

STIC-Biotech/ChemLib

135107

my

From: Marvich, Maria
Sent: Friday, October 15, 2004 8:07 AM
To: STIC-Biotech/ChemLib
Subject: RE:

RECEIVED
OCT 15 2004
STIC/BIOTECH/ChemLib
(STIC)

SEQ ID NO 1 and SEQ ID NO 5.

-----Original Message-----

From: STIC-Biotech/ChemLib
Sent: Friday, October 15, 2004 7:43 AM
To: Marvich, Maria
Subject: RE:

Good morning, now I need the SID NO for 09/911132.
MAUDE

-----Original Message-----

From: Marvich, Maria
Sent: Thursday, October 14, 2004 2:12 PM
To: STIC-Biotech/ChemLib
Subject: RE:

My apologies 09/911132
Yes, this October 5th.

-----Original Message-----

From: STIC-Biotech/ChemLib
Sent: Thursday, October 14, 2004 2:11 PM
To: Marvich, Maria
Subject: RE:

Oh where you talking about Oct of this year? For this 09/011132 the status is it's a NO BIOTECH DATA.
MAUDE

-----Original Message-----

From: Marvich, Maria
Sent: Thursday, October 14, 2004 5:00 AM
To: STIC-Biotech/ChemLib
Subject:

I sent a sequence search request for 09/011132 last October 5 around 2:00. I was wondering what the status of this search was.

Thank you
Maria Bonovich Marvich
United States Patent and Trademark Office
Remsen 2B84

1636 2070

STAFF USE ONLY

Searcher: _____
Searcher Phone: 2- _____
Date Searcher Picked up: 10/8/04
Date Completed: 10/20/04
Searcher Prep/Rev. Time: _____
Online Time: _____

Type of Search

NA Sequence: # _____
AA Sequence: # _____
Structure: # _____
Bibliographic: _____
Litigation: _____
Patent Family: _____
Other: _____

Vendors and cost where applicable

STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: 01
WWW/Internet: _____
Other(Specify): _____

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GenCore version 5.1.6
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OM nucleic - nucleic search, using bw model

Run on: October 20, 2004, 00:09:03 ; Search time 768 Seconds

(without alignments)
10088.731 Million cell updates/sec

Title: US-09-911-132a-1

Perfect score: 1476
Sequence: 1 gcatccctatccagctga.....gcatcccgactaggtacc 1476

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_23sep04:*

1: _geneseqn1980s:*\n2: _geneseqn1980s:*\n3: _geneseqn2000s:*\n4: _geneseqn2001as:*\n5: _geneseqn2001bs:*\n6: _geneseqn2002as:*\n7: _geneseqn2002bs:*\n8: _geneseqn2003as:*\n9: _geneseqn2003bs:*\n10: _geneseqn2003cs:*\n11: _geneseqn2003ds:*\n12: _geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|--------|-------------|--------|-------|-------------|
| 1 | 1476 | 100.0 | 1476 | 6 | AD126549 |
| 2 | 1464 | 99.2 | 1464 | 10 | AD553384 |
| 3 | 1454.2 | 98.5 | 1650 | 8 | AB222773 |
| 4 | 1035.8 | 70.2 | 2523 | 4 | AAKS1495 |
| 5 | 1032.6 | 70.0 | 1587 | 2 | AAQ78135 |
| 6 | 1032.6 | 70.0 | 1587 | 2 | AAT73384 |
| 7 | 1032.6 | 70.0 | 2516 | 12 | ADF45468 |
| 8 | 1032.6 | 70.0 | 2516 | 12 | AD028592 |
| 9 | 1029.8 | 69.8 | 1702 | 12 | ADN43057 |
| 10 | 1021.4 | 69.2 | 1966 | 4 | AAK52479 |
| 11 | 1021.4 | 69.2 | 1491 | 2 | AAQ90640 |
| 12 | 1018.2 | 69.0 | 3076 | 2 | AAT73391 |
| 13 | 1018.2 | 69.0 | 3127 | 2 | AAT73392 |
| 14 | 1008.8 | 68.3 | 2372 | 2 | AAT73393 |
| 15 | 1008.8 | 68.3 | 2484 | 2 | AAT73386 |
| 16 | 1008.8 | 68.3 | 3022 | 2 | AAT73390 |
| 17 | 1008.8 | 68.3 | 3147 | 2 | AAT73389 |
| 18 | 1006.4 | 68.2 | 1464 | 2 | AAQ90639 |
| 19 | 1002.8 | 67.9 | 1597 | 10 | ADH10077 |
| 20 | 1002.8 | 67.9 | 1675 | 10 | ADH10079 |
| 21 | 1002.8 | 67.9 | 1748 | 10 | ADH10087 |

| | | | | | | |
|----|--------|------|------|----|----------|--------------------|
| 22 | 1002.8 | 67.9 | 1777 | 10 | ADH10083 | Adh10083 Human SEA |
| 23 | 1002.8 | 67.9 | 1915 | 10 | ADH10091 | Adh10091 Human SEA |
| 24 | 1002.8 | 67.9 | 1975 | 10 | ADH10095 | Adh10095 Human SEA |
| 25 | 1002.4 | 67.9 | 1904 | 12 | AD080225 | Adg80225 Human gen |
| 26 | 1002.4 | 67.9 | 1918 | 10 | ADH10073 | Adh10073 Human gen |
| 27 | 1002.4 | 67.9 | 7582 | 12 | AD080226 | Adh80226 Human sec |
| 28 | 1002.2 | 67.9 | 1728 | 6 | ABL49916 | Ab149916 SEAP, ins |
| 29 | 1002 | 67.9 | 1779 | 6 | ADH10054 | Adh10054 Human g34 |
| 30 | 1002 | 67.9 | 2051 | 5 | ADH13579 | Adh13579 Rat Mob-5 |
| 31 | 1002 | 67.9 | 2121 | 5 | ADH13580 | Adh13580 Human Mob |
| 32 | 1001.4 | 67.8 | 1634 | 2 | AAV42729 | AAV42729 Human pla |
| 33 | 1001.4 | 67.8 | 1697 | 12 | AD080223 | Adg80223 Human gen |
| 34 | 1001.4 | 67.8 | 7677 | 10 | ACF36695 | ACF36695 Plaemid v |
| 35 | 1000.8 | 67.8 | 1558 | 6 | ABL61146 | Ab161146 SEAP repo |
| 36 | 1000.8 | 67.8 | 1560 | 6 | ABK49457 | Abk49457 Human sec |
| 37 | 1000.8 | 67.8 | 1560 | 9 | ACF36062 | ACF36062 Human sec |
| 38 | 1000.8 | 67.8 | 2029 | 12 | AD080227 | Adg80227 Human gen |
| 39 | 1000.8 | 67.8 | 2645 | 12 | ADM43173 | Adm43173 SEAP exp |
| 40 | 1000.8 | 67.8 | 4260 | 9 | AA162063 | AA162063 PSP-SEAP |
| 41 | 1000.8 | 67.8 | 4260 | 9 | AA160448 | AA160448 PSP-SEAP |
| 42 | 1000.8 | 67.8 | 4260 | 12 | ADP90307 | Adp90307 PSP-SEAP |
| 43 | 1000.8 | 67.8 | 4356 | 12 | ADH97132 | Adh97132 Mammalian |
| 44 | 1000.8 | 67.8 | 4677 | 8 | ACC49134 | Acc49134 Cloning v |
| 45 | 1000.8 | 67.8 | 4846 | 3 | AAA29133 | AAA29133 pNF-Xappa |

ALIGNMENTS

RESULT 1
AD126549
ID AD126549 standard; DNA; 1476 BP.

AC AD126549;

DT 22-APR-2004 (first entry)

DE Bovine b1APII DNA.

KW alkaline phosphatase; resistance gene; zeomycin; G418; heat stability;

KX bovine; b1APII; yeast; gene; ds.

OS Bos taurus.

PN EP1176205-A2.

PD 30-JAN-2002.

PF 21-JUL-2001; 2001EP-00117822.

PR 25-JUL-2000; 2000DE-01036491.

PA (HOFF) ROCHE DIAGNOSTICS GMBH.

PI (HOFF) HOFFMANN LA ROCHE & CO AG F.

PI Mueller R, Thalhofer J, Geipel F, Hoelke W, Glaeser S, Eckstein H;

PI Kirschbaum T, Bonmarquis B;

DR WPI; 2002-173123/23.

PT Preparing eukaryotic alkaline phosphatase, useful as diagnostic reagent

PT and for dephosphorylation, by recombinant expression in yeast selected

PS for high gene copy number.

PS Claim 2; SEQ ID NO 1; 23bp; German.

This invention describes a novel method of preparing eukaryotic alkaline phosphatase in yeast cells, comprising cloning an alkaline phosphatase gene sequence into different vectors, transforming, and expressing and purifying. A first vector is used containing a resistance gene against a selection marker and transformants that have integrated resistance gene and alkaline phosphatase gene into the genome are selected by growth on medium containing a low concentration of selection marker. The gene copy

applicant

CC number is increased by multiple transformation and multiple transformants
CC selected on growth medium under high selection pressure. A second vector
CC containing the alkaline phosphatase gene and a second resistance gene
CC against a second marker is introduced, its copy number increased as for
CC the first resistance gene and clones selected that have many copies of
CC the alkaline phosphatase gene and of both resistance genes, integrated
CC into the genome. The vectors used in the method are pHP10-3 and pHP10-
CC 3/9k. Preferred cells include methylotrophic yeast, particularly *Pichia*
CC *pastoris* and *Hansenula polymorpha* and specifically *P. pastoris* X-33
CC transformed with pHP10-3 and pHP10-3/9k. The amino acid sequence of
CC bovine alkaline phosphatase is known and, working back from this, an
CC optimised codon sequence was designed. This was assembled conventionally
CC from 28 synthetic oligonucleotides to give a sequence having *EcoRI* and
CC *Asp718* recognition sites at the ends to facilitate cloning. The selection
CC markers are particularly zeomycin and G418, respectively. The alkaline
CC phosphatase is used as diagnostic reagent, as part of a conjugate and for
CC dephosphorylation of DNA. This method produces very active, glycosylated
CC alkaline phosphatase with specific activity over 3000, preferably 10000,
CC units/mg and heat stability comparable with that for commercial enzymes.
CC The expression system is resistant and stable and provides high-level
CC expression without any selection pressure. This sequence represents the
CC bovine *bialpi* gene.

XX Sequence 1476 BP; 337 A; 449 C; 441 G; 249 T; 0 U; 0 Other:

Query Match 100.0%; Score 1476; DB 6; Length 1476;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1476; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAATTCCTCATCCAGCTGAGAGGAAACCCCGCTTCTGAGCCGCAAGGAGCCGAG 60
DB 1 GAATTCCTCATCCAGCTGAGAGGAAACCCCGCTTCTGAGCCGCAAGGAGCCGAG 60
QY 61 GCCCTTGATGTAGCCCAAGAGTTGCGCCGATCCAGACGCTGCCAAGATGTCATCTTC 120
DB 61 GCCCTTGATGTAGCCCAAGAGTTGCGCCGATCCAGACGCTGCCAAGATGTCATCTTC 120
QY 121 TTCCTGGGGGATGGATGGGGGTGCTTACGCTGACAGCACTGGATCTTAAAGGGGAG 180
DB 121 TTCCTGGGGGATGGATGGGGGTGCTTACGCTGACAGCACTGGATCTTAAAGGGGAG 180
QY 181 ATGAATGCAAACTGGGACCTTGAGACACCCCTGGCCATGAGACCGTTCATTCGTGCT 240
DB 181 ATGAATGCAAACTGGGACCTTGAGACACCCCTGGCCATGAGACCGTTCATTCGTGCT 240
QY 241 CTGTCCAAACATACACGTGACAGACAGTGGCCAGACAGGCGCAGCACTGCACTGCC 300
DB 241 CTGTCCAAACATACACGTGACAGACAGTGGCCAGACAGGCGCAGCACTGCACTGCC 300
QY 301 TACCTGTGGGGGTCAAGGGCACTACAGAACCATCGTGTAAAGTSCAGCCGCGCTAC 360
DB 301 TACCTGTGGGGGTCAAGGGCACTACAGAACCATCGTGTAAAGTSCAGCCGCGCTAC 360
QY 361 AATCAGTGCACACGACGCTGGGAAATGAGTCACTCTGTATCAACCGGCGCAAGAA 420
DB 361 AATCAGTGCACACGACGCTGGGAAATGAGTCACTCTGTATCAACCGGCGCAAGAA 420
QY 421 GAGAGGAAGCCGTGGAGTGTGACCAACAGAGGTGACAGATGCCCTCCAGCGGG 480
DB 421 GAGAGGAAGCCGTGGAGTGTGACCAACAGAGGTGACAGATGCCCTCCAGCGGG 480
QY 481 GCTACGCGCACACGCTGACACGAAACTGTACTACAGCGGCACTGCTGCTGATGCA 540
DB 481 GCTACGCGCACACGCTGACACGAAACTGTACTACAGCGGCACTGCTGCTGATGCA 540
QY 541 CAGAAAGATGCTGCTGACAGACATCGCGCACAGCTGTCTAACAATGATATTGACGTG 600
DB 541 CAGAAAGATGCTGCTGACAGACATCGCGCACAGCTGTCTAACAATGATATTGACGTG 600
QY 601 ATCCCTGGGTGAGGCGGATGTAATGTTCTCTGAGGGGAGCCCGAGACCTGAATGCCA 660
DB 601 ATCCCTGGGTGAGGCGGATGTAATGTTCTCTGAGGGGAGCCCGAGACCTGAATGCCA 660

QY 661 GATGATGCCAGTGTGAATGAGACTCCGAAAGCAAGACCAAGCTGTGACAGAAATGCGAG 720
DB 661 GATGATGCCAGTGTGAATGAGACTCCGAAAGCAAGACCAAGCTGTGACAGAAATGCGAG 720
QY 721 GCCAAGCACACGAGAGCCCAAGTATGTGGAACCGCACTGCGCTCTTCAGGCGCGAT 780
DB 721 GCCAAGCACACGAGAGCCCAAGTATGTGGAACCGCACTGCGCTCTTCAGGCGCGAT 780
QY 781 GACTCAGTGTAAACACCTCACTGGGCGCTTTGAGCCGCGAGACATGATATATGT 840
DB 781 GACTCAGTGTAAACACCTCACTGGGCGCTTTGAGCCGCGAGACATGATATATGT 840
QY 841 CAGCAAGACCAACCAAGAGACCCGACCTGCGGAGATGACGAGAGCGGCTTCGAAGTG 900
DB 841 CAGCAAGACCAACCAAGAGACCCGACCTGCGGAGATGACGAGAGCGGCTTCGAAGTG 900
QY 901 CTGAGCAGGAACCCCGGGGCTTTTACCTCTTCTGAGAGAGGCGGCTTGAACAACGCT 960
DB 901 CTGAGCAGGAACCCCGGGGCTTTTACCTCTTCTGAGAGAGGCGGCTTGAACAACGCT 960
QY 961 CACCAATGACGGGAAGCTTATATGACGCTGACGCTGAGGGGATGATGTTGACAAATGCCATC 1020
DB 961 CACCAATGACGGGAAGCTTATATGACGCTGACGCTGAGGGGATGATGTTGACAAATGCCATC 1020
QY 1021 GCCAAGGCTTAACGAGCTCACTAGCCGAACTGACACAGCTGATCTTGTCACTGACAGCAC 1080
DB 1021 GCCAAGGCTTAACGAGCTCACTAGCCGAACTGACACAGCTGATCTTGTCACTGACAGCAC 1080
QY 1081 TCCCATGCTTCTCTTTTGTGTGCTACACACTGCTGAGGACCTTCATTTTCGTCTGCGC 1140
DB 1081 TCCCATGCTTCTCTTTTGTGTGCTACACACTGCTGAGGACCTTCATTTTCGTCTGCGC 1140
QY 1141 CCGGCAAGGCTTATGACAGCAAGTCTACACCTGATCTCTATGGAATGGCCAGGC 1200
DB 1141 CCGGCAAGGCTTATGACAGCAAGTCTACACCTGATCTCTATGGAATGGCCAGGC 1200
QY 1201 TATGCGCTTGGCGGGGCTCGAGGCGCGATGTTAATGACAGCAAGGAGAACTCTCA 1260
DB 1201 TATGCGCTTGGCGGGGCTCGAGGCGCGATGTTAATGACAGCAAGGAGAACTCTCA 1260
QY 1261 TACCGGACAGAGCGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1320
DB 1261 TACCGGACAGAGCGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1320
QY 1321 GGTTCGCGGAGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1380
DB 1321 GGTTCGCGGAGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1380
QY 1381 GCGCAGCATATGCTTGTGCGGCTGCTGAGGCGCTTACAGCGACTGCAATCTGCAGCC 1440
DB 1381 GCGCAGCATATGCTTGTGCGGCTGCTGAGGCGCTTACAGCGACTGCAATCTGCAGCC 1440
QY 1441 CCGGCAACCGGCAACGAGCATCCCGGACTAAGGTTACC 1476
DB 1441 CCGGCAACCGGCAACGAGCATCCCGGACTAAGGTTACC 1476
RESULT 2
ADES3384
ID ADES3384 standard; DNA; 1464 BP.
XX
XX ADES3384;
AC
AC 29-JAN-2004 (first entry)
XX
XX Bovine alkaline phosphatase DNA.
DE
DE alkaline phosphatase; mutation; immunoassay; antigen;
XX
XX interference suppressor; bovine; ds; gene.
OS
OS Bos taurus.
XX
XX
FH Key Location/Qualifiers

| | | | | |
|----|--|-----|---------|---|
| FT | CDS | | 1..1464 | /tag=a /product= "alkaline phosphatase" /partial /note= "no start codon given" |
| FT | | | | |
| FT | | | | |
| XX | EPI348760-AZ. | | | |
| PX | | | | |
| PD | 01-OCT-2003. | | | |
| PP | 21-MAR-2003; 2003EP-00006426. | | | |
| PR | 25-MAR-2002; 2002DE-01013201. | | | |
| PA | (HOFF) ROCHE DIAGNOSTICS GMBH. (HOFF) HOFFMANN LA ROCHE & CO AG F. | | | |
| PI | Mueller R, Thalhofer J, Geipel F, Hoeke W, Kirschbaum T; | | | |
| DR | WPI, 2003-769844/73. | | | |
| DR | P-PsDB; ADES3385. | | | |
| PT | New mutants of alkaline phosphatase (AP) where enzymatic activity is reduced a hundred fold, are useful as blocking reagents in AP-based immunoassays. | | | |
| PS | Disclosure; SEQ ID NO 1; 35pp; German. | | | |
| CC | This invention describes a novel mutant of eukaryotic alkaline phosphatase where the wild-type sequence is at least 77% homologous with ADHS3385 and where the alkaline phosphatase activity is reduced by at least 100-fold, relative to the wild type. The mutations described are Asp42, 316 or 357 for Asn, Val, Ala or Ser; Ser92 or 155 for Ala, Gly, Val or Leu; Glu311 for Glu, Asn, Lys, Ile or Met; His320, 358 or 432 for Asn, Phe, Asp or Tyr; or Gly322 for an amino acid larger than Asp. Conjugates of the novel mutant with antibodies are useful in alkaline phosphatase-based immunoassays for antigens as interference suppressors, i.e., they prevent non-specific binding of active alkaline phosphatase based conjugates to vessel walls or first antibodies, a phenomenon that may result in false positive results. The mutants have almost the same tertiary and quaternary structures as wild-type alkaline phosphatase, so are very specific intereference suppressors. This sequence encodes the wild-type bovine alkaline phosphatase described in the disclosure of the invention. | | | |
| SQ | Sequence 1464 BP; 334 A; 446 C; 438 G; 246 T; 0 U; 0 Other; Query Match 99.2%; Score 1464; DB 10; Length 1464; Best Local Similarity 100.0%; Pred. No. 0; Matches 1464; Conservative 0; Mismatches 0; Indels 0; Gaps 0. | | | |
| OY | 7 CTGATCCAGCGTAGAGAATAACCCCCTTCGTGAACGCCGCAGCAGCCCCCTT | 66 | | |
| Db | 1 CTCATTCCAAGTGAGAGAAAAAACCCTTTCTGGAACCGCAAGCACCCAGCCCTT | 60 | | |
| OY | 67 GATGTAGCCAAAGATTGCAGCCCATCCAGACAGCTGCCAAGATGTCACTCTTCTTG | 126 | | |
| Db | 61 GATGTAGCCAAAAGTTGACGCCGANTCCAGACAGCTGCCAABAATGTATCTCTTCTTG | 120 | | |
| OY | 127 GGGAATGGAGTGGGGGTGCTTAACGGTAGACGCCACTCGGATCTTAAAGGGGCAGATGAT | 186 | | |
| Db | 121 GGGGATGGGATGGGGGTGCTTAACGGTAGACGCCACTCGGATCTTAAAGGGGCAGATGAT | 180 | | |
| OY | 187 GGCAAATCGGGACCTGTAGACAACCCCGGCGCATGTGAGCAAGTTCCCATPACGTGGCTGTGCC | 246 | | |
| Db | 181 GGCAAATCTGGGACCTGTAGACAACCCCGGCGCATGTGAGCAAGTTCCCATPACGTGGCTGTGCC | 240 | | |
| OY | 247 AAACATACAAAGTGTGACAGACAGGTGCCAGACAGCGACGACACTGSCACTGTCACTCG | 306 | | |
| Db | 241 AAACATACAAAGTGTGACAGACAGGTGCCAGACAGCGACGACACTGSCACTGTCACTCG | 300 | | |
| OY | 307 TTGTGGGTCAAGGGCACTTACGAACCATCGGTGTAAGTGCAGCCGCCCGCTTACATCAG | 366 | | |

| | | | |
|----|------|--|------|
| Db | 301 | 1GTGGGGTCAAGGGCACTACAGAACCATCGGTGTAAGTGAGAGCCCGGCTCAACATCAG | 360 |
| QY | 367 | TGCAACACGACACGTGAGAAATGAGTGCACGTCTGTGATCAACGGGGCCAGAAAGCAGGG | 426 |
| Db | 361 | TGCAACACGACACGTGAGAAATGAGTGCACGTCTGTGATCAACGGGGCCAGAAAGCAGGG | 420 |
| QY | 427 | AAGGCCGTGGAGAGTGTGACCAACCAAGGGGTGAGCATCGTCCCAAGCCGGGGCCCTAC | 486 |
| Db | 421 | AAGGCCGTGGAGAGTGTGACCAACCAAGGGGTGAGCATCGTCCCAAGCCGGGGCCCTAC | 480 |
| QY | 487 | GCGCACACGCTGAACCCGAACTGGTACTCAGACGCCAGCTGCCTGCTGTATGCAAGAG | 546 |
| Db | 481 | GCGCACACGCTGAACCCGAACTGGTACTCAGACGCCAGCTGCCTGCTGTATGCAAGAG | 540 |
| QY | 547 | AATGGCTGCCAGACATCGCCGCAACAGCTGGTCTTACAACATGATATTTGACGTGATCTTG | 606 |
| Db | 541 | AATGGCTGCCAGACATCGCCGCAACAGCTGGTCTTACAACATGATATTTGACGTGATCTTG | 600 |
| QY | 607 | GGTGGAGGGCCGAAATGTACATGTTTTCTGTAGAGGGACCCCAACCTGTGAATCCAGATGAT | 666 |
| Db | 601 | GGTGGAGGGCCGAAATGTACATGTTTTCTGTAGAGGGACCCCAACCTGTGAATCCAGATGAT | 660 |
| QY | 667 | GCCAGTGTGAATGAGATCCGGAAGAGCAACAGAACTGTGTGCAAGATGAGCAGGCCAAG | 726 |
| Db | 661 | GCCAGTGTGAATGAGATCCGGAAGAGCAACAGAACTGTGTGCAAGATGAGCAGGCCAAG | 720 |
| QY | 727 | CACCAAGGAGGCCAGTATGTGTGGAACCGACCTGCGTCTTCAAGCGGCCGATGATCTCC | 786 |
| Db | 721 | CACCAAGGAGGCCAGTATGTGTGGAACCGACCTGCGTCTTCAAGCGGCCGATGATCTCC | 780 |
| QY | 787 | AGTGTAAACACCTCTCATGTGGGCTCTTTTGAAGCCGGCAGACATGAAAGTATTAATGTTACAGAA | 846 |
| Db | 781 | AGTGTAAACACCTCTCATGTGGGCTCTTTTGAAGCCGGCAGACATGAAAGTATTAATGTTACAGAA | 840 |
| QY | 847 | GACCAACACMAAGAACCCGACCCCTGGCGGAGATGACGGAAGCGGCCCTGCAAGTGTCTAGC | 906 |
| Db | 841 | GACCAACACMAAGAACCCGACCCCTGGCGGAGATGACGGAAGCGGCCCTGCAAGTGTCTAGC | 900 |
| QY | 907 | AGGAACCCCGCGGGGCTTCTACCTTTCGTGAGAGGAGGCCGATTTGAACAACGCTACACAT | 966 |
| Db | 901 | AGGAACCCCGCGGGGCTTCTACCTTTCGTGAGAGGAGGCCGATTTGAACAACGCTACACAT | 960 |
| QY | 967 | GACGGCAAAAGCTTATATGTGCACTGACGTGAGGCATCATGTTTGACAATGCGCATGTGCCAAG | 1026 |
| Db | 961 | GACGGCAAAAGCTTATATGTGCACTGACGTGAGGCATCATGTTTGACAATGCGCATGTGCCAAG | 1020 |
| QY | 1027 | GCTAAACGAGCTCATCTAGGGAACGTGGAACCGTGATCTCTGTGCATGTGAGACCACTCCCAT | 1086 |
| Db | 1021 | GCTAAACGAGCTCATCTAGGGAACGTGGAACCGTGATCTCTGTGCATGTGAGACCACTCCCAT | 1080 |
| QY | 1087 | GTCCTTCTCTTTTGGTGGCTACACACTGCGTGGAGCTTCATTTTCGGTCTGGGCCCGGCG | 1146 |
| Db | 1081 | GTCCTTCTCTTTTGGTGGCTACACACTGCGTGGAGCTTCATTTTCGGTCTGGGCCCGGCG | 1140 |
| QY | 1147 | AAGGCTTTAAGCAGCAAGTCTTACACTCCATCTCTTATGSCAATGGCCCAAGGCTATGCG | 1206 |
| Db | 1141 | AAGGCTTTAAGCAGCAAGTCTTACACTCCATCTCTTATGSCAATGGCCCAAGGCTATGCG | 1200 |
| QY | 1207 | CTTGGCGGGGGCTGGAAGCCCGAATTTAATGTGACGACCAAGCGAGAAACCTCTATACCGG | 1266 |
| Db | 1201 | CTTGGCGGGGGCTGGAAGCCCGAATTTAATGTGACGACCAAGCGAGAAACCTCTATACCGG | 1260 |
| QY | 1267 | CAGCAGGCGAGCCGTGCGCCCTGTGCTAAGCGAGACCCACCGGGGGCGAAGACGTGGCGGTTC | 1326 |
| Db | 1261 | CAGCAGGCGAGCCGTGCGCCCTGTGCTAAGCGAGACCCACCGGGGGCGAAGACGTGGCGGTTC | 1320 |
| QY | 1327 | GCGCAGAGGCCCGCAGGCGCACTTGTGTCAAGGCGTGCAGAGAGACCTTGTGTGGCGAC | 1386 |
| Db | 1321 | GCGCAGAGGCCCGCAGGCGCACTTGTGTCAAGGCGTGCAGAGAGACCTTGTGTGGCGAC | 1380 |
| QY | 1387 | ATCATATGCGCTTTGGGGGCTGTGTGGAACCCGTACACCGAATGTGCAATCTGCAAGCCCGGCG | 1446 |
| Db | 1381 | ATCATATGCGCTTTGGGGGCTGTGTGGAACCCGTACACCGAATGTGCAATCTGCAAGCCCGGCG | 1440 |

DB 1419 CAGGCGGCGTGCCTCCCTGCTAGCAGAGACCCAGGGGGCGAAGCGTGGGTTCGCG 1478
QY 1330 CGAGGCGCCGAGGCGCAGCTGTGTGCAAGGGGTGCAAGAGACCTTCGTGGGCGACATC 1389
DB 1479 CGAGGCGCCGAGGCGCAGCTGTGTGCAAGGGGTGCAAGAGACCTTCGTGGGCGACATC 1538
QY 1390 ATGAGCCTTTGCGGGGCTGCGTGAAGCCCTACACGACTGCAATCTGCCAGGCCCGCCAGC 1449
DB 1539 ATGAGCCTTTGCGGGGCTGCGTGAAGCCCTACACGACTGCAATCTGCCAGGCCCGCCAGC 1598
QY 1450 GCCACGACGATCCCGCACT 1468
DB 1599 GCCACGACGATCCCGCACT 1617
RESULT 4
AAK51495
ID AAK51495 standard; cDNA; 2523 BP.
XX
AC AAK51495:
XX
DT 06-NOV-2001 (first entry)
XX
DE Human polynucleotide SEQ ID NO 40.
XX
KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW tissue growth factor; immunomodulatory; cancer; leukemia;
KW nervous system disorder; arthritis; inflammation; ss.
XX
OS Homo sapiens.
XX
PN WO200157190-A2.
XX
PD 09-AUG-2001.
XX
PF 05-FEB-2001; 2001MO-US004098.
XX
PR 03-FEB-2000; 2000US-00496914.
XX
PR 27-APR-2000; 2000US-00560875.
XX
PR 20-JUN-2000; 2000US-00598075.
XX
PR 19-JUL-2000; 2000US-00620325.
XX
PR 01-SEP-2000; 2000US-00654936.
XX
PR 15-SEP-2000; 2000US-00663561.
XX
PR 20-OCT-2000; 2000US-00693325.
XX
PR 30-NOV-2000; 2000US-00728422.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y;
PI Ma Y, Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;
PI Xue AJ, Yang Y, Wejhtman T, Goodrich R;
XX
DR WPI: 2001-476283/51.
XX
DR P-PSDB; AAM78362.
XX
PT Nucleic acids encoding polypeptides with cytokine-like activities, useful
PT in diagnosis and gene therapy.
XX
PS Claim 1; Page 603-606; 6221p; English.
XX
XX The invention relates to polynucleotides (AAK51456-AAK53435) and the
XX encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to
XX cytokine, cell proliferation or cell differentiation or which may induce
XX production of other cytokines in other cell populations. The
XX polynucleotides and polypeptides are useful in gene therapy, vaccines or
XX peptide therapy. The polypeptides have various cytokine-like activities,
XX e.g. stem cell growth factor activity, haematopoiesis regulating
XX activity, tissue growth factor activity, immunomodulatory activity and
XX activity/inhibin activity and may be useful in the diagnosis and/or
XX treatment of cancer, leukemia, nervous system disorders, arthritis and
XX inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111

CC (AAK52582) and 3666 (AAM8020) are omitted as the relevant pages from the
XX sequence listing were missing at the time of publication
XX
SQ Sequence 2523 BP; 521 A; 856 C; 713 G; 433 T; 0 U; 0 Other;
Query Match 70.2%; Score 1035.8; DB 4; Length 2523;
Best Local Similarity 81.5%; Pred. No. 8, 6e-242;
Matches 1199; Conservative 0; Mismatches 272; Indels 0; Gaps 0;
QY 6 CCTCATCCGAGCTGAGAGAAAACCCCGCTTCTGGAACCGGACGAGCCAGGCCCT 65
DB 107 GGTATCCGAGCTGAGAGAAAACCGGCTTCTGGAACCGGACGAGCTGAGGCCCT 166
QY 66 TGATGTAGCCAAAGAAAGTTGCGCCGATTCAGACAGCTGCGCAAGAAATGTCATCTTCTT 125
DB 167 GGTATGCTGCCAAGAAAGCTGAGCCCTTCAGAAAGTTCGCCAAGAACTATCTTCTTCT 226
QY 126 GGGGATGAGATGAGGAGTGCCTTACGCTGACAGCCACTCGGATCTTAAAGGAGAGATGA 185
DB 227 GGGGATGAGGATGAGGAGTGCCTTACGCTGACAGCCACTCGGATCTTAAAGGAGAGAA 286
QY 186 TGCCAAACTGAGACCTGAGACACCCCTGGCCATGACACAGTTCCCATAGCTGCTGTC 245
DB 287 TGCCAAACTGAGGAGCTGAGACACCCCTGGCCATGACACCGCTTCCATACCTGCTGTC 346
QY 246 CAAGACATCAAGCTGAGACAGAGGTCAGACAGGTCAGACAGGTCAGACAGGTCAGACAG 305
DB 347 CAAGACATCAAGCTGAGACAGAGGTCAGACAGGTCAGACAGGTCAGACAGGTCAGACAG 406
QY 306 GTGTGGGCTCAAGGGCACTACAGAACATCGGTGTAGTGACAGCCGCGCTTAAATCA 365
DB 407 GTGTGGGCTCAAGGGCACTACAGAACATCGGTGTAGTGACAGCCGCGCTTAAATCA 466
QY 366 GTGTGAACAGACAGCTGAGACAGGTCAGACAGGTCAGACAGGTCAGACAGGTCAGACAG 425
DB 467 GTGTGAACAGACAGCTGAGACAGGTCAGACAGGTCAGACAGGTCAGACAGGTCAGACAG 526
QY 426 GAAGGCGGTGGAGGTGTGTCACACAGAGGTCAGACAGGTCAGACAGGTCAGACAGGTC 485
DB 527 GAAGGCGGTGGAGGTGTGTCACACAGAGGTCAGACAGGTCAGACAGGTCAGACAGGTC 586
QY 486 CGGCAACAGGTGAACCGAAATCTGTACTCAGAGCCGACCTGCTGTAGTACAGAA 545
DB 587 CGGCAACAGGTGAACCGAAATCTGTACTCAGAGCTGTACTCAGAGCTGTACTCAGAGCT 646
QY 546 GAATGCTGTGACAGACATGCGCCACAGCTGTGTCTCAACATGAGATATGACCTGATCT 605
DB 647 GAGGGGTGTGACAGACATGCGCCACAGCTGTGTCTCAACATGAGATATGACCTGATCT 706
QY 606 GGTGTGAGGCGCAATGTATCATGTTTCTGAGGGGGACCCAGACCTGTGAATACCAATGA 665
DB 707 TGCGGAGGCGCGAAGTATCATGTTTCTGAGGGGGACCCAGACCTGTGAATATCAAGTGA 766
QY 666 TGCCAGTGTGAATGATGATCGGAGAGCAAGCAAGCACTGTGTGAGAAATGAGAGGCCAA 725
DB 767 TGCCAGTGTGAATGATGATCGGAGAGCAAGCAAGCACTGTGTGAGAAATGAGAGGCCAA 826
QY 726 GCACCAAGGAGCCAGATGTGTGAACCGCACTGCGCTCTTCAAGGCGGCGATGATCT 785
DB 827 GCACCAAGGAGCCAGATGTGTGAACCGCACTGCGCTCTTCAAGGCGGCGATGATCT 886
QY 786 CAGTGTGAACACACTGATGAGGCTCTTGAAGCGGAGCATGAATATATGTTACGA 845
DB 887 GTGTGTGAGCCATCTATGAGGCTCTTGAAGCGGAGCATGAATATATGTTACGA 946
QY 846 AGACCAACCAAGAGACCCGACCTGCGGAGATGACGAGGCGGCTGTCAAGTGTCTAG 905
DB 947 AGACCAACCAAGAGACCCGACCTGCGGAGATGACGAGGCGGCTGTCTGCTGTAG 1006
QY 906 CAGAAACCCCGGGGCTTCTTACTTCTTGTGAGGAGGCGGATGACAGCTGATCA 965
DB 1007 CAGAAACCCCGGGGCTTCTTACTTCTTGTGAGGAGGCGGATGACAGCTGATCA 1066

QY 906 CAGGAACCCCGGGGCTTCTACCTCTTGTGAGAGGAGCGGATTGACCAAGTCA 965
 DB 957 CAGGAACCCCGGGGCTTCTACCTCTTGTGAGAGGAGCGGATTGACCAAGTCA 1016
 QY 966 TGAAGGCAAGCTTATATAGCACTGAGGCGATCATTTGACAAATCCATCCGCA 1025
 DB 1017 TGAAGGCTGTGCTTACAGGAGCTGAGGCGGATGTTGACAGCAATGAGAG 1076
 QY 1026 GGTAAACAGCTCACTAGGCACTGAGCAAGCTGATCTTGTCACTGCAACCACTTCCA 1085
 DB 1077 GGGGGGCACTCAACAGCAGAGAGGACAGCTGACCTCTGTCAACGCTGACCACTCCA 1136
 QY 1086 TGTCTTCTCTTTTGTGAGTACACACTGCGTGGAGACTTCATTTTGGCTGGCCCCCG 1145
 DB 1137 TGTCTTCTCTTTTGTGAGTACACACTGCGGAGAGTCTTCATCTTGGGTTGGCCCCAG 1196
 QY 1146 CAAAGCTTATAGACAGCAAGTCTACACCTTCATCTTATGCAATGGCCCAAGCTATG 1205
 DB 1197 CAAAGCTCAAGGACAGCAAGCAAGCTTACAGTCCATCTGTGACCAATGGCCCGGCTA 1256
 QY 1206 GCTTGGCGGGGCTTCCAGGCGCCATGTTATGAGCAACAAGGAGAACCTTCATACCG 1265
 DB 1257 GTTCAACTAGGCGGTGACAGACGTGAATGAGAGGAGCGGGAGCCCGATTTACCA 1316
 QY 1266 GCAGCAGGCGGCGGTGCGCTGAGTACAGACCCAGGGGAGAGAGTGGCGGCTT 1325
 DB 1317 GCAGCAGGCGGCGGTGCGCTGAGTACAGACCCAGGGGAGAGAGTGGCGGCTT 1376
 QY 1326 CGCGCAGAGGCGCGGAGCGACCTGTGTGACAGCGGTGACAGAGAGACCTTGTGGCG 1385
 DB 1377 TGGCGCGGCGCGGAGCGACCTGTGTGACAGCGGTGACAGAGAGAGCTTGTGGCG 1436
 QY 1386 CATCATGAGCTTTTGGGCGCTGCGTGTGAGGCTTACACGCACTGCAATTTGCCAGCC 1445
 DB 1437 TGTCAATGAGCTTTGCGTGTGAGGCTTACACGCGCTGCGAGCTTGTGGCG 1496
 QY 1446 CAGCGCAGCAGGATCCCGGACTAGAGGTAC 1476
 DB 1497 CTGCAACCAAGCAGCGCGGCAACCAAGTTGCC 1527

RESULT 6
 AAT27384
 ID AAT27384 standard; DNA; 1587 BP.
 XX
 AC AAT27384;
 XX
 DT 20-SEP-1996 (first entry)
 XX
 DE Human alkaline phosphatase coding sequence.
 XX
 KW alkaline phosphatase; label; antibody; IgG; fusion protein; chimera;
 KM immunoassay; de.
 XX
 OS Homo sapiens.
 XX
 PH Key
 FT CDS 1.1587
 FT /cag= a
 FT /product= "Alkaline phosphatase"
 XX
 JF08070875-A.
 XX
 PD 19-MAR-1996.
 XX
 PF 05-SEP-1994; 94JP-00211035.
 XX
 PR 05-SEP-1994; 94JP-00211035.
 XX
 PA (TOYU) TOSOH CORP.
 XX
 DR WPI; 1996-203155/21.

DR P-PSDB; AAR91805.
 XX Recombinant alkaline phosphatase (AP)-antibody fusion protein - comprises
 PT AP fused downstream of antibody heavy or light chain, useful as
 PT immunoassay reagent.
 XX
 PS Example 1; Page 10-12; 44p; Japanese.
 XX
 CC The gene coding for human alkaline phosphatase is fused downstream of a
 CC gene coding for either the variable and CH1 regions of an antibody heavy
 CC chain or an antibody light chain. Coexpression of the H- and L-chain
 CC sequences, one of which is fused to the AP gene, results in production of
 CC AP-labeled antibodies suitable for use in immunoassays. The present
 CC sequence codes for human AP
 XX
 SQ Sequence 1587 BP; 317 A; 515 C; 490 G; 265 T; 0 U; 0 Other:
 Query Match 70.0%; Score 1032.6; DB 2; Length 1587;
 Best Local Similarity 81.4%; Pred. No. 4,5e-241;
 Matches 1197; Conservative 0; Mismatches 274; Indels 0; Gaps 0;
 QY 6 CCTCATCCCAAGTGAAGAGAAACCCGCTTCTGGAACCCGCAAGCCCAAGGCGCT 65
 DB 57 CGTATCCCAAGTGAAGAGAAACCCGCTTCTGGAACCCGCAAGCCCAAGGCGCT 116
 QY 66 TGATGTAGCAAGAAATTCAGCCGATCCAGACAGCTGCGCAAGATGTCATCTTCTT 125
 DB 117 GATGTGCGCAAGAAATTCAGCCGATCCAGAAAGTGTGCGCAAGAACTATCTTCT 176
 QY 126 GGGGAGTGGGATGGGGGTGCTTACGGTGAACGCACTCGGATCTTAAAGGGGAGATGA 185
 DB 177 GGGGAGTGGGATGGGGGTGCTTACGGTGAACGCACTCGGATCTTAAAGGGGAGATGA 236
 QY 186 TGGCAAACTGGGACTTGAACACCCCTGGCCATGAGACAGTTCCATAGCTGCTGTG 245
 DB 237 TGGCAAACTGGGACTTGAACACCCCTGGCCATGAGACAGTTCCATAGCTGCTGTG 296
 QY 246 CAAAGATCAAAAGTGGAGCAGAGTGCAGACAGGAGGAGGACTGCTCACTCACT 305
 DB 297 CAAAGATCAAAAGTGGAGCAGAGTGCAGACAGGAGGAGGACTGCTCACTCACT 356
 QY 306 GTGTGGGGTCAAGGGCACTTACAGAACATCGGTGTAGTGACGCGCCGCTTAACTCA 365
 DB 357 GTGTGGGGTCAAGGGCACTTACAGAACATCGGTGTAGTGACGCGCCGCTTAACTCA 416
 QY 366 GTGCAACAGCAGCAGTGGGAAATGAGTCACTGTGTGATCAACCGGGCCAAAGAACAG 425
 DB 417 GTGCAACAGCAGCAGTGGGAAATGAGTCACTGTGTGATCAACCGGGCCAAAGAACAG 476
 QY 426 GAAGGCGTGGGAGTGTGACACACAGGAGTGCAGCATGCTCCCAAGCCGAGGCTTA 485
 DB 477 AAGGTCAATGAGTGTGTGACACACAGGAGTGCAGCATGCTCCCAAGCCGAGGCTTA 536
 QY 486 CGCGCAGCAGGTGAACCGAAACTGTACTGACAGCGCGCATCTGCTGATGACAGAA 545
 DB 537 CGCACACAGTGAACCGGAACGTGATCAATGCTGATGCTGCTGCTGCTGCTGCTGCT 596
 QY 546 GAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 605
 DB 597 GAGGGGGTGCAGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 656
 QY 606 GGGTGAAGGCGGAATGACATGTTTCTGAGGGGAGCCCGAGACCTGGAATACCAAGTA 665
 DB 657 TGGCGGAGGCGGAATGACATGTTTCTGAGGGGAGCCCGAGACCTGGAATACCAAGTA 716
 QY 666 TGGCAGTGTGATGATGATCGGAAGGACAAAGCTGTGTGAGGAATGAGAGGCA 725
 DB 717 TGGCAGCAGGAATGATGATGATCGGAAGGAACTGTGTGAGGAATGAGAGGCA 776
 QY 726 GCACCAAGGAGCCCAAGTGTGTGAAACGCACTGCGCTCTTCAAGCGGCGCATGACT 785
 DB 777 GCACCAAGGAGCCCAAGTGTGTGAAACGCACTGAGCTCATAGCGGCGCTTGAACA 836

QY 786 CAGTGAACACACCTCATGGGCTCTTTGAGCCGGCAGACATGATATATGTCAGCA 845
 DB 837 GTCGTGACCACTCTATGGGCTCTTTGAGCCGGCAGACATGATATGATCTCCG 896
 QY 846 AAGACCAACCAAGAGACCCGACCTTGCGGAGATGACGAGGCGCCCTCGAATGCTGAG 905
 DB 897 AAGACCCACATGAGACCCCTCCCTGATGAGATGACAGAGGCTGCCCTGCTGTGAG 956
 QY 906 CAGGAACCCCGGGGCTTACTCTCTTCTGAGGAGGAGCCGATGACACGCTGACCA 965
 DB 957 CAGGAACCCCGGGGCTTACTCTCTTGTGAGGAGGAGCCGATGACCATGCTATCA 1016
 QY 966 TCACGGCAAGCTTATATGSCACTGACTAGGCGATCATGTTGACATGSCATCGCA 1025
 DB 1017 TCAGGGGTGAGGCTTACAGGCAAGTCACTAGGCGGTCATGTTGAGAGGCCATTAGAG 1076
 QY 1026 GGTAAAGAGCTCTAGAGGAACTGAGACAGCTGATCTTGTCACTGACAGACCTCCA 1085
 DB 1077 GCGGGCCAGCTCACACGAGGAGGACAGCTGACCTCTGTCACCGCTGACCACTCCA 1136
 QY 1086 TGTCTTCTCTTTTGTGAGGCTACACATGSGTGGGACCTCATTTTGGTCTGCCCCCG 1145
 DB 1137 TGTCTTCTCTTTGAGGCTACCTTTCGAGGAGAGCTCATCTTGGGTTGCCCCAG 1196
 QY 1146 CAGGCTTACAGACAGCACTCTACACTCTCTATGSCAATGSCCAGGCTATGC 1205
 DB 1197 CAGGCTTACAGACAGCACTCTACACTCTCTATGSCAATGSCCAGGCTATGC 1256
 QY 1206 GCTTGGCGGGGCTCGAGGCGCGATTTAATGCGACACAGGAGGAACTCTATACCG 1265
 DB 1257 GTTCAACTCAGGCGTGCAGACAGCTGATGAGAGCGAGGAGGAGCCCGATTACCA 1316
 QY 1266 GCAGCAGGCGGCGGTCGCTGCTAGAGAGCCGAGGAGGAGGAGAGGAGGCTGCT 1325
 DB 1317 GCAGCAGGCGGCGGTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1376
 QY 1326 CCGCGAGGCGCGCAGGCGCAGCTGTGTGACGCGCTGTGACGAGAGACCTTGTGCGCA 1385
 DB 1377 TCGCGGCGGCGCGCAGGCGCAGCTGTGTGATGTGTGAGAGAGCTTGTGTGCGCA 1436
 QY 1386 CATCATGAGCTTGTGCGGCTGTGCTGTGAGAGCTCTACACGACTGCAATCTGCCAGCCCGC 1445
 DB 1437 TGTCTATGAGCTTGTGCTGTGCTGTGAGAGCTCTACACGAGCTGTGAGCTGTGCC 1496
 QY 1446 CACGCGCACAGCATCCCGCACTAGGGTACC 1476
 DB 1497 CTGCAACACGACGCGCGCACCCAGTGC 1527
 RESULT 7
 ADF45468
 ID ADF45468 standard; DNA; 2516 BP.
 XX
 AC ADF45468;
 XX
 DT 12-FEB-2004 (fixed entry)
 XX
 DE Human vasodilator-responsive gene #65.
 XX
 KM Vasodilating substance; vasodilation response gene; vasodepressor;
 KM antihypertensive drug; vasodilation-responsive gene; hypotensive;
 KM vasodilator; human; gene; db.
 XX
 OS Homo sapiens.
 XX
 PN JP200310272-A.
 PD 05-NOV-2003.
 XX
 PF 26-APR-2002; 2002JP-00126514.
 XX
 PR 26-APR-2002; 2002JP-00126514.
 XX

PA (TANAKA) TANAKA T.
 PA (ASAH) ASAH KASEI KK.
 PA (SUMU) SUMITOMO SEIYAKU KK.
 XX
 DR WPI; 2004-015357/02.
 XX
 PT Obtaining vasodilating substance by contracting test substance with
 PT vascular smooth muscle cell, comparing change in gene expression and
 PT selecting vasodilator which increases expression of vasodilation response
 PT genes.
 XX
 PS Claim 6; SEQ ID NO 65; 98bp; Japanese.
 CC The present invention relates to a method for obtaining a vasodilating
 CC substance which increases expression of vasodilation response genes, and
 CC obtaining a vasodepressor which increases or decreases the expression
 CC level of vasodilation response genes. The method is useful for obtaining
 CC vasodilating substance which increases/decreases expression of
 CC vasodilation response genes. The vasodepressor substance obtained by the
 CC method of the invention is useful as an antihypertensive drug. The method
 CC is also useful for identifying the specific vasodilator response genes.
 CC The present sequence represents a human vasodilator-responsive gene.
 XX
 SQ Sequence 2516 BP; 517 A; 853 C; 712 G; 434 T; 0 U; 0 Other;
 Query Match 70.0%; Score 1032.6; DB 12; Length 2516;
 Best Local Similarity 81.4%; Pred. No. 5.2e-241; Mismatches 274; Indels 0; Gaps 0;
 Matches 1197; Conservative 0;

QY 6 CCTATCCAGCTGAGAGGAAACCCCGCTTCTGAAACCGCCAGGAGCCAGGCCCT 65
 DB 102 CGTCATCCAGCTGAGAGGAAACCCCGCTTCTGAAACCGCCAGGAGCCAGGCCCT 161
 QY 66 TGATGAGCCAAAGATTGACGCCGATCCAGACAGCTCCAAAGATGTCATCTTCTT 125
 DB 162 GATGCTCCCAAGAGCTGACGCCCATCAAGAGTCCCAAGAACTCTATCTTCTTCT 221
 QY 126 GGGGATGAGATGGGGGTGCTTACGCTGACAGCCACTCGATCTCTAAAGGGGAGATGA 185
 DB 222 GGGGATGAGATGGGGGTGCTTACGCTGACAGCCACTCGATCTCTAAAGGGGAGATGA 281
 QY 186 TGGCAACTGGGACCTGAGACACCCCTGGCCATGAGACCACTTCCATAGTGTCTGTC 245
 DB 282 TGGCAACTGGGACCTGAGACACCCCTGGCCATGAGACCACTTCCATAGTGTCTGTC 341
 QY 246 CAAGCATACAACTGTGACAGACAGGTGCCAGACAGCCGACCACTGCTTACTT 305
 DB 342 CAAGCATACAACTGTGACAGACAGGTGCCAGACAGCCGACCACTGCTTACTT 401
 QY 306 GTGTGGGCTCAAGGCACTACAGAACCATGCTGTATGTCAGAGCGCCGCTCAATCA 365
 DB 402 GTGTGGGCTCAAGGCACTTCCAGACCATGCTGTATGTCAGAGCGCCGCTTMAACA 461
 QY 366 GTGCAACAGACAGTGGAAATGAGTCACTCTGTGTCAACCGGGCCAAAGACAGG 425
 DB 462 GTGCAACAGACAGTGGAAATGAGTCACTCTGTGTCAACCGGGCCAAAGACAGG 521
 QY 426 GAAAGCGGTGAGAGTGTGACCAACCAAGGTGCAAGATGCTTCCAGCGGGGCTTA 485
 DB 522 AAGGTCAATGAGAGTGTGACCAACCAAGGTGCAAGATGCTTCCAGCGGGGCTTA 581
 QY 486 CCGCAGACAGGTGAAACGAAACTGTACTACAGAGCGCCAGCTGTGTCAGACAGAA 545
 DB 582 CCGCAGACAGGTGAAACGCAACTGTACTACAGAGCTGATCAATGTGCTGCTAGCCGCA 641
 QY 546 GAATGCTGCCAGAGCATGCGCGCAACAGCTGTCTTCAACATGAGATATGAGTATCT 605
 DB 642 GAAAGGCTGCCAGAGCATGCGCGCACTGATCTTCAACATGAGATATGAGTATCT 701
 QY 606 GGTGTGAGCGGATGTATGATTTCTGAGGGGAGCCCAAGACCTGAAATCCAGAGTGA 665
 DB 702 TGGCGGAGCGCAAGTATGATTTCTCATGGGAGCCCAAGACCTGATGATCCAGAGTGA 761

| | | | |
|----|------|---|------|
| QY | 666 | TGGCAGTGTGAATGGAGTCCGGAAGACAGACAGAACTGGTGCAGAAATGGCAGGCCAA | 725 |
| Db | 762 | TGCCACCGCAGATGGAAATACAGGCTGGAGCGGAAGAACTGGTGCAAGGATGCTGGCAAA | 821 |
| QY | 726 | GCACCGAGGAGCCGAGTATGTGTGGAAACCGACCTGCGCTCCCTTCAGGCGGCGATGATCTC | 785 |
| Db | 822 | GCACCAAGGAGTGCCTGTATATGTGGAAACCGACCTGAGCTCATATGCAAGCGGCTCCGTGACCA | 881 |
| QY | 766 | CAGTTAAACACACTCTATGGGCTCTTTTGAGCCGGCAGACATGAAGTATAATGTTCAACA | 845 |
| Db | 882 | GTTGTGTGACCATCTCATGGGGCTCTTTTGAGCCCGGAACACGAATATATGAATCTTCCG | 941 |
| QY | 846 | AGACCACACAAAGAACCCGACCTTGCGGAGATGACGGAAGCGGCGCTTCGAAGTGTGAG | 905 |
| Db | 942 | AGACCCCACTAGAACCCCTCCCTGATGAGATGACAGAGGCTGCTCCCTGCGCTGTGAG | 1001 |
| QY | 906 | CAGAACCCCGGAGGCTTCTACTCTTTCGTGGAGGAAGCGGCATTTGACACGGTCAACA | 965 |
| Db | 1002 | CAGGAACCCCGCGGCTTCTACTCTTTCGTGGAGGCGGCGCATTCAGCAATGGTCAACA | 1061 |
| QY | 966 | TGACGGCAAACTTATATGCACTGACTGAGAGGCATCATGTTTGACATGGCATATCGCCA | 1025 |
| Db | 1062 | TGAGGGTGTGGCTTACAGGACGTCACAGAGCGGTCAATGTTGACACGCGCATTTGAGAG | 1121 |
| QY | 1026 | GAGTTAACAGCTCACTTAACGAACTGGAACGCGTGAATCTTGTCACTGACAGACACTCCCA | 1085 |
| Db | 1122 | GCGGGGCAAGCTCACACAGCAGAGAGAACCTGTAACCTTCGTACCGCTGACACTCCCA | 1181 |
| QY | 1086 | TGTCCTCTCTTTTGTGGTACACACTGCTGTGGAGCTTCATTTTCGTTGCTGGCCCCGG | 1145 |
| Db | 1182 | TGTCCTCTCTTTTGTGGTACACACTGCTGTGGAGCTTCATTTTCGAGTTGGCCCCAG | 1241 |
| QY | 1146 | CAAGGCTTTAGACAGCAAGTCTTACCTTCACTCTTATATGGCAATGGCCAGGCTATGC | 1205 |
| Db | 1242 | CAAGGCTCAGACACAGCAAGTCTTACCTTCACTCTTATATGGCAATGGCCAGGCTATGC | 1301 |
| QY | 1206 | GCTTGGCGGGGCTCGAAGCCCGATGTTAATGGCAGCACAAGCGAGAACCTCATACG | 1265 |
| Db | 1302 | GTTCAACTCAAGCGGTGGACACAGAGTGAATGAGAGCGAGAGGCCGACCTCATACCA | 1361 |
| QY | 1266 | GCAGCAGCGGCGCTGTCCCTCTGTGCTATGCGAAGACCAAGGGGCGAAGACGTGGCGGTGTT | 1325 |
| Db | 1362 | GCAGCAGCGGCGGCTGTCCCTCTGTGCTATGCGAAGACCAAGGGGCGAAGACGTGGCGGTGTT | 1421 |
| QY | 1326 | CGCGGAAGGCGCGAGGGCGACCTGTGTCAAGGCGGTGACGAGAGGAGACCTTCGTGGCGCA | 1385 |
| Db | 1422 | TGCGGCGGCGCGCGAGGGCGACCTGTGTCAATGTGTGAGAGACAGACCTTCGTAGCGCA | 1481 |
| QY | 1386 | CATCATGGCTTTTGTGGGCTGCGTGGAGCCCTTACACCGACTGCATCTGCACGCCCCCGC | 1445 |
| Db | 1482 | TGTATATGCTTTGCTGTGCTGTGTGAGACCCCTTACACGCGCTGTGCGACTGTGGGCTCCCGC | 1541 |
| QY | 1446 | CACCGCCACACAGATCCCGCACTAGGGTACC | 1476 |
| Db | 1542 | CTGCACCAACGACCGCGGCAACCCAGTTGCC | 1572 |

| |
|--|
| RESULT 8 |
| ADO28592 |
| ID ADO28592 standard; cDNA; 2516 BP. |
| XX |
| AC ADO28592; |
| XX |
| DT 12-AUG-2004 (first entry) |
| XX |
| DE Human PPBI encoding cDNA SEQ ID NO:21. |
| XX |
| KM high-grade dysplasia; HGD; oesophageal adenocarcinoma; |
| KW neo-plastic transformation; cancer; cytostatic; gene therapy; human; |
| KM alkaline phosphatase intestinal precursor; PPBI; chromosome 2; gene; ss |
| XX |
| OS Homo sapiens. |
| XX |

| | | |
|----|--|---------------------------------------|
| FH | Key | Location/Qualifiers |
| FT | CDS | 46..1632 /*tag= a /product= "PPBI" |
| FT | | |
| XX | | |
| PN | | MO200404178-A2. |
| XX | | |
| PD | | 27-MAY-2004. |
| XX | | |
| PR | | 13-NOV-2003; 2003WO-US036260. |
| XX | | |
| PA | (GETH) GENENTECH INC. | |
| PL | Smith V; | |
| DR | WPI; 2004-420319/39. | |
| P | P-PSDB; ADO26593. | |
| XX | | |
| PT | Detecting of high-grade dysplasia in cells of a mammalian tissue sample comprises establishing the level of expression in the test tissue sample of the genes. | |
| PT | | |
| XX | | |
| PS | Claim 1; SEQ ID NO 21; 256pp; English. | |
| XX | | |
| CC | The present invention describes a method for detecting high-grade dysplasia (HGD) in cells of a mammalian tissue sample. Also described: | |
| CC | (1) identifying an oesophageal tissue susceptible to oesophageal adenocarcinoma; (2) determining the predisposition of a mammalian tissue to a neo-plastic transformation by detecting HGD in cells of the tissue; | |
| CC | and (3) detecting cancer in a patient. The method can be used in detecting HGD and cancer in cells of a mammalian tissue sample. The methods and compositions of the present invention can be used in treating and preventing HGD and cancer, and in gene therapy. The present sequence encodes human alkaline phosphatase intestinal precursor (PPBI), which is used in the exemplification of the present invention. The human PPBI gene is located on chromosome 2. | |
| CC | | |
| XX | | |
| XX | Sequence 2516 BP; 517 A; 853 C; 712 G; 434 T; 0 U; 0 Other; | |
| QQ | | |
| | Query Match 70.0%; Score 1032.6; DB 12; Length 2516; Best Local Similarity 81.4%; Pred.No. 5,2e+241; | |
| | Matches 1197; Conservative 0; Mismatches 274; Indels 0; Gaps 0 | |
| OY | 6 CCTATCCAGCTGACAGAGAACCCTCGCTTTTGAAACGGCCAGGCAGGCCGCTT | 65 |
| Db | 102 CGTATCCTCCACTGTGAAGAGAACCCGCGCTTCGTGAACCGCCAGGCAGCTGAGGCGCT | 161 |
| OY | 66 TGATGTACCAAGAAATTGGACAGCCGATCCAGACAGCTGGCCAAGTAATCATCTCTTCT | 125 |
| Db | 162 GAATGTCTCCAAGAACTGTGACGCCCATCAGAAAGTCCCAAGAACTCATCTTCTCT | 221 |
| OY | 126 GGGGATGGATGGGGGTGCTTACCGTGAACAAGCCTCGATCTTAAAGGGGCAGATGAA | 185 |
| Db | 222 GGCGGATGGGTTGGGGGTGCCACGGTAGCACAGCAACAGATCTTAAAGGGGCAGAA | 281 |
| OY | 186 TGGCAAATGGGACTTGAGACACCCCTGSCCATGSAACAGTTCCCATAGTGGCTTGT | 245 |
| Db | 282 TGGCAAACTGGGGCTCTGAAGCGCCCCCTGTGGCATGTAGACCGCTTCCATACTGGCTTGT | 341 |
| OY | 246 CAAGACATPACAACGTGAGACAGAGTGGCAGACAGCGCAGGCACTGGCACTGCTTA | 305 |
| Db | 342 CAAGACATPACAATGTGAGACAGAGTGGCAGACAGCGCAGGCACTGGCACTGCTTA | 401 |
| OY | 306 GTGTGGGGTCAAGGGCACTACAGAACCATGGGTAAAGTGAGCGCGCCGCTTACATCA | 365 |
| Db | 402 GTGCGGGGTCAAGGGCACTTCCAGAACCATGGCTTGAAGTGACGCGCCGCTTAA | 461 |
| OY | 366 GTGCAACACGACGCTGGGAATGAGTCAACGCTGTGTGATCAACCGGGCCAAAGAAACAG | 425 |
| Db | 462 GTGCAACACGACCGGGCAATGAGSTCATCTTCGTGTGAAGAACCGGGCCAAAGACAG | 521 |

QY 426 GAAGCGCTGGAGTGTGTGACACCAACAGGGGTGACAGTGTCTCCCAACCGGGGCTTA 485
 DB 522 AAAAGTAGTAGAGGTGTGTACACACAGGGGTGACAGCGCTCCGCAACCGGACCTTA 581
 QY 486 CCGGACACAGGTGAACCGAACTGGTACTGACGCGGACCTTGCTGATGACAGAA 545
 DB 582 CCGACACACAGTGAACCGCAACTGGTACTGATGCTGATGCTGCTGCTGCTGCTGCTG 641
 QY 546 GAATGCTCTCCAGGAATGCGCCGACAGCTGTCTCAACATGAGATTTGACTGATCTCT 605
 DB 642 GAGGGGGTCCAGAGATCGCCACTGAGCTCATCTCCAACTGGAATTTGACCTGATCTCT 701
 QY 606 GGGTGAAGCCGGAATGTATCATGTTTCTTGAGGGGACCCGAGACCTGAAATACCAATGA 665
 DB 702 TGGCGAGGCGCGAAGTACATGTTTCCATGSGGACCCGAGACCTGAGTATCCCACTGA 761
 QY 666 TGCAGTGTGAATGAGTCCGAGAGCAAGCAAACTGTGTGAGAAATGGCAGGCCAA 725
 DB 762 TGCAGACCAAGAAATGGAATCAGGCTGAGCGGGAAGAACTGTGTGAGAAATGGCTGGCAA 821
 QY 726 GGAACCGAGGAGCCCACTATGTGTGAAACCGCACTGGCTCTTCAAGCGCGGATGACTTC 785
 DB 822 GACACGAGGTGCTGTGTATGTGTGAAACGCACTGAGCTCATGCAAGCGCTCCCTGAGACA 881
 QY 786 CAGTGTAAACACCTCATGAGGCTCTTTGAGCCGAGACATGAATATATTTGATGAGT 845
 DB 882 GTCTGTGACCACTCTCATGAGGCTCTTTGAGCCGAGACATGAATATGAGATCTCTCG 941
 QY 846 AATACCAACCAAGAACCCGACCTTGGCGAGATGATGAGAGCGGCTTGCAGAGTGTGAG 905
 DB 942 AATACCCCAACATGAGACCTCTCCCTGATGAGATGAGAGAGGCTCCCTGCTGTGAG 1001
 QY 906 CAGGACCCCGGGGCTTACTCTCTTGAGAGGGAGCGGATTTGACACAGCTACCA 965
 DB 1002 CAGGAACCCCGGGGCTTACTCTTGTGTGAGGGGCGGATGACCAATGATGATCA 1061
 QY 966 TGACGCGCAAGCTTATATGSCACTGACTGAGCGATCATGTTTGAATATGATCGCAA 1025
 DB 1062 TGAGGCTGTGGCTTACAGGACGTCTGAGGGGTCACTTTCAGACGACCATTTGAGAG 1121
 QY 1026 GCGTAAACAGCTCTACTAGCAACGTGATCTTGTCACTGACAGACCATCTCCA 1085
 DB 1122 GCGGGGCCAGCTACACGAGAGAGACAGCTGACCTTGTACCGCTGACCACTGCCA 1181
 QY 1086 TGTCTTCTTTTGTGTGTACACATGCTGGGAACTTCATTTTGGCTGTGGCCCCGG 1145
 DB 1182 TGTCTTCTCTTGTGTGTACACCTTGTGAGGAGCTTCATCTTGGGTTGGCCCCAG 1241
 QY 1146 CAAAGCCTTAGACAGCAAGTCTTACACTCTCTTATGCAATGAGCCAGGCTATGC 1205
 DB 1242 CAAAGCTACGACAGCAAGAAAGCTTACAGTCCATCTGTATGCGCAATGGCCGGGCTACGT 1301
 QY 1206 GCTTGGCGGGGCTCGAGGCCGATGTTATGSCAGACACAGCGAGAACTCTCATACCG 1265
 DB 1302 GTTCAACTCAGCGCTGCGACACAGACTGTATAGAGCGAGACGGGAGCCCCGATTAACA 1361
 QY 1266 GCAGAGGGGGGCGTGGCCCTGAGCTTAGAGGAGCCCAACGGGGCGAAGAGTGGCGTGT 1325
 DB 1362 GCAGAGGGGGGCGTGGCCCTTGTCTGACAGACCCAGAGGGGAGAAAGTGGCGGTGT 1421
 QY 1366 CCGCGAGGCGCGCAGGCGCACCTGTGTGACGCGCTGAGAGAGAGACCTTGTGTGCGCA 1385
 DB 1422 TCGCGGCGGCGCGCAGGCGCACTGTGTGATGTGTGTGAGAGAGAGTGTGTGCGCA 1481
 QY 1386 CATCATGCTTTTGGGGGCTGGGTGTGAGCCCTTACACCACTGCAATCTTCCAGCCCGCG 1445
 DB 1482 TGTCTATGGCTTGTGCTGTCTGTGAGCCCTTACACAGGCTGCGACCTGCGCTCCCGCG 1541
 QY 1446 CACGCGCACAGATCCCGACTAGGGTACC 1476
 DB 1542 CTGCAACCAACGACGCGCGCACCACTCACTGCTCC 1572

RESULT 9
 ID ADN43057
 ID ADN43057 standard; cDNA; 1702 BP.
 XX
 AC ADN43057;
 XX
 DT 29-JUL-2004 (first entry)
 XX
 DE Human secreted protein SECP-43 cDNA.
 XX
 XX cytosolic; anorectic; immunosuppressive; gene therapy; SECP-antagonist;
 KW SECP-agonist; secreted protein; SECP; autoimmune disorder; obesity;
 KW cancer; human; SECP-43; gene; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO2004037987-A2.
 XX
 PD 06-MAY-2004.
 XX
 PF 22-OCT-2003; 2003WO-US033491.
 XX
 PR 22-OCT-2002; 2002US-0420720P.
 XX
 PR 07-NOV-2002; 2002US-0425207P.
 PR 15-NOV-2002; 2002US-0426679P.
 PR 19-NOV-2002; 2002US-0427871P.
 PR 06-JAN-2003; 2003US-0438551P.
 PR 17-JAN-2003; 2003US-0441144P.
 PR 27-JAN-2003; 2003US-0443135P.
 XX
 PA (INCY-) INCYTE CORP.
 XX
 PI Baughn MR, Becha SD, Bhatia UG, Blake JT, Burrill JD, Chawla NK;
 PI Chien D, Elliott VS, Emerling BM, Faveiro KD, Hafalia ALA;
 PI Harnsen BW, Ho A, Ison CH, Khare R, Lee S, Lee SY, Lu DAM;
 PI Margis JP, Murgie J, Nguyen DB, Ramkumar J, Richardson TW;
 PI Swarnakar A, Tang TY, Tran UK, Wang JT, Yue H, Zheng W;
 DR WPI: 2004-365505/34.
 DR P-PDB: ADN42982.
 DR
 PT New human secreted protein (SECP) polypeptide, useful for preparing a
 PT composition for treating a disease associated with decreased expression
 PT or overexpression of functional SECP e.g., autoimmune disorders, obesity
 PT or cancer.
 PS Claim 5; SEQ ID NO 118; 2899p; English.
 XX
 XX The invention describes an isolated human secreted protein (SECP)
 CC polypeptide. Also described are: an isolated polynucleotide encoding the
 CC polypeptide; a recombinant polynucleotide comprising a promoter sequence
 CC operably linked to the polynucleotide; a cell transformed with the
 CC recombinant polynucleotide; a transgenic organism comprising the
 CC recombinant polynucleotide; a method of producing the polypeptide; an
 CC isolated antibody that specifically binds to the polypeptide; a method of
 CC detecting a target polynucleotide in a sample; a method for treating a
 CC disease or condition associated with decreased expression or
 CC overexpression of functional SECP; a method of screening a compound for
 CC effectiveness as an agonist or antagonist of the polypeptide or in
 CC altering expression of the target polynucleotide; a method of screening a
 CC compound that specifically binds to, or that modulates the activity of,
 CC the polypeptide; a method of assessing toxicity of a test compound; a
 CC diagnostic test for a condition or disease associated with the expression
 CC of SECP in a biological sample; a method of diagnosing a condition or
 CC disease associated with the expression of SECP in a subject; a
 CC composition comprising the antibody and a carrier, or the polypeptide, or
 CC agonist or antagonist compound and an excipient a method of preparing a
 CC polyclonal or monoclonal antibody; a method of detecting the polypeptide
 CC in a sample; a method of purifying the polypeptide; a method of
 CC generating an expression profile of a sample that contains
 CC polynucleotides; and an array comprising different nucleotide molecules
 CC affixed in distinct physical locations on a solid substrate, where at
 CC least one of the nucleotide molecules comprises a first oligonucleotide

or polynucleotide sequence specifically hybridizable with at least 30 contiguous nucleotides of the target polynucleotide. The polypeptide is useful for preparing a composition for diagnosing or treating a disease or condition associated with decreased expression or overexpression of CC functional SSCP e.g. autoimmune disorders, obesity or cancer. This CC sequence encodes a human secreted protein.

Sequence 1702 BP; 339 A; 562 C; 513 G; 288 T; 0 U; 0 Other;

Query Match 69.8%; Score 1029.8; DB 12; Length 1702;
Best Local Similarity 81.2%; Pred. No. 2,2e-240;
Matches 1196; Conservative 0; Mismatches 277; Indels 0; Gaps 0;

```

QY 4 TTCTCATCCAGCTGAGAGAGAAACCCCGCTTCTGGAACCGCCAGGAGCCAGGCC 63
DB 141 TCCCTGCGCAGCTGAGAGAGAGAAACCCCGCTTCTGGAACCGCCAGGAGCTGAGGCC 200
QY 64 CTGATGTAGCCAAAGAGTTGACGCCGATCCAGACAGCTGCGCAAGAAATGTCATCTTTC 123
DB 201 CTGATGTAGCTCAAGAAAGTTGACGCCGATCCAGACAGCTGCGCAAGAAATGTCATCTTTC 260
QY 124 TTGGGGGATGGGATGGGGGGTCTTACGCTGACAGCCACTGGAATCTTAAAGGGGAGATG 183
DB 261 CTGGGGGATGGGATGGGGGGTCTTACGCTGACAGCCACTGGAATCTTAAAGGGGAGATG 320
QY 184 AATGGCAACTGGGACCTGAGACACCCCTGGCCATGGAACCACTTCCATACGTGGCTCTG 243
DB 321 AATGGCAACTGGGACCTGAGACACCCCTGGCCATGGAACCACTTCCATACGTGGCTCTG 380
QY 244 TCCAGACATACACAGTGAACAGACAGTGCAGACAGCGCAGAGCACTGCACTGCTTAC 303
DB 381 TCCAGACATACACAGTGAACAGACAGTGCAGACAGCGCAGAGCACTGCACTGCTTAC 440
QY 304 CTGTGTGGGGTCAAGGGCACTACAGAACATCTGCTGTAAAGTGAAGCGCCGCTTACAT 363
DB 441 CTGTGTGGGGTCAAGGGCACTTCCAGAACATCTGCTGTAAAGTGAAGCGCCGCTTAC 500
QY 364 CAGTGCACACGACAGCTGGGAAATGAGGTACAGCTGTGATCAACCGGGGCAAGAAAGCA 423
DB 501 CAGTGCACACGACAGCTGGGAAATGAGGTACATCTCTGTGATCAACCGGGGCAAGAAAGCA 560
QY 424 GGGAGAGCCGTGGAGTGTGACACCAACCGAGGTGACAGATCCTCCAGCCGGGGCC 483
DB 561 GGAAGTCAAGTGAAGTGTGACACCAACCGAGGTGACAGATCCTCCAGCCGGGGCC 620
QY 484 TACCGGACACGGGTGAACCGAAACTGCTACAGACGCGCACTGCTGCTGATGCAAG 543
DB 621 TACCGGACACAGTGAACCGCAACTGCTACAGATGCTGATGCTGCTGCTGAGCCGC 680
QY 544 AAGAAATGCTGCCAGACATCGCCGACAGCTGCTACAAATGATATTTGAAGTATC 603
DB 681 CAGAGAGGGTGCAGAGACATCGCCGACAGCTGCTACAAATGATATTTGAAGTATC 740
QY 604 CTGGGTGAGAGCGGAATGTATCATGTTTCTGAGGGGAGCCCAAGACCTGTAATCCAGAT 663
DB 741 CTGGGGGAGAGCGCGCAAGTATGTTTCCATGAGGAGCCCAAGACCTGTAATCCAGAT 800
QY 664 GATGCCAGTGTGAATGAGTCCGGAAGACAGCAAGCACTGCTGCAAGATGCAAGGCC 723
DB 801 GATGCCAGCGCAAGATGGAATCAAGCTGAGCGGGAAGAACTGCTGCAAGATGCAAGGCC 860
QY 724 AAGCAACAGGAGACCCAGTATGTTGGAACCGCACTGCTGCTTCAAGGGGCGAGATGAC 783
DB 861 AAGCAACAGGAGTCTGTTGTTGTTGGAACCGCACTGAGTCAAGAGGGTCTCTGAGAC 920
QY 784 TCCAGTGTAAACACCTCATGAGGCTCTTGTAGCCGCGACAGATGAAGTAAATGTTTCA 843
DB 921 CAGTCTGTGACCATCTCATGAGGCTCTTGTAGCCGCGACAGATGAAGTAAATGATTCAC 980
QY 844 CAAAGCACACCAAGAGACCCGACCTTGGCGGAGATGACGAGGGCGGCTTCAAGTCTG 903
DB 981 CGAGAGCCCAACCTGAGACCCCTCTGATGAGATGACAGAGGCTGCTGCGCTGCTG 1040

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QY 904 AGCAGAGACCCCGGGGCTTTTACTCTTCTGTGAGAGAGGCCCGCATTTACACGCTAC 963
DB 1041 AGCAGAGACCCCGGGGCTTTTACTCTTCTGTGAGAGAGGCCCGCATTTACACGCTAC 1100
QY 964 CATGACGCAAAAGCTTATATGACACTGATGAGGCGCATATGTTTGAACAATGCAATGGC 1023
DB 1101 CATGAGGGTGTGGCTTACACGACACTGATGAGGCGGTATGTTGACACACGCAATTTAG 1160
QY 1024 AAGGCTTAAGAGTCACTAGACCAAGTGAACAGCTGATCTTGTCACTGACAGCACTCC 1083
DB 1161 AAGGCGGGGCAAGTCACTAGACCAAGTGAACAGCTGATCTTGTCACTGACAGCACTCC 1220
QY 1084 CATGCTTCTCTTTTGTGTGCTACACATGCTGGGAGCACTGCAATTTTGGTCTGGCCCC 1143
DB 1221 CATGCTTCTCTCTTTGTGTGCTACACCTTGCAGAGGAGCTCCATCTTCGGGTGGCCCC 1280
QY 1144 GGCAGAGCTTATGACAGCAAGTCTTACCTCTCATCTCTTATGGAATGGCCAGGCTAT 1203
DB 1281 AGCAGAGCTTATGACAGCAAGTCTTACCTCTCATCTCTTATGGAATGGCCAGGCTAT 1340
QY 1204 GCGCTTGGGGGGGCTCGAGGCCCGATGTTAAATGGCAGACAAAGCAGAGAACCTCATAC 1263
DB 1341 GTGTTCACTACAGGCTGCTGACACGATGAAATGAGAGCGGAGAGCCCGATTTAC 1400
QY 1264 CCGCAGCAGCGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1323
DB 1401 CAGCAGCAGCGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1460
QY 1324 TTGCGCGAGAGGCCCGCAGCGGCACTGTGTGACAGCGGCTGCAAGAGAGACCTTCTGG 1383
DB 1461 TTGCGCGAGAGGCCCGCAGCGGCACTGTGTGACAGCGGCTGCAAGAGAGACCTTCTGG 1520
QY 1384 CACATGATGGCTTTTGGGGGCTGCGGTGAGGCCCTACACGCACTGCAATCTGCCAGCCCC 1443
DB 1521 CATGTATGACCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1580
QY 1444 GCCACCGCACAGCATTCGCCGACCTAGAGGTACC 1476
DB 1581 GCCTGACACAGCAGCGCGGACCCAGTTGGC 1613

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RESULT 10
AAK52479
ID AAK52479 standard; cDNA; 1966 BP.
XX
AC AAK52479;
XX
XX 06-NOV-2001 (first entry)
XX
DE Human polynucleotide SEQ ID NO 2008.
XX
XX Human; cytokine; cell proliferation; cell differentiation; gene therapy;
XX vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
XX tissue growth factor; immunomodulatory; cancer; leukaemia;
XX nervous system disorder; arthritis; inflammation; ss.
OS Homo sapiens.
XX
XX MO200157190-A2.
XX
PD 09-AUG-2001.
XX
PF 05-FEB-2001; 2001WO-US004098.
XX
XX 03-FEB-2000; 2000US-00496914.
XX 27-APR-2000; 2000US-00560875.
XX 20-JUN-2000; 2000US-00598075.
XX 19-JUL-2000; 2000US-00620325.
XX 01-SEP-2000; 2000US-00654936.
XX 15-SEP-2000; 2000US-00663561.
XX 20-OCT-2000; 2000US-00693325.
XX 30-NOV-2000; 2000US-00728422.
XX

PA (HVS-) HVSQ INC.
XX Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y;
PI Ma Y, Zhao QH, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;
PI Xue AJ, Yang Y, Wejhrman T, Goodrich R;
XX MPI; 2001-476283/51.
DR P-PSDB; AAM79346.
XX
PT Nucleic acids encoding polypeptides with cytokine-like activities, useful
in diagnosis and gene therapy.
PS
XX Claim 1; Page 4413; 6221pp; English.
XX
CC The invention relates to polynucleotides (AAK51456-AAK53435) and the
CC encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to
CC cytokine, cell proliferation or cell differentiation or which may induce
CC production of other cytokines in other cell populations. The
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC peptide therapy. The polypeptides have various cytokine-like activities,
CC e.g. stem cell growth factor activity, haematopoiesis regulating
CC activity, tissue growth factor activity, immunomodulatory activity and
CC activity/inhibin activity and may be useful in the diagnosis and/or
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111
CC (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the
CC sequence listing were missing at the time of publication
XX
SQ Sequence 1966 BP; 381 A; 667 C; 579 G; 339 T; 0 U; 0 Other;
Query Match 69.2%; Score 1021.6; DB 4; Length 1966;
Best Local Similarity 81.3%; Pred. No. 2,3e-238;
Matches 1197; Conservative 0; Mismatches 274; Indels 1; Gaps 1;
QY 6 CCTCATCCAGCTGAGAGAGAAACCCGCTTGTGAAACCGGACGAGCCGACCT 65
DB 107 CCGTATCCAGCTGAGAGAGAAACCGGCTTGTGAAACCGGACGAGCTGAGCCCT 166
QY 66 TGAATGAGCAG 125
DB 167 GATGCTGCGAAG 226
QY 126 GGGGAGTGGAGTGGGGGCTCTACGCTGACAGGCACTCGGATCTTAAAGGGGAGATGA 185
DB 227 GGGGAGTGGGTTGGGGGCTCCACGCTGACAGGCACTCGGATCTTAAAGGGGAGAGAA 286
QY 186 TGGCAAACTGGGAGCTGAGACACCCCTGAGCATGACAGTTCCTTCCATAGCTGCTGTCT 245
DB 287 TGGCAAACTGGGAGCTGAGACACCCCTGAGCATGACAGTTCCTTCCATAGCTGCTGTCT 346
QY 246 CAAGCATCAACCTGAG 305
DB 347 CAAGCATCAACCTGAG 406
QY 306 GTGTGGGCTCAAGGGGCACTACAGAACATCGGTGTAAGTGCAGCGCCGCTTAACTAATCA 365
DB 407 GTGTGGGCTCAAGGGGCACTTCCAGAACATCGGTGTAAGTGCAGCGCCGCTTAACTAATCA 466
QY 366 GTGCACACAGACAGCTGGGAGATGAGGTCACTGTGTATCAACCGGGGCAAGAAAGCAGG 425
DB 467 GTGCACACAGACAGCTGGGAGATGAGGTCACTGTGTATCAACCGGGGCAAGAAAGCAGG 526
QY 426 GAAAGCCGTGGAGTGGTGAACCAACCAAGGTTGAGCATGTCTCCGACCGGGGCTTAA 485
DB 527 AAGTCTAGTAGAGTGGTGAACCAACCAAGGTTGAGCATGTCTCCGACCGGGGCTTAA 586
QY 486 CCGGACACAGGTGAACCGAAACTGTACTCAAGCGCGGACCTGCTGATGACAGAA 545
DB 587 CCGGACACAGGTGAACCGAACTGTACTCAAGTGTGACATGCTGCTGCTGCTGCTGCTGCTG 646
QY 546 GAATGGCTGCGAGAGATGCGCGACAGCTGTCTTAAACATGATGATTTGACGTGATCTCT 605
DB 647 GGAGGGGTGCGAGAGATGCGCGACAGCTGTCTTAAACATGATGATTTGACGTGATCTCT 706

QY 606 GGGTGGAGGCGGAATGTATCATGTTTCTGAGGGGAGCCCGACAGCCCTGAATACCCAGATGA 665
DB 707 TGGCGAGAGCGCAAGTACATGTTTCCATAGGGAGCCCGACAGCCCTGATACCCAGCTGA 766
QY 666 TGGCAGTGTGATGAGAGTCCGGAAGACAGACAGAACTGTGTGACAGAAATGGCAGGCGCA 725
DB 767 TGGCAGCAGAGATGAGAACTAGGCTGAGCGGGAGAACTGGTGCAGAAATGGCTGGCAAA 826
QY 726 GCACCAAGGAGCCCATGATGTGTGGAACCGCATGCGCTCTTACAGGGGCGCGATGATCTC 785
DB 827 GCACCAAGGAGT 886
QY 786 CAGTGTATACACCTCATAGGCTCTTGTGAGCGCGGACAGCATGAAATGTAATGTTACACA 845
DB 887 GTCTGTGACCATCTCATAGGCTCTTGTGAGCGCGGACAGCATGAAATGTAATGTAATGTA 946
QY 846 AGACCACACCAAGAGACCGGACCTGTGCGAGATGACGAGAGCGGCTGTCAAGTGTGAG 905
DB 947 AGACCACACCTGAGACCCCTCTGTATGAGATGACAGAGGTGCTGTGCGCTGTGAG 1006
QY 906 CAGGAACCCCGGGGCTTCTACCTTGTGTGAGGAGGAGCGCATTTGACACGCTGACCA 965
DB 1007 CAGGAACCCCGGGGCTTCTACCTTGTGTGAGGAGGAGCGCATTTGACACGCTGACCA 1066
QY 966 TGAAGGCAAGGCTTATGAGCACTGAGAGCGCATGTTTGTGACATGCGCATGCGCA 1025
DB 1067 TGAAGGCTGTGCTTACAGGACCTCATGAGGCGGTCAATGTTGACAGCGCATTTGAGAG 1126
QY 1026 GAGTACAGAGCTCATAGTACAGTACAGTACAGTACAGTACAGTACAGTACAGTACAGT 1085
DB 1127 GCGGGGCGAGCTGACACAG 1186
QY 1086 TGTCTTCTCTTGT 1145
DB 1187 TGTCTTCTCTTGT 1246
QY 1146 CAGGCTTTAGACAGCAAGTCTTACCTCATCTCATCTCATCTCATCTCATCTCATCTCATCT 1205
DB 1247 CAGGCTTTAGACAGCAAGTCTTACCTCATCTCATCTCATCTCATCTCATCTCATCTCATCT 1306
QY 1206 GCTTGGCGGGGCTTGAAGGCGCGGAGTGAATGAGCAGCAAGAGCAAGAGCAAGAGCAAG 1265
DB 1307 GTTCAACTCAGGCGGAGGAG 1366
QY 1266 GAGCAGAGC-GAGCGTCCCTGCTGCTAGCAGAGACCCAGGGGCGAAGAGCTGGCGGTCT 1324
DB 1367 CCAGCAGGCGGGGAGTGCCTCTGTCTCGAGACCCAGAGGCGGAGAGAGAGAGAGAGAG 1426
QY 1325 TCGGCGAGAGGCGGAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1384
DB 1427 TTTGCGGAGGCGGAGAGGAG 1486
QY 1385 ACATCATGAGCTTTTGGGCTGTGCTGAGAGCCCTACACCGAGTGCATTTGCGAGCCCG 1444
DB 1487 ATGTATGAGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1546
QY 1445 CCAGCGCAACAGCATCTCCCGACTAGGCTACC 1476
DB 1547 CCTGCACCAACAGCATCTCCCGACTAGGCTACC 1578
RESULT 11
AA090640
ID AA090640 standard; cDNA to mRNA; 1491 BP.
XX
XX AA090640;
AC
XX
XX
DT 24-JUL-1995 (first entry)
XX
XX Human enteric alkaline phosphatase cDNA mutant 1491 bp.
DE Human enteric alkaline phosphatase; homogeneous quality production;
XX
XX
KW

KM clinical diagnosis; ds.
 XX Homo sapiens.
 OS
 XX Key Location/Qualifiers
 FH mat_peptide 1..1491
 FT /tag= a
 FT /note= "truncated HIP"
 PN JP06284885-A.
 PD 11-OCT-1994.
 XX
 PF 02-APR-1993; 93JP-00076883.
 XX
 PR 02-APR-1993; 93JP-00076883.
 XX
 XX (TOYU) TOSOH CORP.
 XX
 DR MPI, 1994-362592/45.
 XX
 DR P-PSDB; AAR75700.
 XX
 PT Recombinant human enteric alkaline phosphatase - for cheap and large
 PT scale prodn. of homogeneous HIP.
 XX
 PS Claim 4; Page 3-5; 9pp; Japanese.
 XX
 CC AA090640 encodes AAR75700 the human enteric alkaline phosphatase (HIP)
 CC mutant 1491 bp. Using recombinant DNA techniques homogeneous quality HIP
 CC mutants could be produced, avoiding the problems associated with poor
 CC quality labelled enzymes in clinical diagnosis
 XX
 SQ Sequence 1491 BP; 309 A; 471 C; 461 G; 250 T; 0 U; 0 Other;

Query Match 69.2%; Score 1021.4; DB 2; Length 1491;
 Best Local Similarity 82.1%; Pred. No. 2.3e-238;
 Matches 1155; Conservative 0; Mismatches 256; Indels 0; Gaps 0;

QY 6 CCTCATCCAGCTGAGAGAGAAACCCGCTTCTTGAAACCGCAGGACGCCAGCCCT 65
 DB 57 CGTCATCCAGCTGAGAGAGAAACCCGCTTCTTGAAACCGCAGGACGCCAGCCCT 116
 QY 66 TGAATGAGCCAAAGTGGAGCCGATCCAGACAGCTGCCAAGATGTCATCTCTT 125
 DB 117 GGAATGCTGCCAAGAGCTGAGCCCATCCAGAAAGTGGCCAAAGACCTCATCTCT 176
 QY 126 GGGGAGTGGAGTGGGGTGCCTACGGTGAACGCCCATCGATCTTAAAGGGCAGATGA 185
 DB 177 GGGCGATGGGTGGGGGTGCCACGGTGAACGCCCATCGATCTTAAAGGGCAGATGA 236
 QY 186 TGGCAAACTGGGACCTTGAGACACCCCTGGCCATGAGCAAGTTCCTATCGTGTCT 245
 DB 237 TGGCAAACTGGGGCTTGAGACGCCCTGGCCATGAGACCGCTTCCATACCTGTCT 296
 QY 246 CAAGACATTAAGTGGAGCAGACAGTGGCCAGACAGGCGAGCACTGCCATCTTACCT 305
 DB 297 CAAGACATTAAGTGGAGCAGACAGTGGCCAGACAGGCGAGCACTGCCATCTTACCT 356
 QY 306 GTGTGGGGTCAAGGGCACTACAGAAACCATCGGTGTAAGTGACAGCGCCGCTTAAATCA 365
 DB 357 GTGTGGGGTCAAGGGCACTTCCAGACCATCGGTGTAAGTGACAGCGCCGCTTAAATCA 416
 QY 366 GTGCAACACGACAGCTGGGAATGAGTCACTGTGTATCAACCGGGCCAAAGAAAGAGG 425
 DB 417 GTGCAACACGACAGCTGGGAATGAGTCACTGTGTATCAACCGGGCCAAAGAAAGAGG 476
 QY 426 GAAGCGGTGGAGTGTGACCAACCAAGGTGACAGCAAGCTCCCAAGCGGGCGCTTA 485
 DB 477 AAAGTCAAGTGAAGTGTGACCAACCAAGGTGACAGCAAGCTCCCAAGCGGGCGCTTA 536
 QY 486 CGGCACACAGGTGAACCGAAATGTGTACTGACAGCGCGAAGCTGCTGTATGACAGAA 545
 DB 537 CGGCACACAGGTGAACCGCAACTGTGTACTGATGCTGACATGCTCTCCAGCCGCCCA 596

QY 546 GAATGGCTCCAGACATGCGCCGACAGCTGTCTTACATAGATATTGACGTATCTCT 605
 DB 597 GGAGGGGTCCAGACATGCGCCGACAGCTGTCTTACATAGATATTGACGTATCTCT 656
 QY 606 GGGTGAAGGCCGAATGTATCATGTCTTCTGAGGGGACCCCAAGACCTGAATACCAGATGA 665
 DB 657 TGGCGGAGGCCGCAAGTATCATGTCTTCTGAGGGGACCCCAAGACCTGAATACCAGATGA 716
 QY 666 TGGCATGTGAATGTAGTCCGGAAGACAAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 725
 DB 717 TGGCATGTGAATGTAGTCCGGAAGACAAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 776
 QY 726 GCACGAGGAGGCCAGTATGTGTGAAACCGCACTGGCTCTTTCAGAGCGCGATGATCTC 785
 DB 777 GCACGAGGAGGCCAGTATGTGTGAAACCGCACTGAGCTATGCAAGGCTCCCTGAGACCA 836
 QY 786 CAGTGTACACACCTCATGAGGCTCTTGTAGCCGAGACATGAAATGATATGTTACAGA 845
 DB 837 GTCTGTGACCAATCTCATGAGGCTCTTGTAGCCGAGACATGAAATGATATGATCTCCG 896
 QY 846 AGACCAACACAAAGACCCGACCTTGGCGGAGATGACGAGGCGGCTTCAAGTGTGAG 905
 DB 897 AGACCCCAACACTGACCCCTCCCTGATGAGATGACAGAGGCTGCTGCTGCTGAG 956
 QY 906 CAGGAACCCCGGGGGCTTACCTCTTGTGAGGAGGAGCGCATTTGACCAAGCTCAGCA 965
 DB 957 CAGGAACCCCGGGGGCTTACCTCTTGTGAGGAGGAGCGCATTTGACCAAGCTCAGCA 1016
 QY 966 TGAACGCAAGCTTATATGACACTGACAGCGATCATGTTTGAATGCAATGCCATGCCAA 1025
 DB 1017 TGAAGGTGTGCTTACAGGACAGTCACTGAGGCGGATGTTTCAAGAGCCCATTTAGAG 1076
 QY 1026 GGCTAACAGCTCTACTAGGAACTGACACGCTGATCTTTGCTACCTGACACCATCTCCA 1085
 DB 1077 GGGGGGCAAGCTCACAGGAGGAGGACAGCTGACCTTGTGACCGCTGACCATCTCCA 1136
 QY 1086 TGTCTCTCTTTTGGTGGCTACACACTGCTGTGGAGCTTCATTTTGGTCTGGCCCGG 1145
 DB 1137 TGTCTCTCTTTTGGTGGCTACACACTGCTGTGGAGCTTCATTTTGGTCTGGCCCGG 1196
 QY 1146 CAAGGCTTGAACAGCAAGTCTTACACTCTCATCTTATGCAATGAGCCAGCTATGC 1205
 DB 1197 CAAGGCTTGAACAGCAAGTCTTACACTCTCATCTTATGCAATGAGCCGAGCTATGC 1256
 QY 1206 GCTTGGCGGAGCTGAGGCGCGATTTATGACAGCAAGGAGGAAACCTCATACCG 1265
 DB 1257 GTTCAACTCAGGCGGTGCGACACAGCTGAATGAGACGAGAGCGGAGCCCGATTACCA 1316
 QY 1266 GCAGCAGGCGGCGCTGCGCTGCTAGCGAGACCCAGGGGGGGAAGAGCTGGCGGT 1325
 DB 1317 GCAGCAGGCGGCGCTGCGCTGCTAGCGAGACCCAGGGGGGGAAGAGCTGGCGGT 1376
 QY 1326 CGGCGAGGCGGCGAGGCGCACTGCTGACAGCGGCTGAGAGAGACCTTCTGGCGCA 1385
 DB 1377 TGGCGGCGGCGGAGGCGCACTGCTGACAGCGGCTGAGAGAGACCTTCTGGCGCA 1436
 QY 1386 CATCATGACCTTTTGGGCTGCGGTGAGGCTTACACCGACTGCAATCTGCC 1436
 DB 1437 TGTCTATGCGCTTGTGCTGTGAGGCTTACACCGACTGCAATCTGCC 1487

RESULT 12
 AAT27391
 ID AAT27391 standard; DNA; 3076 BP.
 XX
 AC AAT27391;
 XX
 DT 23-SEP-1996 (first entry)
 XX
 DE Human IgG CH1-hinge-CH2 region-alkaline phosphatase fusion pXPD.
 XX
 KM alkaline phosphatase; label; antibody; IgG; H-chain; constant region;


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Db      2121 TGAGGGTGTGGCTTACAGGAGCTACCTGAGGCGGTGATGTTGACGAGCCATTGAGAG 2180
QY      1026 GGCTAACGAGCTCATTAGGAACTGACACGCTGATCCTTGTACCTGACAGACCACTCCCA 1085
Db      2181 GGGCGGCGCTCAGACGAGAGGAGACAGCTGACCTCTGTACCGCTGACCACTCCCA 2240
QY      1086 TGTCTTCTTCTTGTGCTTACACATGCGTGGAGACCTCCATTTTGTGCTGGCCCCCG 1145
Db      2241 TGTCTTCTTCTTGTGCTTACACATGCGTGGAGACCTCCATTTTGTGCTGGCCCCCG 2300
QY      1146 CAAGGCTTAAACAGCACTCTTACACCTTCTTATGCAATGCGCCAGCTATGC 1205
Db      2301 CAAGGCTCAGAGAGAGAAAGCTTACAGCTTCTTATGCAATGCGCCAGCTATGC 2360
QY      1206 GCTTGGCGGGGCTGAGGCGCGGATGTTATGAGCAACAGCGAGAACTCTCATACCG 1265
Db      2361 GTTCAACTCAGGCTGCGACAGACGTGATGAGACGAGCGGAGCGCCGATTATCA 2420
QY      1266 GCAGAGAGCGCGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1325
Db      2421 GCAGAGAGCGCGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2480
QY      1326 CGCGGAGGCGCGCGAGCGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1385
Db      2481 TCGCGGCGCGCGCGAGCGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2540
QY      1386 CATCATGCGCTTGGCGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1428
Db      2541 TGTCTTGGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2583

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RESULT 14
AAT27393
ID AAT27393 standard; DNA; 2372 BP.

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XX      AAT27393;
XX      23-SEP-1996 (first entry)
XX      Human Igg CH1-hinge-linker-alkaline phosphatase fusion pCH1P1.
XX      alkaline phosphatase; label; antibody; Igg; H-chain; constant region;
XX      immunoglobulin gamma; fusion protein; chimera; immunosassay; ds.
XX      Homo sapiens.
OS      Synthetic.
XX      Key Location/Qualifiers
FH      Key 212..503
FT      exon /tag= a
FT      exon /note= "precise start position is unclear"
FT      exon 892..2372
FT      exon /tag= b
FT      exon /transl_except= pos:948..950, aa:Ser
FT      exon /transl_except= pos:951..953, aa:Thr
FT      exon /note= "end position corresponds to termination codon;
FT      exon nucleotides 906..956 encode a 17 amino acid linker and
FT      exon nucleotides 957..2366 are derived from the alkaline
FT      exon phosphatase gene"

```

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XX      JP08070875-A.
XX      PD 19-MAR-1996.
XX      PF 05-SEP-1994; 94JP-00211035.
XX      PR 05-SEP-1994; 94JP-00211035.
XX      PA (TOYU ) TOSOH CORP.
XX      WPI: 1996-203155/21.
XX      DR P-PSDB; AAW03141.
XX

```

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PT      Recombinant alkaline phosphatase (AP)-antibody fusion protein - comprises
PT      AP fused downstream of antibody heavy or light chain, useful as
PT      immunosassay reagent.
XX      Example 1; Page 40-43; 44pp; Japanese.
XX      The gene coding for human alkaline phosphatase is fused downstream of a
XX      gene coding for either the variable and CH1 regions of an antibody heavy
XX      chain or an antibody light chain. Coexpression of the H- and L-chain
XX      sequences, one of which is fused to the AP gene, results in production of
XX      AP-labelled antibodies suitable for use in immunosassays. The present
XX      sequence is an insert from plasmid pCH1P-1 coding for human Igg heavy
XX      chain constant region sequences (CH1-hinge) fused to a partial AP-coding
XX      region via a 17 amino acid linker
SQ      Sequence 2372 BP; 481 A; 781 C; 710 G; 400 T; 0 U; 0 Other;

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Query Match 68.3%; Score 1008.8; DB 2; Length 2372;

Best Local Similarity 82.2%; Pred. No. 3.1e-235;

Matches 1160; Conservative 0; Mismatches 252; Indels 0; Gaps 0;

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QY      17 CTGAGAGAGAAACCCCGCTTCTGGAACCCGCGAGGAGCCAGCCCTTATGATGACCA 76
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QY      137 TGGGGGCTCTACGCTGACAGCCACTCGGATCTTAAAGGGGAGATGAATGCAAACTGG 196
Db      1075 TGGGGGCTCTACGCTGACAGCCACTCGGATCTTAAAGGGGAGATGAATGCAAACTGG 1134
QY      197 GACCTGAGACACACCCCTGCGCATGAGACCACTTCCATAGTGGCTCTGTCCAAAGCATACA 256
Db      1135 GACCTGAGACACACCCCTGCGCATGAGACCACTTCCATAGTGGCTCTGTCCAAAGCATACA 1194
QY      257 ACGTGCAGACAGGCTGCGACAGCGGAGGACATGCGCACTGCTGCTGCTGCTGCTGCTGCT 316
Db      1195 ACGTGCAGACAGGCTGCGACAGCGGAGGACATGCGCACTGCTGCTGCTGCTGCTGCTGCT 1254
QY      317 AGGCGCACTTACAGAACCTATGCTGTAGTGCAGCGCCCGCTTACATCATGTGCAACAGCA 376
Db      1255 AGGCGCACTTACAGAACCTATGCTGTAGTGCAGCGCCCGCTTACATCATGTGCAACAGCA 1314
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Db      1315 CACGTGGAATGAGGTACGCTGTGTATCAACCGGGGCCAAGAAAGCAGAGAAAGCCCTGG 1374
QY      437 GAGTGTGACACCAACCAAGGCTGACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 496
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QY      497 TGAACCGAAACTGTACTCAGACCGCGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 556
Db      1435 TGAACCGCGAATGTGACTCAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1494
QY      557 AGGACATGCGCGCACAGTGTGTCTAACCAATGATATTGAGTGTATCCTGGTGTGAGAGCC 616
Db      1495 AGGACATGCGCGCACAGTGTGTCTAACCAATGATATTGAGTGTATCCTGGTGTGAGAGCC 1554
QY      617 GAATGTACATGTTTCTGAGGGGAGCCCGAGACCTGAAATACCAAGATATGCAAGTGTGA 676
Db      1555 GAATGTACATGTTTCTGAGGGGAGCCCGAGACCTGAAATACCAAGATATGCAAGTGTGA 1614
QY      677 ATGAGTCCGGAAGAGACAGAGAACTGTGTGAGAAATGAGAGCCAGCAAGCAGAGAG 736
Db      1615 ATGAGTCCGGAAGAGACAGAGAACTGTGTGAGAAATGAGAGCCAGCAAGCAGAGAG 1674
QY      737 CCCAGTATGTGTGAACCGGCACTGCGCTCTTCAAGGGGCGGAGATGATCCAGTGTAAAC 796
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 DB 1795 TGGACCCCTCTCTGATGATGATGACAGAGCTGCTCCCTGCTGAGACGAAACCC 1854
 QY 917 GGGGCTTCTACCTCTTGTGAGAGGAGCGGCAATGACCGGACCATGACGAGCAAG 976
 DB 1855 GCGGCTTCTACCTCTTGTGAGAGGAGCGGCAATGACCGGACCATGACGAGCTGTG 1914
 QY 977 CTATATGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 1036
 DB 1915 CTATACGAGGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 1974
 QY 1037 TCACATGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 1096
 DB 1975 TCACATGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 2034
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 DB 2095 ACAGCAAGTCTACACCTCTCTATGACGACGACGACGACGACGACGACG 1254
 QY 1217 GCTGAGGCGCGATGTTAATGACGACGACGACGACGACGACGACGACG 1276
 DB 2155 GCTGAGGCGCGATGTTAATGACGACGACGACGACGACGACGACGACG 1214
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 QY 1337 CGGAGGCGACCTGCTGACGACGACGACGACGACGACGACGACGACGACG 1396
 DB 2275 CGGAGGCGACCTGCTGACGACGACGACGACGACGACGACGACGACGACG 1334
 QY 1397 TTGCGGCTGCTGAGAGCCCTTACCGACGACGACGACGACGACGACG 1428
 DB 2335 TTGCGGCTGCTGAGAGCCCTTACCGACGACGACGACGACGACGACG 2366
 RESULT 15
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 ID AAT27386 standard; DNA; 2484 BP.
 AC AAT27386;
 XX
 DT 23-SEP-1996 (first entry)
 XX
 DE Human IgG H-chain constant region-alkaline phosphatase fusion pVPS.
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 KW alkaline phosphatase; label; antibody; IgG; H-chain; C-region; CH1;
 KW fusion protein; chimera; immunoassay; ds.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 FH Key location/Qualifiers
 FT exon 212..503
 FT exon /*tag= a
 FT exon /*note= "precise start position is unclear"
 FT exon 892..936
 FT exon /*tag= b
 FT exon 1055..2484
 FT exon /*tag= c
 FT exon /*note= "end position corresponds to termination codon;
 FT exon nucleotides 1069..2478 are derived from the alkaline
 XX exon phosphatase gene"

PN JP08070875-A.
 XX
 PD 19-MAR-1996.
 XX
 PF 05-SEP-1994; 94JP-00211035.
 XX
 PR 05-SEP-1994; 94JP-00211035.
 XX
 PA (TOYO) TOSOH CORP.
 XX
 XX WPI; 1996-203155/21.
 DR P-PSDB; AAR91807.
 XX
 PT Recombinant alkaline phosphatase (AP)-antibody fusion protein - comprises
 PT AP fused downstream of antibody heavy or light chain, useful as
 PT immunoassay reagent.
 XX
 PS Example 1; Page 15-18; 44p; Japanese.
 PS
 CC The gene coding for human alkaline phosphatase (AP) is fused downstream
 CC of a gene coding for either the variable and CH1 regions of an antibody
 CC heavy chain or an antibody light chain. Coexpression of the H- and L-
 CC chain sequences, one of which is fused to the AP gene, results in
 CC production of AP-labelled antibodies suitable for use in immunoassays.
 CC The present sequence is an insert from plasmid pVPS coding for human IgG
 CC heavy chain constant region sequences (CH1-hinge) fused to a partial AP-
 CC coding region
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 Query Match 68.3%; Score 1008.8; DB 2; Length 2484;
 Best Local Similarity 82.2%; Pred. No. 3.2e-235;
 Matches 1160; Conservative 0; Mismatches 252; Indels 0; Gaps 0;
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 DB 1067 CTGAGAGAGAGAAACCCGCTTCTGGAACCGGACGACGACGACGACGACG 1126
 QY 77 AGAAGTTGACGCGGATCCAGACAGCTGCGCAAGATCTCTCTCTTGGGGAGTGG 136
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 QY 137 TGGGGTGCCTACGAGGACGACGACGACGACGACGACGACGACGACGACG 196
 DB 1187 TGGGGTGCCTACGAGGACGACGACGACGACGACGACGACGACGACGACG 1246
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 QY 257 ACCTGACAGACAGGTCGACGACGACGACGACGACGACGACGACGACGACG 316
 DB 1307 ATGTGACAGACAGGTCGACGACGACGACGACGACGACGACGACGACGACG 1366
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 DB 1367 AGGCAACTACAGAAACCATCGGTGTAAGTGACGACGACGACGACGACGACG 1426
 QY 377 CACGTGGATGAGGTCACTGTGATCAACCGGCGCAAGAAAGCAGGAAAGCCGTG 436
 DB 1427 CACGTGGATGAGGTCACTGTGATCAACCGGCGCAAGAAAGCAGGAAAGCCGTG 1486
 QY 437 GAGTGTGACACACACGAGGTGACGATGCTCCCAAGCGGGGCTTACGCCACAG 496
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 QY 497 TGAACGGAACCTGTGATCAAGCGGACGCTGCTGATGACAGAGAAAGTGGCTGC 556
 DB 1547 TGAACGGAACCTGTGATCAAGCGGACGCTGCTGATGACAGAGAAAGTGGCTGC 1606
 QY 557 AGGACATGCGCGGACGCTGTCTACACATGATGATTAAGTGTGATGAGAGGCC 616
 DB 1607 AGGACATGCGCGGACGCTGTCTACACATGATGATTAAGTGTGATGAGAGGCC 1666

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Listing first 45 summaries

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| 3 | 1327 | 89.9 | 2542 | 4 US-09-305-681-5 | Sequence 5, Appl1 |
| 4 | 1002.4 | 67.9 | 1956 | 3 US-08-867-352-20 | Sequence 20, Appl1 |
| 5 | 1000.8 | 67.8 | 4989 | 4 US-09-693-011-12 | Sequence 12, Appl1 |
| 6 | 1000.8 | 67.8 | 5083 | 4 US-09-693-011-11 | Sequence 11, Appl1 |
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| 9 | 1000.8 | 67.8 | 6408 | 4 US-09-693-011-10 | Sequence 9, Appl1 |
| 10 | 1000.8 | 67.8 | 7076 | 4 US-09-837-863-20 | Sequence 20, Appl1 |
| 11 | 1000.8 | 67.8 | 7076 | 4 US-09-837-863-21 | Sequence 21, Appl1 |
| 12 | 1000.8 | 67.8 | 7092 | 4 US-09-837-863-19 | Sequence 19, Appl1 |
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| 14 | 1000.8 | 67.8 | 7573 | 4 US-09-837-863-27 | Sequence 27, Appl1 |
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| 36 | 139.4 | 9.4 | 5293 | 4 US-09-900-708-1 | Sequence 1, Appl1 |
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| 38 | 120.8 | 8.2 | 220 | 3 US-09-263-933-22 | Sequence 22, Appl1 |
| 39 | 120.8 | 8.2 | 220 | 4 US-09-919-901-22 | Sequence 22, Appl1 |
| 40 | 120.8 | 8.2 | 220 | 4 US-10-191-966-22 | Sequence 22, Appl1 |
| 41 | 114.8 | 7.8 | 1074 | 4 US-09-270-767-13264 | Sequence 13264, A |
| 42 | 92.2 | 6.2 | 709 | 4 US-09-270-767-1586 | Sequence 1586, A |
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| 44 | 76.8 | 5.2 | 200 | 4 US-09-900-708-4 | Sequence 4, Appl1 |
| 45 | 67.4 | 4.6 | 1368 | 2 US-08-738-172-3 | Sequence 3, Appl1 |

ALIGNMENTS

RESULT 1
US-09-305-681-1
; Sequence 1, Application US/09305681

; Patent No. 6406899

; GENERAL INFORMATION:

; APPLICANT: TITLE OF INVENTION: Highly active alkaline phosphatase

; NUMBER OF SEQUENCES: 54

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)

; CURRENT APPLICATION DATA:

; FILING DATE: US/09/305,681

; CLASSIFICATION:

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1798 base pairs

; TYPE: nucleotide

; STRANDEDNESS: single strand

; TOPOLOGY: linear

; MOLECULE TYPE: genomic DNA

; US-09-305-681-1

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| DB | 167 | TGATGATGAGCAAGAGATTGAGCGGATCCAGACAGTGTCCAGAAATGTCTTCTT | 226 |
| QY | 126 | GGGGGATGGGATGGGGGCTCTACGCTGACAGCACTGGGATCTTAAAGGGGAGATGA | 185 |
| DB | 227 | GGGGGATGGGATGGGGGCTCTACGCTGACAGCACTGGGATCTTAAAGGGGAGATGA | 286 |
| QY | 186 | TGGCAAACTGGGACCTGAGACACCCCTGGCCATGAGCAAGTCCATACGTGGCTGTC | 245 |
| DB | 287 | TGGCAAACTGGGACCTGAGACACCCCTGGCCATGAGCAAGTCCATACGTGGCTGTC | 346 |
| QY | 246 | CAAGACATCAACGTGAGACAGACAGGTGCCAGACAGCCGACATCTGCACTGCTACCT | 305 |
| DB | 347 | CAAGACATCAACGTGAGACAGACAGGTGCCAGACAGCCGACATCTGCACTGCTACCT | 406 |

QY 306 GTGTGGGGTCAAGGGCACTACAGAACCATCGGTGTAGTGAGCCGCCGCTACATCA 365
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Db 407 GTGTGGGGTCAAGGGCACTACAGAACCATCGGTGTAGTGAGCCGCCGCTACATCA 466
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QY 1206 GCTTGGCGGGGCTCGAGGCGCGATGTATGAGCAGACAAAGGAGAAACCTCATACCG 1265
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QY 1266 GAGACAGGGGCGTGCCTTGTGTAGCAGAACCAACGGGGGGAAGAGTGGCGGTGT 1325
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RESULT 2
US-09-305-681-3
; Sequence 3, Application US/09305681
; Patent No. 6406899
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Highly active alkaline phosphatase
; NUMBER OF SEQUENCES: 54
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/305,681
; FILING DATE:
; CLASSIFICATION:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2460 base pairs
; TYPE: nucleotide
; STRANDEDNESS: single strand
; TOPOLOGY: linear
; MOLECULE TYPE: genomic DNA
US-09-305-681-3
Query Match 90.7%; Score 1338.2; DB 4; Length 2460;
Best Local Similarity 94.4%; Pred. No. 0;
Matches 1388; Conservative 0; Mismatches 83; Indels 0; Gaps 0;
QY 6 CCTATCCCAAGTGAAGAGAAACCCCGCTTCTGTGAACCGCCAGGACCCAGCCCT 65
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Db 122 CTTCATCCCAAGTGAAGAGAAACCCCGCTTCTGTGAACCGCCAGGACCCAGCCCT 181
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QY 66 TGAATGACCAAGAGTGTGACGCGATCCAGACAGCTCCCAAGATGTCTCTTCTT 125
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Db 182 TGAATGACCAAGAGTGTGACGCGATCCAGACAGCTCCCAAGATGTCTCTTCTT 241
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QY 126 GGGGAGTGGATGGGGGTGCTTACGAGTACAGCCACTCGATCTTAAAGGGGACAGTAA 185
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Db 242 GGGGAGTGGATGGGGGTGCTTACGAGTACAGCCACTCGATCTTAAAGGGGACAGTAA 301
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QY 186 TGGCAAACTGGGACCTTGAAGACACCCCTGGCCATGGAACCAATTCCTATCGTGTCTG 245
| | | | |
Db 302 TGGCAAACTGGGACCTTGAAGACACCCCTGGCCATGGAACCAATTCCTATCGTGTCTG 361
| | | | |
QY 246 CAAAGCATACAAAGTGAAGACAGACAGTGCACAGCCAGGCACTGCACTGCTTACT 305
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Db 362 CAAAGCATACAAAGTGAAGACAGACAGTGCACAGCCAGGCACTGCACTGCTTACT 421
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QY 306 GTGTGGGGTCAAGGGCAACTACAGAACCATCGGTGTATGATGAGCGCGCTCAATCA 365
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Db 422 GTGTGGGGTCAAGGGCAACTACAGAACCATCGGTGTATGATGAGCGCGCTCAATCA 481
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QY 366 GTTGCAACACGACAGTGGGAATGAGTCACTGTGTATCAACCGGGGCCAAGAAAGCAG 425
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Db 482 GTTGCAACACGACAGTGGGAATGAGTCACTGTGTATCAACCGGGGCCAAGAAAGCAG 541
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QY 486 CCGGCACACGCTGAACCGAATCTGTACTCAGACGCGCACTGCTGTGTATGACAGAA 545
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Db 602 TGCACACACGCTGAACCGTGAATCTGTACTCAGACGCGCACTGCTGTGTATGACAGAA 661
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841 GCACCGAGGAGCCAGTATGTGTGAAACCGACGAGCTCTTTCAGGACCAATGACCC 900
QY 786 CAGTGAACACACCTGATGGGCTCTTTGAGCCGGAGACATGAATATTAATTTGACGA 845
DB 901 CAGTGAACACACCTGATGGGCTCTTTGAGCCGGAGACATGAATATTAATTTGACGA 960
QY 846 AGACCAACACCAAGACCCGACCTGGGAGATGACGAGGCGGCTTCGAAAGTGTGAG 905
DB 961 AAGACCCCAACCAAGACCCGACCTGGGAGATGACGAGGCGGCTTCGAAAGTGTGAG 1020
QY 906 CAGGAACCCCGGGGCTTTTACTCTTCTGAGGAGGAGCCGATTTGACCACTGACCA 965
DB 1021 CAGGAACCCCGGGGCTTTTACTCTTCTGAGGAGGAGCCGATTTGACCACTGACCA 1080
QY 966 TCAGCGCAAGGCTTATATGACCTGACCTGAGGAGATCATGTTGACATGACCATGGCAA 1025
DB 1081 TCAGCGCAAGGCTTATATGACCTGACCTGAGTACATGATGATTTGACATGACCATGGCAA 1140
QY 1026 GGTAAACGAGCTCATAGCGAACTGAGACAGCTGATCTTGTCTGACAGACCACTGCCA 1085
DB 1141 GGTAAACGAGCTCATAGCGAACTGAGACAGCTGATCTTGTCTGACAGACCACTGCCA 1200
QY 1086 TGTCTTCTTTTGTGCTGCTACACATCGTGGGAGCTTCATTTTGTGCTGCTGCGG 1145
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QY 1146 CAAGGCTTGAACAGAGTCTTACACCTCCATCTTATGGAATGAGCCAGGCTATGC 1205
DB 1261 CAAGGCTTGAACAGAGTCTTACACCTCCATCTTATGGAATGAGCCAGGCTATGC 1320
QY 1206 GCTTGGCGGGGCTCGAGGCCGATGTTATGACAGACAGAGGAAACCTCATATCCG 1265
DB 1321 GCTTGGCGGGGCTTAAAGCCGATGTTATGACAGACATTAAGAGAGAACCCCTCGATCCG 1380
QY 1266 GAGAGAGGCGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1325
DB 1381 GAGAGAGGCGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1440
QY 1326 GCGGAGAGGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1385
DB 1441 GCGGAGAGGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1500
QY 1386 CATCATGCGCTTGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1445
DB 1501 CATCATGCGCTTGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1560
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DB 1561 TGGCCTCTCCGACGCGCGCACCTGCGGCGC 1591

RESULT 4
US-08-867-352-20
Sequence 20, Application US/08867352
Patent No. 6060273
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Multicistronic expression units and their use
NUMBER OF SEQUENCES: 25
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25 (EPA)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/867,352
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/387,847
FILING DATE:
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:

LENGTH: 1956 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
CLONE: pSQ2-SEAP (Berger et al., 1988)
FEATURE:
NAME/KEY: CDS
LOCATION: 43..1560
OTHER INFORMATION: /note= "human SEAP gene; flanked
OTHER INFORMATION: by 5'-EcoRI and 3'-HindIII restriction cleavage
OTHER INFORMATION: sites"
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 94..1560
OTHER INFORMATION: /product= "mature protein"
PUBLICATION INFORMATION:
AUTHORS: Berger, J.
AUTHORS: Hauber, U.
AUTHORS: Hauber, R.
AUTHORS: Geiger, R.
AUTHORS: Cullen, B. R.
JOURNAL: Gene
VOLUME: 66
PAGES: 1-10
DATE: 1988
PUBLICATION INFORMATION:
AUTHORS: Millan, J. L.
JOURNAL: J. Biol. Chem.
VOLUME: 261
PAGES: 3112-3115
DATE: 1986
US-08-867-352-20

Query Match
Best Local Similarity 67.9%; Score 1002.4; DB 3; Length 1956;
Matches 1177; Conservative 0; Mismatches 291; Indels 0; Gaps 0;

QY 6 CCTCATCCAGCTGAGAGAGAAACCCGCTTCTGGAACCGCCAGGAGCCAGGCTT 65
DB 93 CATCATCCAGCTGAGAGAGAAACCCGACTTCTGGAACCGCCAGGAGCCAGGCTT 152
QY 66 TGAATGACCAAGAGTTCAGCCGATCCAGACAGCTCCAAAGATGTCATCTTCTT 125
DB 153 GGGTCCGCGCAAGAGCTGACGCTGACAGACAGCCGCAAGAACTTCATCTTCTT 212
QY 126 GGGGATGGAGTGGGGGTGCTTACGCTGACAGCCACTCGATCTTAAAGGGAGATGAA 185
DB 213 GGGGATGGAGTGGGGGTGCTTACGCTGACAGCTGACAGATCTTAAAGGGAGATGAA 272
QY 186 TGGCAACTGGACCTGAGACACCCCTGGCCATGAGCAAGTTCCATACGTGCTGTC 245
DB 273 GGAACAACCTGGGGCTGAGATACCCCTGGCCATGAGCAAGTTCCATACGTGCTGTC 332
QY 246 CAAGCATACAGCTGAGACAGAGTGCACAGCCAGCCAGGACATGCTGCTTACTT 305
DB 333 CAAGCATACAGCTGAGACAGAGTGCACAGCCAGCCAGGACATGCTGCTTACTT 392
QY 306 GTGTGGGTGCAAGGCACTACAGAACCATCGGTGTAAGTCAAGGCGCCGCTACATCA 365
DB 333 GTGTGGGTGCAAGGCACTTCCAGACATTTGCTTGAAGTCAAGGCGCCGCTTAAACA 452
QY 366 GTGCAACACGACGCTGGGAAATGAGTACGCTTGTGTATCAACCGGCTCAAGAAAGCAG 425
DB 453 GTGCAACACGACGCGGCAACGAGGTATCTCCGTATGATGGGCTCAAGAAAGCAG 512
QY 426 GAAAGCCCTGGAGTGTGACCAACCAAGGAGTGAAGATCTTCCAGGCGGGCTTA 485
DB 513 GAAAGTGGAGTGTGACCAACCAAGGAGTGAAGATCTTCCAGGCGGGCTTA 572

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|----|------|---|------|
| QY | 486 | CGCGCAACGGGTGAACCGAAACGTGATCTACAGACGCCGCACTCGCTGCTGATGCAAGAA | 545 |
| Db | 573 | CGCCCAACGGGTGAACCGCAACGTGATCTCGAAGCGCACTGCTGCTCGGCGCCGCCA | 632 |
| QY | 546 | GAATGGCTCGCAGAGCATCGCCGCGCACAGCTGGTCTCAACACATGGATATTAAGTCGTATCT | 605 |
| Db | 633 | GGAGGGGTGCCAGAGCATCGCTAAGCAGCTCATCTCCAAACATGGACATTAAGCGTATCT | 692 |
| QY | 606 | GGGTGGAGGCCGAATGTACATGTTTCCGTAGGGGGAACCCAGAACCCTGAAATACCCAGATGA | 665 |
| Db | 693 | AGGTGGAGGCCGAAGATACATGTTTCCATGGGAACCCCAAGACCTGTGTACCAAGATGA | 752 |
| QY | 666 | TGCCAGTGTGAATGGAGTCCGGGAAGACAAGAACCTGGTGCAGAAATGGCAGGCGCA | 725 |
| Db | 753 | CTACAGCCCAAGGTGGAGCAAGCTGTGACGGGAAGAAATTTGGTGCAGAAATGGCTGGGGA | 812 |
| QY | 726 | GCACCGAGGAGGCCAGTATGTGTGGAAACCGACCTGCTCTTCAGGCGGCGCATGATCTC | 785 |
| Db | 813 | GGCGCAGGGGTGCGCGGTATGTGTGAAACCGCACGTAGCTCATGCAAGGCTTCCCTGAGACC | 872 |
| QY | 786 | CAGTGTAAACACCTCATGAGGCTCTTTTGAGCCGGCAGACATGAAGTATATGTTCAACA | 845 |
| Db | 873 | GTGTGTGACCACTCATGAGGTCTCTTTGAGCCTGGAACTGAAATACGAATCTCACCG | 932 |
| QY | 846 | AGACCAACCAAGAGCCCGACCCCTGGCGGAGTGAACGAGACGGCCCTGCAGAGTGTAG | 905 |
| Db | 933 | AGACTCTCAACTGAAACCCCTCCCTGATGTAAGATGAAGAGGCTGCCCTGCGCTGTGAG | 992 |
| QY | 906 | CAGGAACCCCGGGGCTTCTACCTCTTCGTGGAAGGAGCGGCATTTGACACGGTCAACA | 965 |
| Db | 993 | CAGGAACCCCGGGGCTTCTCTCTCTTCGTGGAAGGTGTGTGCATTCAGACATGGTTCATCA | 1052 |
| QY | 966 | TGACGGCAAAAGTTATATGSGACTGACTGAGGCCATATGTTTGAACAATGCCATTCGCCAA | 1025 |
| Db | 1053 | TGAAGAAGGGGTTACCGGGCACTGACTGGAACGATCAATGTTCAACGACGGCATTTGAGAG | 1112 |
| QY | 1026 | GGCTTAACAGCTCACTAAGCACTGGAACAGCTGATCTTGTTCACCTGCAGACCACTGCCA | 1085 |
| Db | 1113 | GGCGGGCCAGCTCAACCAAGCGAAGGAACAAGCTAGCCTCGTCACTGCGACACACTCCCA | 1172 |
| QY | 1086 | TGTCCTCTCTTTGGTGGCTACACACTGCGTGGAGCCTTCATTTTCGCTTGGCCCCCGG | 1145 |
| Db | 1173 | CGTCTTCTCTTTGGAGGCTACCCCTCGAGGGAGCTCAATCTTCGGGGCTGGCCCCCTGG | 1232 |
| QY | 1146 | CAAGGCTTAAACACAGTACTTAACTCCATCTCTTAATGGCAATGGCCCAAGCTATAGC | 1205 |
| Db | 1233 | CAAGGCCCGGGAACAGAAAGGCTTACAGCTCTCTCTTAACGAAACGGTCCAGGCTAATGT | 1292 |
| QY | 1206 | GCTTGGCGGGGCTGAGAGGCCGATGTTAATATGGCAGCAACAAGCAGAAACCTCATACCG | 1265 |
| Db | 1293 | GCTACAGAACGGCGCCGCCGCGATGTTTACGAAAGCAAGACGGGAGACCCCGAGTATCG | 1352 |
| QY | 1266 | GCAGCAGGCGGCGCTGCTCTGTAGCGAAGCCACGGGGGCGAAGAGCTGGCGGTCTT | 1325 |
| Db | 1353 | GCAGCAGTACAGAGTGGCCCTTGGAAAGAAAGACCCACGCAAGGCGAGAGCTGGGCGTGT | 1412 |
| QY | 1326 | CGCGGAGAGCCCGCAGAGGGCAACTGGTGTCAACGCGCTGAGAGAGAGACCTTCGTGGCGCA | 1385 |
| Db | 1413 | CGCGGCGGCGCCGCAAGGCGCACTGTGTTCACGCGCTGACAGAGCAGACCTTTCATATGCGCA | 1472 |
| QY | 1386 | CATCATGGACTTTTGGGGGCTGCGTGGAGACCCCTTAACAACGACTGCAATTCGACAGCCCGC | 1445 |
| Db | 1473 | CGTATATGGCTTTCGCGCGCTGCTGTGAAGCTTAACAACGCGCTGTGCACCTGGGGCCCCCGC | 1532 |
| QY | 1446 | CACCGGCACACAGACTCCCGACTAGGCT | 1473 |
| Db | 1533 | CGGCACCAACGACGCGCGCGCAACCCGGGT | 1560 |

RESULT 5
US-09-693-011-12
; Sequence 12, Application US/09693011
; Patent No. 6632978

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/ GENERAL INFORMATION:
/ APPLICANT: Kaelin, Edgar
/ APPLICANT: Luyten, Marcel
/ APPLICANT: Zetves, Hans-Gunter
/ TITLE OF INVENTION: Transgenic Animals For Studying
/ TITLE OF INVENTION: Regulation Of Genes
/ FILE REFERENCE: 4-31176A
/ CURRENT APPLICATION NUMBER: US/09/693,011
/ CURRENT FILING DATE: 2000-10-20
/ NUMBER OF SEQ ID NOS: 12
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 12
/ LENGTH: 4969
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: DNA CONSTRUCT
/ US-09-693-011-12

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| Query Match | Similarity | Score | No. 00.8 | DB 4 | Length 4989 |
|--------------|--------------|---------------------------|-----------------------|-------------------------------|-------------|
| Best Local | Similarity | 80.1% | Pred. No. 8e-242 | | |
| Matches 1176 | Conservative | 0 | Mismatches 252 | Indels | Gaps 0 |
| QY | 6 | CCTCATCCCAAGCTGAGGAGGAAAA | CCCCGCGCTTCTGGA | CCGCCAGGCAAGCCCAAGCCCT | 65 |
| DB | 1134 | CATCATCCCAAGTTAGAGAGAGAA | CCCGCACTTCTGGA | CCGGAGGCAACCCAGGCCCT | 1193 |
| QY | 66 | TGATGTAGCCAAAGATTGCA | AGCCGATCCAGACAGCTGCCA | AGATATCATCTCTTCTT | 125 |
| DB | 1194 | GGGTGCGCCCAAGAACTGCA | AGCTTGCAAGACAGCCGCA | AGAACTCATCATCTTCTCT | 1253 |
| QY | 126 | GGGGATGGAATGGGGGTGCT | TAAGTGTACAGCACCTCGGAT | CTCTAAAGGGGAGAGAA | 185 |
| DB | 1254 | GGGGGATGGAATGGGGGTGCT | TAAGTGTACAGCACCTCGGAT | CTCTAAAGGGGAGAGAA | 1313 |
| QY | 186 | TGGCAATCTGGGACCTGAG | CACCCCTGGGCATGAGC | AGATCCCATACGTGGCTGTG | 245 |
| DB | 1314 | GGACAACTGGGGCTTAGAT | ACCCCTGGGCATGAGC | CGCTTCCCATATGTGGCTGTG | 1373 |
| QY | 246 | CAGAATATACACGTGAG | CAGACAGGTGCCAGAC | AGGCGAGGCACTGCACTGCTTACT | 305 |
| DB | 1374 | CAAGACATACATGTATAG | CAAAACATGTGCCAGAC | AGTGAAGCCACAGCCAGCGCTACT | 1433 |
| QY | 306 | GTGTGGGGGTCAAGGGCA | CTACAGAACCATCGTGTAT | GAATGTGACAGCGCCCGCTTACATCA | 365 |
| DB | 1434 | GTGCGGGGTCAAGGGCA | CTTCCAGAACCATTTGGCTT | GTAGTGAAGCCCGCCCGCTTTAACCA | 1493 |
| QY | 366 | GTGCAACCGACACGTGG | GAATGTGAGATCAACCGGGC | CAAGAAAGGAGG | 425 |
| DB | 1494 | GTGCAACCGACACGCGG | CAACGAGTATCTCCGTAT | GTGAATGGGCAAGAAAGGAGG | 1553 |
| QY | 426 | GAAAGCCCTGGGAATGTGT | GCACACCAACAGGGGTG | CAACATATGCTCCCGACGCGGGCTTA | 485 |
| DB | 1554 | GAAATGATGGGAATGTGT | GCATACCAACAGAGTGC | ACACGCGCTGCGACGCGCACCTTA | 1613 |
| QY | 486 | CGCGCAACGGGTGAACCG | AAACTGTGTACTAGACGCG | CACTGTCTCTGTATGCACAGAA | 545 |
| DB | 1614 | CGCCCAACGGGTGAACCG | CAACTGTGTACTAGACGCG | CACTGTCTCTGTATGCACAGAA | 1673 |
| QY | 546 | GAAATGCTGCGCAGACAT | CGCCGACAGCTGTGTAT | CAACATGTGATTTTACACGTGATCT | 605 |
| DB | 1674 | GGAGGGGTGCGCAGACAT | CGCTTACGACGCTATCT | CAACATGTGACATTTACGATGATCT | 1733 |
| QY | 606 | GGGTGGAAGCCGAATGT | ATACATGTTTCTGAGGGG | AGACCCCAAGCTTAATACCCAGATGA | 665 |
| DB | 1734 | AGGTGGAAGCCGAATGT | ATCATGTTTCCGATGGAA | CCCAAGCCCTGTAGTACCAAGATGA | 1793 |
| QY | 666 | TGCCAGTGTGAATGAAG | TCCCGAGAGCAAGACAG | AACTGAGTGAAGATGGCAGGCA | 725 |
| DB | 1794 | CTACAGCCAAAGTGGG | ACAGGCTGAGCGGAA | GAATCTGGTGTGAGGAATGTGCTGCGGAA | 1853 |
| QY | 726 | GCACCGGGAAGCCAGT | ATGTGTGGAACCGCACT | GGCTCTCTTGAAGCGGCGCATGATCT | 785 |

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Db      1854 GGCACAGGATGCCCGGTATGTGTGAACCGCACTGAGCTCATGACAGCTTCCCTGAGACC 1913
Qy      786 CAGTGTAAACACACTCATGAGGAGCTCTTTGAGCCGGCAGACATGAGATTAATGTTGACGA 845
Db      1914 GTCTGTGACCCATCTATGAGGTCTTTTGAAGCTTGAGAGACATGAATAAGAGATCCACCG 1973
Qy      846 AGACCAACACCAAGAGACCCGACCTTGCGAGATGACGAGAGCGGCCCTTGCAAGTGTGAG 905
Db      1974 AGACTCCACACTGAGACCCCTCCCTGATGAGATGACAGAGGCTGCCCTGGGCTGTGAG 2033
Qy      906 CAGGAACCCCCGGGGGTTTACTCTTCTTGAGAGGAGCCGATTTGACCAAGGTACCA 965
Db      2034 CAGGAACCCCCGGGGGTTTCTCTCTTGAGAGGAGGTGATGACCATGAGTATGA 2093
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Qy      1026 GGCTAAAGAGCTCACTAGCGAATGGAACGCTGATCTTGTCTACCTGACAGACCACTCCCA 1085
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Qy      1086 TGTCTTCTCTTTTGTGTGCTACACACTGCTGTGAGGAGCTCTCATTTTGGTCTGCCCCG 1145
Db      2214 CGTCTTCTCTCTTGTGAGGCTACCCCTGCGAGGAGCTCATCTTGTGGCTGGCCCCCTG 2273
Qy      1146 CAAGGCTTAGACAGAGAGTCTTACACTCATCTCTTATGGAATGAGCCAGGCTATG 1205
Db      2274 CAAGGCTTGGAGAGAGAGGCTTACACGAGTCTCTCTATACGAGAAAGGCTCAGGCTATG 2333
Qy      1206 GCTTGGCGGGGCTCGAGGCGCGAGTGAATGAGCAGACAGAGAGAAACCTCATATCG 1265
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Qy      1266 GAGAGAGGCGCGCTGCGCTGCTGCTAGCAGAACCCAGCGGGCGAGAAAGTGGCGGT 1325
Db      2394 GAGAGAGTGAAGAGTCCCTGAGCAGAAAGCCAGCGAGAGAGAGTGGCGGTGT 2453
Qy      1326 CGCGGAGGCGCGCAGAGCGCACCTGTGTGACGAGCGGTGAGAGAGACCTTGTGTGCGCA 1385
Db      2454 CGCGGCGCGCGCGCAGAGCGCACCTGTGTGACGAGCGGTGAGAGAGACCTTGTGTGCGCA 2513
Qy      1386 CATCATGCGCTTTTGGCGGCTGTGTGAGGCTTACACCGACTGCAATCTGCCAGCCCCG 1445
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RESULT 6
US-09-693-011-11

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; Sequence 11, Application US/09693011
; Patent No. 6632978
; GENERAL INFORMATION:
; APPLICANT: Kaslin, Edgar
; APPLICANT: Luyten, Marcel
; APPLICANT: Ziermes, Hans-Gunter
; TITLE OF INVENTION: Regulation Of Genes
; FILE REFERENCE: 4-31176A
; CURRENT APPLICATION NUMBER: US/09/693,011
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 5083
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: DNA CONSTRUCT
US-09-693-011-11
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Query Match 67.8%; Score 1000.8; DB 4; Length 5083;
Best Local Similarity 80.1%; Pred. No. 8e-242;
Matches 1176; Conservative 0; Mismatches 292; Indels 0; Gaps 0;

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Qy      6 CCTCATCCGAGTGAAGAGAAACCCCGCTTCTTGAAACCGCCAGGACCCAGCCCT 65
Db      1134 CATCATCCGAGTGAAGAGAAACCCCGACTTCTGAAACCGCCAGGACCCGAGCCCT 1193
Qy      66 TGATGAGCAAGAGTGTGAGCCGATCCAGACAGCTCCCAAGATGATCTCTTCT 125
Db      1194 GGTGTCGCAAGAGCTGCAAGCTTCAACAGACAGCCGCAAGAACTTATATCTTCT 1253
Qy      126 GGGGAGTGGAGTGGGGGTGCTTACCGTGAACGCCACTCGATCTTAAAGGGCAGATGA 185
Db      1254 GGGGAGTGGAGTGGGGGTGTCTAGGTGACAGCTCCAGGATCTTAAAGGGCAGAG 1313
Qy      186 TGGCAAACTGGGACTTGAAGACACCCCTGAGCAAGGACCAAGTCCCATACGTGTCTC 245
Db      1314 GGAACAACCTGGGGCTGAGATACCCCTGGCCATGAGACCGCTTCCATATGTGTCTGTG 1373
Qy      246 CAAGACATACAACTGAGCAAGACAGGTGCGAGACAGCCAGGCACTGCACTGCTACT 305
Db      1374 CAAGACATACAACTGAGCAAGACAGGTGCGAGACAGCCAGGCACTGCACTGCTACT 1433
Qy      306 GTGTGGGTCAAGGGCACTACAGAACCATGCTGTATGAGTGAAGCGCCGCTACATCA 365
Db      1434 GTGGGGGTCAAGGGCACTTCCAGACCATTTGTGTGATGAGTGAAGCGCCGCTTAAACA 1493
Qy      366 GTGCAACAGACAGTGGGAATGAGTGAAGTCTGTGTATCAACGGGCGCAAGAAAGCAG 425
Db      1494 GTGCAACAGACAGTGGGCAAGAGTATCTCCCTGTATGATCGGGCGCAAGAAAGCAG 1553
Qy      426 GAAAGCGTGGGAGTGTGACACCAAGGTTGAGATGCTCCAGCGGGGCTCA 485
Db      1554 GAAAGTGTGGGAGTGTGACACCAAGGTTGAGATGCTCCAGCGGGGCTCA 1613
Qy      486 CGCGCACAGGTGAACCGAACTGTACTACAGACCGCACCTGCTGTGATGACAGAA 545
Db      1614 CGCGCACAGGTGAACCGCAACTGTACTCCGAGCGCGACCTGTGCTGGGCCGCA 1673
Qy      546 GAATGCTGCGAGACATGCGCGACAGCTGCTTCAACAATGATATTGACGTATCT 605
Db      1674 GAGAGGGGTGCGAGGACATGCTTACAGCAGCTATCTCAAAATGACATTTGACGTATCT 1733
Qy      606 GGGTGAAGCGGAATGATGTTTCTGAGGGGAGCCGCAACCTGAAATCCAGATGA 665
Db      1734 AGGTGAAGCGGAATGATGTTTCTGAGGGGAGCCGCAACCTGAAATCCAGATGA 1793
Qy      666 TGCCAGTGTGAATGAGTCCGGAAGAGCAAGACAGAACTGTGTGAGAAATGAGCAGGCGCA 725
Db      1794 CTACAGCAAGTGTGAGACAGGCTGAGCGGGAAGAAATGTGTGAGAAATGAGCAGGCGCA 1853
Qy      726 GCAACCAAGAGCCAGATATGTGTGAGACCGCATGCGCTCTTCAAGGCGCGATGATC 785
Db      1854 GCGCCAGGAGTCCCGATATGTGTGAGACCGCATGAGCTCATGAGGCTTCCCTGAGACC 1913
Qy      786 CAGTGTAAACACCTCATGAGGCTCTTGAAGCCGCGACATGAAGTAAATGTTACGA 845
Db      1914 GTCTGTACCACTCATGAGGCTCTTGAAGCTTGAAGACATGAATACGAGATCCACG 1973
Qy      846 AGACCAACCAAGAGACCCGACCTTGCGAGATGACGAGGCGGCTTGAAGTGTGAG 905
Db      1974 AGACTCCACACTGAGACCCCTCCCTGATGAGATGACAGAGGCTGCCCTGGGCTGTAG 2033
Qy      906 CAGGAACCCCCGGGGGTTTCTCTTCTTGAGAGGAGGCGCATTTGACAGCGTACCA 965
Db      2034 CAGGAACCCCCGGGGGTTTCTCTTCTTGAGAGGAGGCTGCACTGAGCTATCA 2093
Qy      966 TGACGGCAAGCTTATATGAGACTGAGAGGCAATCATGTTTGAACATGCAATGCGCA 1025
Db      2094 TGAAGCAGAGGCTTACCGGAGCTGACTGAGACGATCATGTTTGAACGAGCCATTGAGAG 2153
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| | | | |
|----|------|---|------|
| OY | 1026 | GGCTTACAGAGCTCACTTACGMAACTGTGACACCGGTATCTTTGACTGTGAGACAACCTCCA | 1085 |
| Db | 2154 | GCGGGGCAGAGCTCACCAAGCGAGAGSACAAGCTAGAGCTTCGTCACTGCGACACTGCCA | 2213 |
| OY | 1086 | TGTCCTTCCTTTTGGTGGCTACACACTGCGTGGAGCTCCATTTTTCGGTCTGGCCCCGG | 1145 |
| Db | 2214 | CGTCCTTCCTTCGGAGGAGCTACCCCTCGAGAGGAGCTCCATCTTCGGGGCTGGCCCCGG | 2273 |
| OY | 1146 | CAAGGCCCTTACACAGCAGTGCCTTACACTCCATCTCTATATGGCAATGGCCCCAGGCTATGC | 1205 |
| Db | 2274 | CAAGGCCCGGAGACGAAAGGCTCTACCGGTCTCTTATACGAAACGATCCAGAGCTATGT | 2333 |
| OY | 1206 | GCTTGGCGGGGGCTCGAGGCCGATGTTTATATGCGACACAAGCGAGAACTCTCATACG | 1265 |
| Db | 2334 | GCTCAGAGACGGGCGCGCGCGGAGTGTACCGAAGACGACAGCGGAGACCCCGAGTATCG | 2393 |
| OY | 1266 | GCAGCAGCGCGCGCGTGGCTTCGTCTAGCGAGACCCAAGGGGGCGAAGACGTGGCGGTGT | 1325 |
| Db | 2394 | GCAGCAGTCACACAGTGGCCCTTGGACGAAAGAACCCACCAAGCGCGGAGACGTGGCGGTGT | 2453 |
| OY | 1326 | CGCGGAGAGGCCCGACAGGGCGACCTGTGTACAGGCGGTGAGAGGAGACCTTCGTGGCGCA | 1385 |
| Db | 2454 | CGCGGCGGGCCCGACAGGCGCACCTGTGTACAGGCGGTGAGAGACGACCTTTCATATGCCCA | 2513 |
| OY | 1386 | CATCATGGCCTTTTGGGGCTGTGTGAGACCTTACACCGACTTGCAATCTGCAGGCCCGGC | 1445 |
| Db | 2514 | CGTCATGGCCTTTTCGCGCGCTGTGAGACCTTACACCGCTGCGACTGTGGGCCCGCGC | 2573 |
| OY | 1446 | CACGCGCCACAGCATCCCGGACTAGGTT | 1473 |
| Db | 2574 | CGGCACACCGACGCGCGCACCGCGGT | 2601 |

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RESULT 7
; US-09-932-581-25
; Sequence 25, Application US/09932581
; Patent No. 6686159
; GENERAL INFORMATION:
; APPLICANT: Andrews, William H.
; APPLICANT: Foster, Christopher A.
; APPLICANT: Fraser, Stephanie
; APPLICANT: Mohammadpour, Hamid
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR MODULATING
; TITLE OF INVENTION: TELOMERASE REVERSE TRANSCRIPTASE (TERT) EXPRESSION
; FILE REFERENCE: SIER-005
; CURRENT APPLICATION NUMBER: US/09/932,581
; CURRENT FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: 60/227,865
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: 60/230,174
; PRIOR FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: 60/238,345
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 5928
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic expression plasmid
; US-09-932-581-25

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| | | | | |
|-----------------------|--------------|--|----------------|-------------|
| Query Match | 67.8% | Score 1000.8 | DB 4 | Length 5928 |
| Best Local Similarity | 80.1% | Pred. No. 8,4e-242 | | |
| Matches 1176 | Conservative | 0 | Mismatches 292 | Indels 0 |
| | | | Gaps | 0 |
| QY | 6 | CCTCATCCAGCTGAGAGAAACCCGCTTTCTGGAACCGCAGCAGCCAGCCCT | 65 | |
| DB | 358 | CATCATCCAGTTGAGAGAGAACCCGACCTTCTTGGAACCGCAGCAGCCAGCCCT | 417 | |
| QY | 66 | TGATTTAGCCAAAGTTGCAAGCCATCAGCAGCTGCCAAGATGTCATCTCTTCTT | 125 | |

| | | | |
|---|------|---|------|
| D | 418 | GGGTGGCGCCAAAGAGCTGCGAGCCTGGACAAGACGCGCCAAAGAACTCATCATCTTCT | 477 |
| Q | 126 | GGGGGATGGATGGGGGGTGGCTTACGTGTGACAGCACTTCGATCTCTAAAGGGGCAAGTAA | 185 |
| D | 478 | GGGGCATGGATGGGGGTGTCTTACGTGTGACAGCTCCAGATCTCTAAAGGGGCAAGAA | 537 |
| Q | 186 | TGGCAATGGGACCTTGACACCCCTGGCCATGTGAACCATGCCATTCAGTGGGCTGTG | 245 |
| D | 538 | GGACAACTGGGGGCTTGAGATACCTTCGGCCATGGACCGCTTCCCATATGTGGCTGTG | 597 |
| Q | 246 | CAAGACATACACGTGTGACAGACAGGTGTCCAGACAGCGCAGGCACTGCTTACT | 305 |
| D | 598 | CAAGACATACATGTGAACAACATGTGTCCAGACAGTGTGAACCAAGCAAGGCTTACT | 657 |
| Q | 306 | GTGTGGGTCAAGGGCAACTACAGAACCATGTGTGTATGTGACAGCCGCGCTTCAATCA | 365 |
| D | 658 | GTGCGGGGTCAAGGGCAACTTCCAGACCAATTGGCTTGTAGTCAAGCCGCGCTTAAACA | 717 |
| Q | 366 | GTGCAACACGACACTGTGGAAATGAGTTCACGTCTGTATCAACCGGGCCAAAGAAAGAG | 425 |
| D | 718 | GTGCAACACGACAGCGCGGCAAGAGTTCATCTCGTATGTAAATGGGCAAGAAAGCAG | 777 |
| Q | 426 | GAAAGCCCTGGGAGTGTGTGACCAACAACAAGGGTACAGATATCCCGAGCGGGGCTTA | 485 |
| D | 778 | GAAGTCAATGGGAATGTGTAAACCAACAACAAGTGTACAGACGCTTCGCAAGCGGCACTTA | 837 |
| Q | 486 | CGCGCAACGGTGAACCGAAATGTGTATCTAGACGCGGACCTGCTGTCTGTACAGAA | 545 |
| D | 838 | CGCCCAACGGTGAACCGCAACTGTACTGGACGCGGACGTGCTGTGCGCGCCGCA | 897 |
| Q | 546 | GAAATGCTGTCCAGGACATCGCCGACAGTGTGTCTTACAACATGTGATATTGACGTGATCT | 605 |
| D | 898 | GGAGGGGTGTCCAGGACATCGTACAGAGCTCATCTTCMAACATGTGACATYGCATGATCT | 957 |
| Q | 606 | GGGTGGAGGGCCGAATGTATCATGTTCCTGAGGGGAGCCCAAGACCTGTGATACCAATGA | 665 |
| D | 958 | AGGTGAGAGCCGAAGTATCATGTTCCTGATGTGAAACCCCAAGACCTGTGATACCAATGA | 1017 |
| Q | 666 | TGCCAGTGTGATGTGAGTCCGGAAGGACAAGACAGAACCTGTGTGAGGATGTGGAGCCCA | 725 |
| D | 1018 | CTACAGCCAGATGTGGACACAGGCTGTGAGCGGAAACATCTGTGTGAGGATGTGGTCGGA | 1077 |
| Q | 726 | GCACCAAGGAGCCCAATGTGTGTGAAACCGCACTGCGCTCTTACAGCGGCGGATGACTC | 785 |
| D | 1078 | GCGCAGAGGTGTCCCGGTATGTGTGAAACCGCACTGAGCTCATGTGACGCGCTTCCGTGACC | 1137 |
| Q | 786 | CAGTGTACAACTCATGTGGGCTCTTTGAGCCGCGGACGACATGTAAATATATGTTTACGA | 845 |
| D | 1138 | GTCGTGTGACCATCTCATGTGGGTCTCTTTGAGCCTGTGAGACATGTAAATTCGATTCACCG | 1197 |
| Q | 846 | AGACCAACCAAGAGACCCGACCTGTGGGAGATGTACGGAAGCGGCGCTGTCAAGTGTGAG | 905 |
| D | 1198 | AGACTTCACACTGGAACCTCTCTCTGTATGTGAATATACAGAGGCTGCTGCGGCTGTGAG | 1257 |
| Q | 906 | CAGAAACCCCGGGGCTTTCATCTTTCGTGTGAGGAGGCGCGATTGACACAGGTCACCA | 965 |
| D | 1258 | CAGAAACCCCGGGGCTTCTCTCTCTGTGTGAGGGGTGTGTGACATGACATGTGTATCA | 1317 |
| Q | 966 | TGACGGCAAACTTATATGTGCACTGTGAGGCGATATATGTTTGAACATGTCCATTCGCCA | 1025 |
| D | 1318 | TGAAGAAGAGGGCTTATCCGGGCACTGACTGTGAGCATATGTTGTGACAGACGCAATTTGAG | 1377 |
| Q | 1026 | GGCTTACGAGCTCACTAGCGAATGTGACACGCTATCTTGTCACTGACAGACCACTGCCA | 1085 |
| D | 1378 | GGCGGGCAGCTTACACAGCGAGGAGGACAGCTTGAAGCTGTCACTGCGCACCACTGCCA | 1437 |
| Q | 1086 | TGTCCTCTCTTTGTGTGTGACACACTGTGCGTGTGGACCTTCAATTTTGTGCTGTGCCCCG | 1145 |
| D | 1438 | CGTCTTCTCTCTGTGGAAGTACACCCCTGTGAGGGAGCTTCAATCTTTGGGGTGTGCCCCGTG | 1497 |
| Q | 1146 | CAAGGCTTGAACAGCAATGTCTTACACTCATCTTCTTATGTGCAATATGGCCCAAGGCTATGC | 1205 |
| D | 1498 | CAAGGCTTGAACAGCAATGTCTTACAGGTCCTCTTATGTGGAACAGGTCACAGGCTATGT | 1557 |

Db 2587 CGGCACACCGGCGCGCGGCGGT 2614

RESULT 9

US-09-693-011-9
; Sequence 9, Application US/09693011
; Patent No. 6632978
; GENERAL INFORMATION:
; APPLICANT: Kaelin, Edgar
; APPLICANT: Luyten, Marcel
; APPLICANT: Zewes, Hans-Gunter
; TITLE OF INVENTION: Transgenic Animals For Studying
; TITLE OF INVENTION: Regulation Of Genes
; FILE REFERENCE: 4-31176A
; CURRENT APPLICATION NUMBER: US/09/693,011
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 6408
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: TARGETING SEQUENCE
US-09-693-011-9

Query Match 67.8%; Score 1000.8; DB 4; Length 6408;
Best Local Similarity 80.1%; Pred. No. 8.7e-242;
Matches 116; Conservative 0; Mismatches 292; Indels 0; Gaps 0;

QY 6 CCTCATCCCGAGCTGAGAGGAAAAACCCCGCTTGTGAAACCGGCAAGCCAGGCGCT 65
DB 1147 CATCATCCCGAGCTGAGAGGAAAAACCCCGCTTGTGAAACCGGCAAGCCAGGCGCT 1206
QY 66 TGAATAGCCCAAGATTGTCAGCCGATCCAGACAGCTGCGCAAGATTCATCTCTTCT 125
DB 1207 GGGTCCGCGCAAGAGTGTGAGCTGTGACAGACAGCCGCGCAAGATTCATCTCTTCT 1266
QY 126 GGGGAGTGGAGTGGGGTGTCTACGCTGACAGCCACTCGGATCTTAAAGGGGAGATGA 185
DB 1267 GGGGAGTGGAGTGGGGTGTCTACGCTGACAGCCACTCGGATCTTAAAGGGGAGATGA 1326
QY 186 TGGCAAACTGGGACCTGAGACACCCCTGGGCAATGACCAATTCCTAGTGTCTCTGTC 245
DB 1327 GGAACAACTGGGACCTGAGATACCCCTGGGCAATGACCAATTCCTAGTGTCTCTGTC 1386
QY 246 CAAGACATACCAAGTGTGACAGAGTGTGACAGAGCGAGGCACTGCGCTTACCT 305
DB 1387 CAAGACATACCAAGTGTGACAGAGTGTGACAGAGCGAGGCACTGCGCTTACCT 1446
QY 306 GTGTGGGGTCAAGGGCACTACAGAACATCGGTGTAAGTGCAGCCGCGCTTACATCA 365
DB 1447 GTGTGGGGTCAAGGGCACTTCCAGAACATTTGGCTTGAAGTGCAGCCGCGCTTAAACA 1506
QY 366 GTTCAACACGACAGTGGGATGAGTCACTGTGTATCAACCGGGCCAAAGAGAGG 425
DB 1507 GTTCAACACGACAGTGGGATGAGTCACTGTGTATCAACCGGGCCAAAGAGAGG 1566
QY 426 GAAGGCGGTGGAGTGTGACACACAGGATGTGACATGCTCCCGGCGGCGCT 485
DB 1567 GAAGTGTGGAGTGTGACACACAGGATGTGACATGCTCCCGGCGGCGCT 1626
QY 486 CGGCAACAGGTGAACCGAAATGTGATCTGAGACCGGCACTGCTGTATGACAGAA 545
DB 1627 CGGCAACAGGTGAACCGAAATGTGATCTGAGACCGGCACTGCTGTATGACAGAA 1686
QY 546 GAATGCTGTGACAGACATGCGCGCACTGCTGTATGACATGATTTGACGTGATCT 605
DB 1687 GAGGGGTGTGACAGACATGCTGTGACAGCTGTATGACATGATTTGACGTGATCT 1746
QY 606 GGGTGAAGCGGATGTGACATGTTTCTGTAGGGGACCGGCACTGATACCAAGATGA 665

Db 1747 AGGTGAGGCGGAAAGTATGTTTGTGATGGGAAACCCAGACCTGTAGTACCAATGA 1806
QY 666 TGGCATGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 725
DB 1807 CTACAGCCAAAGGTGGAGCAGGCTGAGGAGGAAATGTGTGACAGAAATGTGTGAGAA 1866
QY 726 GCACAGGAGGCCAGTATGTGTGAAACCGCACTGCGCTCTTCAAGGCGGCGATGATCT 785
DB 1867 GCGCCAGGAGTGGCGGATGTGTGAAACCGCACTGAGTGTATGACAGGCTTCCCTGAGACC 1926
QY 786 CAGTGTACACACTGTATGAGGCTCTTTGAGCCGCAAGATGATATGTTTACGA 845
DB 1927 GTCTGTAGCCACTCATGAGGTCTTTGAGCTGTGAGCATGATGATGATGATGATGATG 1986
QY 846 AGACCAACCAAGAGACCCGAGCTGCGGAGATGAGAGGCGGCGCTGCAATGCTGAG 905
DB 1987 AGACTCACACTGAGACCCCTCTGATGAGATGAGAGAGGCTGCGCTGCTGCTGAG 2046
QY 906 CAGAAACCCCGGGGCTTCTACCTCTTGTGAGGAGGCGGCGATGACCAAGGTCACCA 965
DB 2047 CAGAAACCCCGGGGCTTCTTCTCTTGTGAGGAGGCTGCGATGACCAATGATCA 2106
QY 966 TGAAGCAAGCTTATATGACACTGATGAGGAGTATGTTGACATGCTATGCGCA 1025
DB 2107 TGAAGCAAGGCTTATATGAGCACTGATGAGGAGTATGTTGACATGCTATGAGAG 2166
QY 1026 GGTAAACAGCTTATGAGCACTGATGAGGAGTATGTTGACATGCTATGCGCA 1085
DB 2167 GGGGAGGAGCTTATGAGCACTGATGAGGAGTATGTTGACATGCTATGCGCA 2226
QY 1086 TGTCTTCTTGTGAGGCTTATGAGCACTGATGAGGAGTATGTTGACATGCTATGCGCA 1145
DB 2227 GGTCTTCTTGTGAGGCTTATGAGCACTGATGAGGAGTATGTTGACATGCTATGCGCA 2286
QY 1146 CAGGCTTATGAGCACTGATGAGGAGTATGTTGACATGCTATGCGCA 1205
DB 2287 CAGGCTTATGAGCACTGATGAGGAGTATGTTGACATGCTATGCGCA 2346
QY 1206 GCTTGGCGGGGCTGAGGCGGATGTTATGAGCACTGATGAGGAGTATGCGCA 1265
DB 2347 GCTTGGCGGGGCTGAGGCGGATGTTATGAGCACTGATGAGGAGTATGCGCA 2406
QY 1266 GCAGAGGCGGCGGCTTATGAGCACTGATGAGGAGTATGCGCA 1325
DB 2407 GCAGAGTATGAGCACTGATGAGGAGTATGCGCA 2466
QY 1326 CGGCGAGGCGGCGGCTTATGAGCACTGATGAGGAGTATGCGCA 1385
DB 2467 CGGCGAGGCGGCGGCTTATGAGCACTGATGAGGAGTATGCGCA 2526
QY 1386 CATCATGCGCTTGTGCGGCTGCGGAGTATGAGCACTGATGAGGAGTATGCGCA 1445
DB 2527 CATCATGCGCTTGTGCGGCTGCGGAGTATGAGCACTGATGAGGAGTATGCGCA 2586
QY 1446 CACCGGCAACGATGCGGAGTATGAGCACTGATGAGGAGTATGCGCA 1473
DB 2587 CGGCACACCGGCGCGCGGCGGT 2614

RESULT 10

US-09-837-863-20
; Sequence 20, Application US/09837863
; Patent No. 6468754
; GENERAL INFORMATION:
; APPLICANT: Greene, Amy
; APPLICANT: Zhou, Hua
; APPLICANT: Thode, Silke
; APPLICANT: Jarnigan, Kurt
; TITLE OF INVENTION: Vector and Method for Targeted Replacement and Disruption
; FILE REFERENCE: 025.1US
; CURRENT APPLICATION NUMBER: US/09/837,863
; CURRENT FILING DATE: 2001-04-17

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; PRIOR APPLICATION NUMBER: US 60/198,498
; PRIOR FILING DATE: 2000-04-18
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 20
; LENGTH: 7076
; TYPE: DNA
; ORGANISM: vector
US-09-837-863-20

Query Match      67.8%; Score 1000.8; DB 4; Length 7076;
Best Local Similarity 80.1%; Pred. No. 9e-242;
Matches 1176; Conservative 0; Mismatches 292; Indels 0; Gaps 0;

QY 6 CCTCATCCAGCTGAGAGGAAACCCGCTTCTGAAACCCGCGAGGAGCCGACCT 65
Db 1349 CATCATCCAGTTGAGAGAGAGAACCCGACTTCTGAAACCCGAGGAGCAGCCGACCT 1408

QY 66 TGATGTAGCCAGAAAGTTGACGCGATCCAGACAGCTGCCAAGATGTCACTCTTCTT 125
Db 1409 GGGTGGCGCCAGAAAGCTGACGCTGACAGACAGCGCCAGAAACCTCATCTTCTCT 1468

QY 126 GGGGGATGGAGTGGGGGTGCTTACGGGTGACAGCACTCCGATCTTAAAGGGGAGATGA 185
Db 1469 GGGCGATGGAGTGGGGGTGCTTACGGGTGACAGCTCCAGATCTTAAAGGGGAGAGAA 1528

QY 186 TGGCAAACTGGGACTGAGACACCCCTGGCATGAGACCAATTCCATAGTGGCTGTTC 245
Db 1529 GGAAGAACTGGGGCTCGAGATACCCCTGGCATGAGACCCCTTCCATATGTGGCTGTTC 1588

QY 246 CAAGACATTCACAGTGGACAGACAGGTGCCAGACAGCGACGACCTTGCCTTACCT 305
Db 1589 CAAAGACATTCACAGTGGACAAACATGTGCCAGACAGTGGAGCCACAGCCGCTTACCT 1648

QY 306 GTGTGGGGTCAAGGGCACTACAGAACATCGGTGTAAAGTGAACCGCCGCGCTACAAATCA 365
Db 1649 GTGTGGGGTCAAGGGCACTTCCAGAACATGTGTGAAGTGAACCGCCGCGCTTAAATCA 1708

QY 366 GTGCAACACGACAGCTGGAGATGAGGTCACTGTGTATCAACCGGGCCAAAGAACAG 425
Db 1709 GTGCAACACGACAGCTGGGGACAGAGGTCACTGTGTATGAAATCGGGCCAAAGAACAG 1768

QY 426 GAAAGCCGTGGAGTGTGTACCAACCAAGGTGACGATGCTTCCCAAGCCGGGGCTTA 485
Db 1769 GAAAGTCAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1828

QY 486 CGCGCACAGGTGAACCGAACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 545
Db 1829 CGCGCACAGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1888

QY 546 GAATGGCTGCGACGACATGCGCGCACAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 605
Db 1889 GGAAGGGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1948

QY 606 GGGTGAAGCCGAAATGTATATTTTCTTGAAGGGAGCCCAAGACCTGAAATCCAGATGA 665
Db 1949 AGGTGAAGCCGAAAGTATATCTTTCGATGTGGAACCCCAAGACCTGATATCCAGATGA 2008

QY 666 TSCCATGTGAATGAGTCCGAGAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 725
Db 2009 CTACAGCCAGAGTGGAGCAAGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2068

QY 726 GCACCAAGGAGCCAGATATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 785
Db 2069 GCGCCAGAGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2128

QY 786 CAGGTGAACACCTTCATGTGGGCTCTTTTGAAGCCGCGACAGATGAAGTATATGTTCAGCA 845
Db 2129 GTCTGTGACCATTCATGTGGGCTCTTTTGAAGCCGCGACAGATGAAGTATATGTTCAGCA 2188

QY 846 AGACCAACCAAGAGCCCGAGCTGGCGGAGTGAACGAGGGGGGGCTGGCAAGTGTCTAG 905
Db 2189 AGATCTCAACACTGTGACCTCTCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2248
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QY 906 CAGAAACCCCGGGGCTTCTAACCCTTGTGTGAGGAGGAGCGCATTTGACCAAGGTACCA 965
Db 2249 CAGAAACCCCGGGGCTTCTTCTTCTTGTGTGAGGAGGTGTGTGTGTGTGTGTGTGTGTGT 2308

QY 966 TGACGGCAAGGCTTATATGCACTGATGAGCGATCATGTTTGAACATGCGCATGCCAA 1025
Db 2309 TGAAGACAGGGCTTACCGGGGCACTGATGAGCATGATGTTTGCAGACGCGCATTTGAGAG 2368

QY 1026 GGTACAGAGCTCACTACAGAACTGAGACAGCTGTATCTTGTTCATGTGACAGACATCCCA 1085
Db 2369 GGGGAGGAGCTCACTACAGAGAGAGAGACAGCTGTAGCTTGTCACTGTGCGACACTCCCA 2428

QY 1086 TGTCTTCTCTTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1145
Db 2429 GGTCTTCTCTTCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2488

QY 1146 CAAGGCTTTAGACAGCAAGTCTTACACCTCCATCTTATGTGCAATGGCCAGGCTATGC 1205
Db 2489 CAAGGCTTTAGACAGCAAGGCTTACACCGTCTCTTATACGAAACGGTCCAGGCTATGT 2548

QY 1206 GCTTGGCGGGGCTGAGAGCGCCGATGTATATGTGACACCAAGCGAGAACCCCTCATACG 1265
Db 2549 GCTTGAAGACGCGCGCCGCGATGTATATGTGACAGAGCGAGAGCGGAGCCCGAGTATGC 2608

QY 1266 GCAGCAGGCGGCGCTGCGCTTGTGCTGAGAGACCAAGGGGGCGAAGAGCTGTGCTGTG 1325
Db 2609 GCAGCAGTGTGAGAGTGTGCTTGTGAGAGAGAACCAAGCGAGAGCTGTGCTGTG 2668

QY 1326 CGCGGAGGCGCGGAGCGGACCTGTGTGACAGCGGTGAGAGAGAGACCTTGTGTGTGCGCA 1385
Db 2669 CGCGGCGGCGCGGAGCGGACCTGTGTGACAGCGGTGAGAGAGAGACCTTGTGTGTGCGCA 2728

QY 1386 CATCATGCGCTTTTGGGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1445
Db 2729 CATCATGCGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2788

QY 1446 CACCGCACAGCAATCCCGGACTAGGCT 1473
Db 2789 CCGGACACAGCAAGCGCGGCGGCGGCT 2816

RESULT 11
US-09-837-863-21
; Sequence 21, Application US/09837863
; Patent No. 6468754
; GENERAL INFORMATION:
; APPLICANT: Greene, Amy
; APPLICANT: Zhou, Hua
; APPLICANT: Thode, Silke
; APPLICANT: Jarnigan, Kurt
; TITLE OF INVENTION: Vector and Method for Targeted Replacement and Disruption
; FILE REFERENCE: 025.1US
; CURRENT APPLICATION NUMBER: US/09/837,863
; PRIOR FILING DATE: 2001-04-17
; PRIOR APPLICATION NUMBER: US 60/198,498
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 21
; LENGTH: 7076
; TYPE: DNA
; ORGANISM: vector
US-09-837-863-21

Query Match      67.8%; Score 1000.8; DB 4; Length 7076;
Best Local Similarity 80.1%; Pred. No. 9e-242;
Matches 1176; Conservative 0; Mismatches 292; Indels 0; Gaps 0;

QY 6 CCTCATCCAGCTGAGAGGAAACCCGCTTCTGAAACCCGCGAGGAGCCGACCT 65
Db 1349 CATCATCCAGTTGAGAGAGAGAACCCGACTTCTGAAACCCGAGGAGCAGCCGACCT 1408
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QY 66 TGATGAGCAAGATTGCGCGCATCCAGACAGCTGCCAAGATGTCCTCTTCT 125
 DB 1409 GGGTGGCCGCAAGAGTTGAGCTTGCAACAGACGCGCCAAAGAACTCATCTTCT 1468
 QY 126 GGGGATGGGATGGGGGTGCTTACCGGTGACAGCCACTCGATCTTAAAGGGGAGATGA 185
 DB 1469 GGGCGATGGGATGGGGGTGTCTACGGTGAACAGCTGCAGGATCTTAAAGGGGAGAA 1528
 QY 186 TGGCAAACTGGGACCTGAGACACCCCTGGCCATGAGCAAGTCCCATACGTGCTGTG 245
 DB 1529 GGCAAACTGGGGCTGAGATACCCCTGGCCATGAGCAAGCTTCCCATATGTGCTGTG 1588
 QY 246 CAAGACATTCAGTGGAGAGAGAGGAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGG 305
 DB 1589 CAAGACATTCAGTGGAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1648
 QY 306 GTGTGGGGTCAAGGGGCACTACAGAAACCATCGGTGTAAAGTGCAGCGCCCGCTACATCA 365
 DB 1649 GTGTGGGGTCAAGGGGCACTTCCAGAACATTTGGCTTGAAGTGCAGCGCCCGCTTAAACA 1708
 QY 366 GTTCAACAGCACAGTGGGATAGGTCACTGTGTATCAACCGGGCCAAAGAAAGAG 425
 DB 1709 GTTCAACAGCACAGTGGGATAGGTCACTGTGTATCAACCGGGCCAAAGAAAGAG 1768
 QY 426 GAAAGCGGTGGGATGTGACCAACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 485
 DB 1769 GAAAGCGGTGGGATGTGACCAACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1828
 QY 486 CGCGCACAGCGTGAACCGAAACTGTGTACTGACAGCGGACCTGCTGTATGACAGAA 545
 DB 1829 CGCGCACAGCGTGAACCGCACTGTGTACTGACAGCGGACCTGCTGTATGACAGAA 1888
 QY 546 GAAAGCTGTGACAGACATGCGCCGACAGCTGTGTCAACATGATGATTTGACGTGTCT 605
 DB 1889 GAGGGGTGTGACAGACATGCGCTACGACGCTCATCTCAACATGATGATTTGACGTGTCT 1948
 QY 606 GGGTGGAGCGGATGTATCACTGTTCTGAGGGGAGGAGGAGGAGGAGGAGGAGGAGG 665
 DB 1949 AGGTGGAGCGGATGTATCACTGTTCTGAGGGGAGGAGGAGGAGGAGGAGGAGGAGG 2008
 QY 666 TGGCAGTGTGATGAGTCCGAGAGCAAGACAACTGTGTGACAGGATGAGGAGGAG 725
 DB 2009 CTACAGCCCAAGGTGGAGCAAGGCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2068
 QY 726 GCAACAGGAGCCCAATGTGTGAAACGCACTGCGCTCTTCAAGCGGCGGATGATCTC 785
 DB 2069 GCGCCAGGAGCCCAATGTGTGAAACGCACTGAGCTCATGAGGCTTCCCTGAGACC 2128
 QY 786 CAGTGTAAACACACTGAGGCTCTTTGAGCGGAGAGACATGATGATTAATGTTACGA 845
 DB 2129 GTCTGTGACCACTTATGAGGTCTTTGAGCCTGAGAGATGATTAATGATGATGATG 2188
 QY 846 AGACACACCAAGAGACCCGACCTTGGAGAGATGACGAGAGCGGCGCTGCAAGTGTGAG 905
 DB 2189 AGACACACCAAGAGACCCCTCTGATGAGATGACGAGAGCTGCGCTGCGCTGTGAG 2248
 QY 906 CAGGAACCCCGGGGCTTCTACTCTTCTGTGAGGAGGAGGCGGATGACACGCTGACCA 965
 DB 2249 CAGGAACCCCGGGGCTTCTACTCTTCTGTGAGGAGGAGGCGGATGACACGCTGATCA 2308
 QY 966 TAAAGCGCAAGCTTATATGAGCACTGAGGAGATCAATTTGACAAATGCTATGCGCA 1025
 DB 2309 TAAAGCGAGGCTTATACCGGCACTGAGAGATCAATTTGACAAATGCTATGAGAG 2368
 QY 1026 GGTAAAGAGCTACTAGCAAGTGAACGCTGATCTTGTACTGACAGACCACTGCCA 1085
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 QY 1086 TGTCTTCTCTTTTGTGCTACACACTGCGTGGAGCTTCATTTTGGTCTGAGCCCTCG 1145
 DB 2429 CGTCTTCTCTCTTGTGAGGAGTACCCCTGCGAGGAGGAGCTCATCTTGGGCTGAGCCCTG 2488

QY 1146 CAAGCCTTAAAGACAGAGTCTTACACTTCATCTCTATGAGCAATGAGCCAGGCTATG 1205
 DB 2489 CAAGCCTTAAAGACAGAGTCTTACACTTCATCTCTATGAGCAATGAGCCAGGCTATG 2548
 QY 1206 GCTTGGCGGGGCTTCAGAGCCCGATGTTAATGAGCAGACAGGAGGAACTTCATACG 1265
 DB 2549 GCTTGGCGGGGCTTCAGAGCCCGATGTTAATGAGCAGACAGGAGGAGGAGGAGGAGG 2608
 QY 1266 GCAGCAGGAGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1325
 DB 2609 GCAGCAGTACAGAGTCCCTGAGCAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2668
 QY 1326 CGCGCAGGAGGCGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1385
 DB 2669 CGCGCAGGAGGCGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2728
 QY 1386 CATCATGAGCTTTTGGGGTGTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1445
 DB 2729 CATCATGAGCTTTTGGGGTGTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2788
 QY 1446 CACCGCAGCAGATCCCGGCTAGGCT 1473
 DB 2789 CCGCAGCAGCAGATCCCGGCTAGGCT 2816

RESULT 12
 US-09-837-863-19
 ; Sequence 19, Application US/09837863
 ; Patent No. 6468754
 ; GENERAL INFORMATION:
 ; APPLICANT: Greene, Amy
 ; APPLICANT: Zhou, Hue
 ; APPLICANT: Thode, Silke
 ; TITLE OF INVENTION: Vector and Method for Targeted Replacement and Disruption
 ; FILE REFERENCE: 025, IUS
 ; CURRENT APPLICATION NUMBER: US/09/837,863
 ; CURRENT FILING DATE: 2001-04-17
 ; PRIOR APPLICATION NUMBER: US 60/198,498
 ; PRIOR FILING DATE: 2000-04-18
 ; NUMBER OF SEQ ID NOS: 27
 ; SOFTWARE: Patentin version 3.0
 ; SEQ ID NO 19
 ; LENGTH: 7092
 ; TYPE: DNA
 ; ORGANISM: vector
 ; US-09-837-863-19

Query Match 67.8%; Score 1000.8; DB 4; Length 7092;
 Best Local Similarity 80.1%; Pred. No. 9e-242;
 Matches 116; Conservative 0; Mismatches 292; Indels 0; Gaps 0;

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; Patent No. 6468754
; GENERAL INFORMATION:
; APPLICANT: Greene, Amy
; APPLICANT: Zhou, Hua
; APPLICANT: Thode, Slike
; APPLICANT: Jarnigan, Kurt
; TITLE OF INVENTION: Vector and Method for Targeted Replacement and Disruption
; FILE REFERENCE: 025.1US
; CURRENT APPLICATION NUMBER: US/09/837,863
; CURRENT FILING DATE: 2001-04-17
; PRIOR APPLICATION NUMBER: US 60/198,498
; PRIOR FILING DATE: 2000-04-18
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 22
; LENGTH: 7092
; TYPE: DNA
; ORGANISM: vector
US-09-837-863-22

Query Match 67.8%; Score 1000.8; DB 4; Length 7092;
Best Local Similarity 80.1%; Pred. No. 9e-242;
Matches 1176; Conservative 0; Mismatches 292; Indels 0; Gaps 0;

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DB 1349 CATCATCCAGATTGAGAGGAGAAACCCGACTTCTGGAACCCGAGGACGCCAGGCCCT 1408
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QY 786 CAGTGTAAACACTCTATGAGGCTCTTGTAGCCGCGACATGAATGATATGTTACGA 845
Db 2129 GTCTGTGACCACTCTATGAGGCTCTTGTAGCCCTGAGACATGAATGATATGACCCG 2188
QY 846 AGACCAACCAAGAGACCCGACCTGTGAGATGACAGGAGCGGCTCTGCAAGTGTGAG 905
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QY 906 CAGGAAACCCCGGGGCTTCTACTCTTCTGTGAGGAGCGGCAATGACACGCTCA 965
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; Patent No. 6468754
; GENERAL INFORMATION:
; APPLICANT: Greene, Amy
; APPLICANT: Zhou, Hua
; APPLICANT: Rhode, Slike
; APPLICANT: Jarnigan, Kurt

; TITLE OF INVENTION: Vector and Method for Targeted Replacement and Disruption
; TITLE OF INVENTION: of an Integrated DNA Sequence
; FILE REFERENCE: 025.1US
; CURRENT APPLICATION NUMBER: US/09/837, 863
; CURRENT FILING DATE: 2001-04-17
; PRIOR APPLICATION NUMBER: US 60/198,498
; PRIOR FILING DATE: 2000-04-18
; NUMBER OF SEQ. ID NOS: 27
; SOFTWARE: PatentIn version 3.0
; SEQ. ID NO 27
; LENGTH: 7573
; TYPE: DNA
; ORGANISM: vector
US-09-837-863-27
Query Match 67.8%; Score 1000.8; DB 4; Length 7573;
Best Local Similarity 80.1%; Pred. No. 9,2e-242;
Matches 1176; Conservative 0; Mismatches 292; Indels 0; Gaps 0;
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| 43 | 997.6 | 67.6 | 7469 | 9 | US-09-776-167A-6 | Sequence 6, Appl |
| 44 | 997.6 | 67.6 | 7469 | 9 | US-10-053-637-3 | Sequence 3, Appl |
| 45 | 993.4 | 67.3 | 1561 | 15 | US-10-053-637-3 | Sequence 3, Appl |

ALIGNMENTS

| | | | | | | | | | |
|---|-----|---|-----|--|--|--|--|--|-------------------|
| RESULT 1 | | | | | | | | | |
| US-09-911-132a-1 | | | | | | | | | |
| ; Sequence 1, Application US/09911132A | | | | | | | | | |
| ; Publication No. US20030096341A1 | | | | | | | | | |
| ; GENERAL INFORMATION: | | | | | | | | | |
| ; APPLICANT: Roche Diagnostics GmbH | | | | | | | | | |
| ; TITLE OF INVENTION: Expression of Alkaline Phosphatase in Yeast | | | | | | | | | |
| ; FILE REFERENCE: RDID 0073US | | | | | | | | | |
| ; CURRENT APPLICATION NUMBER: US/09/911,132A | | | | | | | | | |
| ; CURRENT FILING DATE: 2002-08-28 | | | | | | | | | |
| ; NUMBER OF SEQ ID NOS: 38 | | | | | | | | | |
| ; SOFTWARE: PatentIn version 3.1 | | | | | | | | | |
| ; SEQ ID NO 1 | | | | | | | | | |
| ; LENGTH: 1476 | | | | | | | | | |
| ; TYPE: DNA | | | | | | | | | |
| ; ORGANISM: Bovine | | | | | | | | | |
| US-09-911-132a-1 | | | | | | | | | |
| Query Match | | | | | | | | | |
| Best Local Similarity 100.0%; Pred. No. 0; | | | | | | | | | |
| Matches 1476; Conservative 0; Mismatches 0; Indels 0; Gaps 0; | | | | | | | | | |
| Score 1476; DB 10; Length 1476; | | | | | | | | | |
| Qy | 1 | GAATTCCTATCCACGAGAGAAACCCCGCTTGTGAACCGCAGAGCCAG | 60 | | | | | | Sequence 22, Appl |
| Db | 1 | GAATTCCTATCCACGAGAGAAACCCCGCTTGTGAACCGCAGAGCCAG | 60 | | | | | | Sequence 26, Appl |
| Qy | 61 | GCCCTGATGTAGCAAGAGTTGACCGGATTCAGACAGCTGCCAAGAAATGTCATCTTC | 120 | | | | | | Sequence 10, Appl |
| Db | 61 | GCCCTGATGTAGCAAGAGTTGACCGGATTCAGACAGCTGCCAAGAAATGTCATCTTC | 120 | | | | | | Sequence 3, Appl |
| Qy | 121 | TTCTTGGGAGATGGAGTGGGGTCTTACGTCAGACGCACTGGAATCTTAAAGGGGCGAG | 180 | | | | | | Sequence 5, Appl |
| Db | 121 | TTCTTGGGAGATGGAGTGGGGTCTTACGTCAGACGCACTGGAATCTTAAAGGGGCGAG | 180 | | | | | | Sequence 16, Appl |
| Qy | 181 | ATGAATGCAAACTGGGAGCCTGAGACACCCCTGGCCATGAGACCAATTCCTATGCTGCT | 240 | | | | | | Sequence 16, Appl |
| Db | 181 | ATGAATGCAAACTGGGAGCCTGAGACACCCCTGGCCATGAGACCAATTCCTATGCTGCT | 240 | | | | | | Sequence 2, Appl |

Db 181 ATGAATGCGAACTGGGACCTTGAGACACCCCTGGCCATGAGACCAATTCCCATACGTGGCT 240
Qy 241 CTGTCCAAACATACACGTGACAGACAGTGGCCAGACAGCGCCAGGCACTGGCACTTGGC 300
Db 241 CTGTCCAAACATACACGTGACAGACAGTGGCCAGACAGCGCCAGGCACTGGCACTTGGC 300
Qy 301 TACCTGTGTGGGGTCAAGGGCACTACAGAACCATCGTGTAAAGTACACCGCCGCTAC 360
Db 301 TACCTGTGTGGGGTCAAGGGCACTACAGAACCATCGTGTAAAGTACACCGCCGCTAC 360
Qy 361 AATCAGTCAACACGACAGCTGGGAAATGAGTCACTCTGTATCAACCGGCGCAAGAAA 420
Db 361 AATCAGTCAACACGACAGCTGGGAAATGAGTCACTCTGTATCAACCGGCGCAAGAAA 420
Qy 421 GGAGGGAAGCGCTGGGAGTGTGACACACAGGCTGACAGATGCTCCCAAGCCGGG 480
Db 421 GGAGGGAAGCGCTGGGAGTGTGACACACAGGCTGACAGATGCTCCCAAGCCGGG 480
Qy 481 GCTACGCGCACACGCTGAAACGAACTGTACTACAGCGCGACCTGCTGCTGATGCA 540
Db 481 GCTACGCGCACACGCTGAAACGAACTGTACTACAGCGCGACCTGCTGCTGATGCA 540
Qy 541 CAGAAATATGCTGCTGCAAGACATCGCGCACAGCTGGTCTTACAAATGATATGACGTG 600
Db 541 CAGAAATATGCTGCTGCAAGACATCGCGCACAGCTGGTCTTACAAATGATATGACGTG 600
Qy 601 ATCTGGGTGGAGGCGCAATGTATCATGTTCTGAGGGGAGCCCAACCTGAAATCCCA 660
Db 601 ATCTGGGTGGAGGCGCAATGTATCATGTTCTGAGGGGAGCCCAACCTGAAATCCCA 660
Qy 661 GATGATGCGCAGTGTGATGAGTCCGGAAGACAAAGCAGACCTGTGACAGAAATGGCAG 720
Db 661 GATGATGCGCAGTGTGATGAGTCCGGAAGACAAAGCAGACCTGTGACAGAAATGGCAG 720
Qy 721 GCCAAGCACAGGAGGCCAGATATGTGTGAAACCGCACCTGCGCTCTTACAGCGCGCAT 780
Db 721 GCCAAGCACAGGAGGCCAGATATGTGTGAAACCGCACCTGCGCTCTTACAGCGCGCAT 780
Qy 781 GACTCAGTGTAAACACCTCATGAGGCTCTTTGAGCGGCGAGACATGAAATATATGTT 840
Db 781 GACTCAGTGTAAACACCTCATGAGGCTCTTTGAGCGGCGAGACATGAAATATATGTT 840
Qy 841 CAGCAAGACACACCAAGAGACCCGACCTGTGCGGAGATGACGAGCGCGCCCTGCAAGTG 900
Db 841 CAGCAAGACACACCAAGAGACCCGACCTGTGCGGAGATGACGAGCGCGCCCTGCAAGTG 900
Qy 901 CTGAGCAGGAACCCCGGGGCTTCTTACTCTTGTGTGAGGAGGCGCATTTGACACAGGT 960
Db 901 CTGAGCAGGAACCCCGGGGCTTCTTACTCTTGTGTGAGGAGGCGCATTTGACACAGGT 960
Qy 961 CACCATGACGGGAAGCTTATATGACATGACGAGGCGATCATGTTTGAACAATGCAATC 1020
Db 961 CACCATGACGGGAAGCTTATATGACATGACGAGGCGATCATGTTTGAACAATGCAATC 1020
Qy 1021 GCCAAGGCTTAACGAGCTCACTAGCGAACTGACACGCTGATCTTGTCACTGCAAGCAC 1080
Db 1021 GCCAAGGCTTAACGAGCTCACTAGCGAACTGACACGCTGATCTTGTCACTGCAAGCAC 1080
Qy 1081 TCCCATGTCTTCTTGTGTGTGCTACACATGCGTGGGACCTCCATTTTGGTCTGGGC 1140
Db 1081 TCCCATGTCTTCTTGTGTGTGCTACACATGCGTGGGACCTCCATTTTGGTCTGGGC 1140
Qy 1141 CCGGGAAGGCGCTTGAACAGACAGTCTACACCTCATCTCTATGGAATGGCCCAAGGC 1200
Db 1141 CCGGGAAGGCGCTTGAACAGACAGTCTACACCTCATCTCTATGGAATGGCCCAAGGC 1200
Qy 1201 TATGCGCTTGGCGGGGCTCGAGGCCGATGTTAATGAGCAGCAAGGAAACCTCTCA 1260
Db 1201 TATGCGCTTGGCGGGGCTCGAGGCCGATGTTAATGAGCAGCAAGGAAACCTCTCA 1260
Qy 1261 TACCGGACAGAGCGGCGCTGCGCTGCTGCTAGCGAGACCAACGAGGGGCAAGACGTGGG 1320
Db 1261 TACCGGACAGAGCGGCGCTGCGCTGCTGCTAGCGAGACCAACGAGGGGCAAGACGTGGG 1320

Qy 1321 GGTTCGCGCGAGGCGCCGAGCGGACCTGATGTCAGGCGTGCAGAGAGACCTTGGT 1380
Db 1321 GGTTCGCGCGAGGCGCCGAGCGGACCTGATGTCAGGCGTGCAGAGAGACCTTGGT 1380
Qy 1381 GCGCAGCATATGACCTTTGCGGGCTGCGTGAAGCCCTTACACGACTGCAATGCGCAGC 1440
Db 1381 GCGCAGCATATGACCTTTGCGGGCTGCGTGAAGCCCTTACACGACTGCAATGCGCAGC 1440
Qy 1441 CCGGCAACCGGCAACAGCATCCCGCATGAGGTACC 1476
Db 1441 CCGGCAACCGGCAACAGCATCCCGCATGAGGTACC 1476

RESULT 2
US-10-395-790A-1
; Sequence 1, Application US/10395790A
; Publication No. US20040072316A1
; GENERAL INFORMATION:
; APPLICANT: Roche Diagnostics Corp.
; TITLE OF INVENTION: Production of weakly active or inactive mutants of alkaline phosph
; FILE REFERENCE: RDID 02028US
; CURRENT APPLICATION NUMBER: US/10/395,790A
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1464
; TYPE: DNA
; ORGANISM: Bovine
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1464)
; OTHER INFORMATION:
US-10-395-790A-1

Query Match 99.2%; Score 1464; DB 16; Length 1464;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1464; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 CTCATCCAGCTGAGAGAGAAAACCCGCTTCTTGAAACGCGCAGACGCCAGGCCCTT 66
Db 1 CTCATCCAGCTGAGAGAGAAAACCCGCTTCTTGAAACGCGCAGACGCCAGGCCCTT 60
Qy 67 GATGAGCAGAAAGTTGACGCCATCCAGACAGTGGCCAAAGATGTATCTTCTTGG 126
Db 61 GATGAGCAGAAAGTTGACGCCATCCAGACAGTGGCCAAAGATGTATCTTCTTGG 120
Qy 127 GGGGATGGGATGGGGGCTGCTTACGGTGAACGCACTCGGATCTTAAAGGGGAGATGA 186
Db 121 GGGGATGGGATGGGGGCTGCTTACGGTGAACGCACTCGGATCTTAAAGGGGAGATGA 180
Qy 187 GGGCAATCGGACCTGAGACACCCCTGGCATGACAGTTCACATGCTGCTGTCC 246
Db 181 GGGCAATCGGACCTGAGACACCCCTGGCATGACAGTTCACATGCTGCTGTCC 240
Qy 247 AAGACATCAACGTGGAACAGACAGTGGCCAGACAGGCACTGCGCATGCTTACTG 306
Db 241 AAGACATCAACGTGGAACAGACAGTGGCCAGACAGGCACTGCGCATGCTTACTG 300
Qy 307 TGTGGGATCAAGGGGCACTACAGAACATCGGTGTAATGACGCGCCGCTTACATGAG 366
Db 301 TGTGGGATCAAGGGGCACTACAGAACATCGGTGTAATGACGCGCCGCTTACATGAG 360
Qy 367 TGCACACAGACAGTGGGAATGAGGTCACTGTGTATCAACCGGCGCAAGAAACAGAG 426
Db 361 TGCACACAGACAGTGGGAATGAGGTCACTGTGTATCAACCGGCGCAAGAAACAGAG 420
Qy 427 AAGGCGTGGGATGAGTGAACCAACAGGCTGACAGATGCTCTCCAGCGGGGCTTAC 486
Db 421 AAGGCGTGGGATGAGTGAACCAACAGGCTGACAGATGCTCTCCAGCGGGGCTTAC 480

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QY 487 GCGCACCGGTGAACCGAACTGTACTAGACGCCGACCTGCTGTATGACAGAAAG 546
DB 481 GCGCACCGGTGAACCGAACTGTACTAGACGCCGACCTGCTGTATGACAGAAAG 540
QY 547 AATGCTGCCAGGACATCGCCGACAGCTGTGTCTAACAACTGATATTTGAAGTATCTTG 606
DB 541 AATGCTGCCAGGACATCGCCGACAGCTGTGTCTAACAACTGATATTTGAAGTATCTTG 600
QY 607 GGTGAGGCGCGAATGTAATGTTTCTGTAGAGGAGACCCCAAGCCCTGAATCCCAATGAT 666
DB 601 GGTGAGGCGCGAATGTAATGTTTCTGTAGAGGAGACCCCAAGCCCTGAATCCCAATGAT 660
QY 667 GCCAGTGTGAATGAGTCCGGAAGAGCAAGCAGACCTGTGTGAGAAATGTCAGAGCCAG 726
DB 661 GCCAGTGTGAATGAGTCCGGAAGAGCAAGCAGACCTGTGTGAGAAATGTCAGAGCCAG 720
QY 727 CACCAAGGAGCCCAAGTATGTGTGAACCGCACTGCGCTCTTTCAGGCGCGCATGACTCC 786
DB 721 CACCAAGGAGCCCAAGTATGTGTGAACCGCACTGCGCTCTTTCAGGCGCGCATGACTCC 780
QY 787 AGTGTAAACACCTCATGCGGCTCTTTGAGCCGCGACATGAAGTAAATGTTTCAAGCA 846
DB 781 AGTGTAAACACCTCATGCGGCTCTTTGAGCCGCGACATGAAGTAAATGTTTCAAGCA 840
QY 847 GACCAACCAAGGAGCCGACCTGTGCGGAGATGACGAGGCGCGCTGCAAGTGTGAGC 906
DB 841 GACCAACCAAGGAGCCGACCTGTGCGGAGATGACGAGGCGCGCTGCAAGTGTGAGC 900
QY 907 AGGAAACCCCGGGGCTTTCTACCTCTTGTGTGAGGAGGCGCGATTGACCAAGTCAACAT 966
DB 901 AGGAAACCCCGGGGCTTTCTACCTCTTGTGTGAGGAGGCGCGATTGACCAAGTCAACAT 960
QY 967 GACGCGAAGCTTAAATGTGACACTGACTGAGCGCATGATGTTTGAACAATGCTCATGCCAAG 1026
DB 961 GACGCGAAGCTTAAATGTGACACTGACTGAGCGCATGATGTTTGAACAATGCTCATGCCAAG 1020
QY 1027 GCTAAGCACTCATGTCGCAAGCTGAGCAGGCTGATCTTGTGCTGCTGACAGCACTCCAT 1086
DB 1021 GCTAAGCACTCATGTCGCAAGCTGAGCAGGCTGATCTTGTGCTGCTGACAGCACTCCAT 1080
QY 1087 GTCTTCTCTTTTGTGTGCTTACACACTGCGTGGAGCTTCCATTTTGGGTGCGCCCGGCG 1146
DB 1081 GTCTTCTCTTTTGTGTGCTTACACACTGCGTGGAGCTTCCATTTTGGGTGCGCCCGGCG 1140
QY 1147 AAGGCTTAAAGACAGCAAGTCTTACACCTTCATCTTATGTGCAATGCGCCGACTATGCG 1206
DB 1141 AAGGCTTAAAGACAGCAAGTCTTACACCTTCATCTTATGTGCAATGCGCCGACTATGCG 1200
QY 1207 CTGTGCGGGGGGCTGAGGCGCGGATGTTAATGAGAGCAAGCGAGAAACCTCATACCGG 1266
DB 1201 CTGTGCGGGGGGCTGAGGCGCGGATGTTAATGAGAGCAAGCGAGAAACCTCATACCGG 1260
QY 1267 CAGCAGGCGGCGCTGCGCTTGTGCTGAGAGACCAAGCGGGGCGAAGAGCTGTGCGGTGTC 1326
DB 1261 CAGCAGGCGGCGCTGCGCTTGTGCTGAGAGACCAAGCGGGGCGAAGAGCTGTGCGGTGTC 1320
QY 1327 GCGCAGGCGCGCGAGCGCACTGTGTGACAGGCGTGCAGAGAGAGACTTGTGTGCGCGAC 1386
DB 1321 GCGCAGGCGCGCGAGCGCACTGTGTGACAGGCGTGCAGAGAGAGACTTGTGTGCGCGAC 1380
QY 1387 ATCATAGGCTTTTGTGCGGGGCTGTGTGAGGCTTACACCGACTGTGCAATCTGCCAGCCCGCC 1446
DB 1381 ATCATAGGCTTTTGTGCGGGGCTGTGTGAGGCTTACACCGACTGTGCAATCTGCCAGCCCGCC 1440
QY 1447 ACCGACCAAGCATCCCGCACTAG 1470
DB 1441 ACCGACCAAGCATCCCGCACTAG 1464

```

RESULT 3
 US-10-053-637-9
 ; Sequence 9, Application US/10053637
 ; Publication No. US20030158132A1

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; GENERAL INFORMATION:
; APPLICANT: KOVESDI, IMRE
; TITLE OF INVENTION: METHOD OF ENHANCING BONE DENSITY OR FORMATION
; FILE REFERENCE: 206211
; CURRENT APPLICATION NUMBER: US/10/053,637
; CURRENT FILING DATE: 2002-01-22
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 1597
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: SEAP/RGD fusion protein
; NAME/KEY: CDS
; LOCATION: (11)..(1585)
; OTHER INFORMATION:
; NAME/KEY: misc feature
; LOCATION: (1538)..(1570)
; OTHER INFORMATION: RGD domain
US-10-053-637-9

Query Match 67.9%; Score 1002.8; DB 15; Length 1597;
Best Local Similarity 80.1%; Pred. No. 1.7e-285;
Matches 1178; Conservative 0; Mismatches 292; Indels 0; Gaps 0;

QY 6 CCTCATCCCACTGAGAGAGAAACCCGCTTTCTGTGAACCCGACAGCCAGCCGCT 65
DB 61 CATCATCCCACTGAGAGAGAAACCCGCTTTCTGTGAACCCGACAGCCAGCCGCT 120
QY 66 TGATGTAGCAAGAAAGTTTCAGCCGATCCAGACAGCTGTGCAAGATGATCTCTTT 125
DB 121 GGGTCCGCGCAAGAACTCAGCTGACAGAGCGCGCAAGACCTCATATCTTCT 180
QY 126 GGGGAGTGGAGTGGGGGCTCTACGCTGACAGCACTCGGATCTTAAAGGCGAGATGAA 185
DB 181 GGGGAGTGGAGTGGGGGCTCTACGCTGACAGCACTCGGATCTTAAAGGCGAGATGAA 240
QY 186 TGGCAAACTGGGACTGGAACACCCCTGGCATGACCAAGTTCCATACGTGCTGTG 245
DB 241 GGAACAACTGGGGCTGGAATACCCCTGGCATGACCAAGTTCCATACGTGCTGTG 300
QY 246 CAAGACATACACGTGAGAGAGACAGGTGCGAGCAGCGAGGACCTGCGCACTGCTACCT 305
DB 301 CAAGACATACACGTGAGAGAGACAGGTGCGAGCAGGTGCGAGGACCTGCGCACTGCTACCT 360
QY 306 GTGTGGGGTCAAGGGGCACTAAGAACATCGGTGTATGTGAGCGCGCGCTACATGA 365
DB 361 GTGTGGGGTCAAGGGGCACTAAGAACATCGGTGTATGTGAGCGCGCGCTTAAACGA 420
QY 421 GTGTGGGGTCAAGGGGCACTAAGAACATCGGTGTATGTGAGCGCGCGCTTAAACGA 480
DB 426 GAAAGCGGTGAGAGTGTGACCAACCAAGGCTGAGCATGCTCTCCGACCGGGGCTTA 485
QY 481 GAAAGCGGTGAGAGTGTGACCAACCAAGGCTGAGCATGCTCTCCGACCGGGGCTTA 540
DB 486 CGGCAACAGGTGAACCGAAACTGTGATCTCAGAGCGCGCACTGCTGTGATGACAGAA 545
QY 541 CGGCAACAGGTGAACCGAAACTGTGATCTCAGAGCGCGCACTGCTGTGATGACAGAA 600
DB 546 GAATGCTGCCAGAGCATGCGCGCAAGCTGTGTCTAACCAATGATATTTGACGTGATCT 605
QY 601 GGAGGGGTGCCAGACATGCTACGAGCTCATCTTCCAACTGAGCAATGACGTGATCT 660
DB 606 GGTGTAGGCGCAATGTATATGTTTCTGTGAGGAGACCCCAAGCCCTGAATACCAATGA 665
QY 661 AGTGTAGGCGCAATGTATGTTTCTGTGAGGAGACCCCAAGCCCTGAATACCAATGA 720
DB 666 TGCAGTGTGAATGAGTGTGCGGAGAGCAAGGCAAGCTGTGAGAGATGCGAGCCAA 725
QY 721 CTACAGCCCAAGGTGGAGCAGGCTGAGCGGAGAAATCTGTGTGAGAAATGCTGCGCGAA 780

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| | | | |
|---|------|--|------|
| Qy | 726 | GCACCGAGGAGGCGCAGTATGNTGGAAACCGCACTGGCGCTCTTCAAGCGGGCCGATGATCTC | 785 |
| Db | 781 | GCGCCAGGAGGTGCCCGATATGATGGAAACCGCACTGAGCTCATGCAAGGCTTCCCTGGAGCC | 840 |
| Qy | 786 | CAGTGTAAACACACTCATGGGCTCTTTGAGCCGGCAGACATGAAGTATATATGTTTCAGCA | 845 |
| Db | 841 | GTCTGTGACCCCATCTCATGGGTCTCTTTGAGCTGGAGACATGAAATATACAGATTCACCG | 900 |
| Qy | 846 | AGACCAACACAAAGAACCCGACCTTGGCGGAGATGACGAGGGCGGGCCCTGCAGTGTGAG | 905 |
| Db | 901 | AGACTCCACACTGAGACCCCTCCCTCATGAGATGACAGAGGGCTGCCCCCTCGCTCTGAG | 960 |
| Qy | 906 | CAGGAACCCCCCGGGCTTCTACCTCTTGGTGAAGGAGGCCGATTTGACACGSGTCACA | 965 |
| Db | 961 | CAGGAACCCCCCGGGCTTCTCTCTTGGAGGGGTGGTGGATGACCAATGATCATCA | 102 |
| Qy | 966 | TGACGGCAAAAGCTTATATGCACTGACTGAGGCGATCATGTTTGAACATGCCATCGCCA | 1021 |
| Db | 1021 | TGAAAGCAGGGCTTACCGGGCACTGACTGACGATCATGTTTCAGACGCGCATTGAGAG | 108 |
| Qy | 1026 | GGCTTAACGAGCTCACTAGCGAACTGGAACGCTGATCTTTGTCACTGCAAGACACTTCCCA | 1081 |
| Db | 1081 | GGCGGGCCAGCTCACACAGGAGAGAGACAGCTGAGCCCTGTCACTGCCAGACCACTCCCA | 1141 |
| Qy | 1086 | TGCTTCTCTTTTGGGAGCTACACACTGAGTGGAGACCTTCATTTTCGATCTGGCCCCGG | 1144 |
| Db | 1141 | CGTCTTCTCTTCCGAGAGCTACCCCTGGAGAGAGCTCATCTTGGGCTGGCCCCCTGG | 1201 |
| Qy | 1146 | CAAGGCTTTAGACAGCAAGTCTTCACTCTCATCTCTTATGSCAATGAGCCAGGCTATGC | 1201 |
| Db | 1201 | CAAGGCCCGGGAACAGAAAGGCTTACACGGTCTCTCTTATACGAAACGGTTCAGAGCTATGT | 1261 |
| Qy | 1206 | GCTTGGCGGGGCTCGAAGGCCCGATGTTTAAATGGCAGACAAAGCGAGAAACCTCATACCG | 1261 |
| Db | 1261 | GCTCAAGGACGGCGCCCGGCCGAGATGTTAACGAGAGCGAGACGGGAGGCCCGCAGATATGG | 1321 |
| Qy | 1266 | GCAGCAGGCGGGCCGTCGCCCTTGGCTTAGCGAGAACCCAGGGGGCGAAAGCGTGGCGGTGT | 1321 |
| Db | 1321 | GCAGCAGTCAAGCATGTGCCCCCTTGGACGAAAGAACCCAGCAGGCGGAGACGTGGCGGTGT | 1381 |
| Qy | 1326 | CGCGGAGAGGCCCGCAGAGCGCACCTGTGTGACGCGCGCTGACGAGAGAGACCTTGTGTGCGCA | 1381 |
| Db | 1381 | CGCGGCGGGCCCGCAGAGCGCACCTGTGTTCACGSGCGTGCAGAGCAGACCTTATAGCGCA | 1441 |
| Qy | 1386 | CATCATGGCCCTTTGGGGGCTGGGTGAGAGCCCTTACACCACTGCAATGTGCCAGCCCCGGC | 1441 |
| Db | 1441 | CGTCAATGGCTTTCGGCGGCTGTGTGAGAGCCCTTACACCCGCTTCGACCTTGGCCGCCCCCGC | 1501 |
| Qy | 1446 | CACCGCACACAGCATCTCCCGACTGAGGATC 1475 | |
| Db | 1501 | CGGCACCAACGACGCCCGCGCACCCGGGTTTC 1530 | |
| RESULT 4 | | | |
| US-10-053-637-11 | | | |
| : Sequence 11, Application US/10053637 | | | |
| : Publication No. US20030158132A1 | | | |
| GENERAL INFORMATION: | | | |
| : APPLICANT: KOVESDI, IMRE | | | |
| : TITLE OF INVENTION: METHOD OF ENHANCING BONE DENSITY OR FORMATION | | | |
| : FILE REFERENCE: 206211 | | | |
| : CURRENT APPLICATION NUMBER: US/10/053, 637 | | | |
| : CURRENT FILING DATE: 2002-01-22 | | | |
| : NUMBER OF SEQ ID NOS: 28 | | | |
| : SOFTWARE: PatentIn version 3.1 | | | |
| : SEQ ID NO 11 | | | |
| : LENGTH: 1675 | | | |
| : TYPE: DNA | | | |
| : ORGANISM: Artificial Sequence | | | |
| : FEATURE: | | | |
| : OTHER INFORMATION: SeqP/Decorain fusion | | | |
| : NAME/KEY: CDS | | | |

| | LOCATION: (11) .. (1663) | OTHER INFORMATION: |
|----------------------------|--|--------------------|
| | NAME/KEY: misc_feature | |
| | LOCATION: (1544) .. (1663) | |
| | OTHER INFORMATION: decorsin domain | |
| | US-10-053-637-11 | |
| Query Match | 67.9% Score 1002.8; DB 15; Length 1675; | |
| Best Local Similarity | 80.1% Pred. No. 1.7e-285; | |
| Matches 1178; Conservative | 0; Mismatches 292; Indels 0; Gaps 0 | |
| Qy | 6 CCTCATCCCACTGAGAGAGAAAACCCCGCTTCTGAAACCGCCAGGACCCAGGCCCT | 65 |
| Db | 61 CATCATCCCACTTGGAGAGAGAACCCCGACTTCTGAAACCGCGAGGACCGAGGCCCT | 120 |
| Qy | 66 TGATGTAGCCCAAGAGTTGTCAGCCCGATCCCAACAGTTCGCAAGATTCCTCTTCT | 125 |
| Db | 121 GGGTGTCCGCCAAGAGCTGCAAGCCTGCAACAACAGCCCGCAAGAACTCATCATCTTCT | 180 |
| Qy | 126 GGGGATGGAGTGGGGGTGCTTACGGTGCAGCCCACTGGATTCCTAAAGGGGACAGTGA | 185 |
| Db | 181 GGGGATGGAGTGGGGGTGCTTACGGTGCAGCTGCAAGATTCCTAAAGGGGACAGTGA | 240 |
| Qy | 186 TGGCAACTGGGACCTGAGACACCCCTGGCCATGGAACAATTCCCATGCTGCTGTC | 245 |
| Db | 241 GGAACAACCTGGGGCTGAGATACCCCTGGCCATGGAACCGCTTCCCATGTGGGCTCTGTC | 300 |
| Qy | 246 CAAAGCATATCAACGTGACAGACAGGTGCAGACAGCCAGGACATGCTACCT | 305 |
| Db | 301 CAAAGCATATCAATGTAGCAAAACATGTGCCAGACAGTGGAGCCACAGCCACCGCTTACT | 360 |
| Qy | 306 GTGTGGGGTCAAGGGCAACTACAGAACCATCGTGTAAAGTGCAGCCGCCCTCGTCAATCA | 365 |
| Db | 361 GTGGGGGGTCAAGGGCAACTTCCAGACCATTTGGCTTGAAGTGCAGCCGCCCTTTAACCA | 420 |
| Qy | 366 GTGCAACACGACAGTGGGAATGAGTGCATCGTGTGATTCACACGGGGCAAGAAAGACGG | 425 |
| Db | 421 GTGCAACACGACAGTGGGAATGAGTGCATCGTGTGATTCACACGGGGCAAGAAAGACGG | 480 |
| Qy | 426 GAAAGCCCTGGAGATGTGTGACACACACAGGGGTGACAGTGCCTCCAGCCGGGGCTTA | 485 |
| Db | 481 GAAATGATGGGAATGTGTGACACACACAGTGTGACAGTGCCTCCAGCCGGGGCTTA | 540 |
| Qy | 486 CGCGCACAGGTGAACCGAACTGTGACTCAGAGCGCGCACTGCTGCTGATGCACAGAA | 545 |
| Db | 541 CGCGCACAGGTGAACCGCAACTGTGACTCAGAGCGCGCACTGCTGCTGCTGCGCGCA | 600 |
| Qy | 546 GAATGGCTGCAGGACATCGCCGACAGCTGTGTCAACAATGTGATTTAGAGTATCT | 605 |
| Db | 601 GGAAGGGGTGCAGGACATCGTGTGAGCTATCTTCAACAATGTGATTTAGAGTATCT | 660 |
| Qy | 606 GGGTGGAGGCGGAATGTACATGTTTCTGAGGGGAACCCAGACCCCTGAATACCCAGATGA | 665 |
| Db | 661 AGGTGGAGGCGGAATGTACATGTTTCTGAGGGGAACCCAGACCCCTGAATACCCAGATGA | 720 |
| Qy | 666 TGCCAGTGTGAATGAGATGCCGGAAGGACAAACAACAACCTGGTGCAGGAATGGCAGGCCAA | 725 |
| Db | 721 CTAAAGCCAAAGTGGACCAAGCTGGACGGGAAGATGTGTGACAGGAATGGCTGGCGAA | 780 |
| Qy | 726 GCACCAAGGAGCCCAAGTATGTGTGAAACCGCACTGCGCTCTTCCAGCGGCGATGACTC | 785 |
| Db | 781 GCGCAGGGGTGCCGGTATGTGTGAAACCGCACTGAGGCTTCAAGCAGGCTTCCCTGGACCC | 840 |
| Qy | 786 CAGTGTAAACACCTCATGGGCTCTTTGAGCCCGGACAGACATGAAGTATTAATGTTACAGA | 845 |
| Db | 841 GTCTGTGATCCCATATCAGGGTCTCTTTGAGCCCTGGAACATGAATATCGAGATCACCG | 900 |
| Qy | 846 AGACCAACCAAGGACCCGACCTCGGCGGAATGACGGAAGCCGCGCTCGCAAGTCTGAG | 905 |
| Db | 901 AGACTTCACACTGAAACCTCTCTGATGGAATGACAGAGGCTGCTTCCGCTGCTGAG | 960 |
| Qy | 906 CAGGAACCCCGGGGCTTTTACCTCTTGTGTGAGGAGGCGGCATTTGACACGCTCACCA | 965 |

| | | | | |
|-----------------------|--------------|--|----------------|-------------|
| Query Match | 67.9% | Score 1002.8 | DB 15 | Length 1748 |
| Best Local Similarity | 80.1% | Pred. 1.7e-285 | | |
| Matches 1178 | Conservative | 0 | Mismatches 292 | Indels 0 |
| | | | Gaps 0 | |
| Oy | 6 | CCTCATCCGACGTGAGAGAAAACCCCGCTCTTGAAACCGCCAGGACGCCAGGCGCT | 65 | |
| | | | | |
| Db | 61 | CATCATCCCACTTGAGAGAGAAACCCGCACTCTTGAAACCGCAGGACGAGCCGAGGCGCT | 120 | |

| | | | |
|----|------|--|------|
| OY | 66 | TGATGTAGCCAAAGAAAGTTGGACGGCGGATCCAGACAGCTGGCCAAAGATGTCAATCCCTCTT | 125 |
| Dp | 121 | GGGTGCGCCCAAGAGCTGCAGCTTGCAAGACAGCCGCCAAGAACTCAATCATTTTCT | 180 |
| OY | 126 | GGGGGATGGGTATGGGGGTGCTTACGTTGACAGCCACTCGGATCCTAAAGGGGAGATGAA | 185 |
| Dp | 181 | GGGGGATGGGATGGGGGTGTCTACGTGTGACAGCTGCCAGGATCCTTAAAGGGGAGAA | 240 |
| OY | 186 | TGGCAAACTGGGACTTGAGACACCCCTGGCCATGGACCAAGTTCCCATAGTGGCTCTGTC | 245 |
| Dp | 241 | GGACAAACTGGGGGCTGAGATATACCCCTGGCCATGGACCGCTTCCCATATGGGCTCTGTC | 300 |
| OY | 246 | CAAAACATATCAAGTGGACAGACAGGTGCCAGACAGCGCAGGCACTGCCACTGCTCACT | 305 |
| Dp | 301 | CAAAACATATCAATATGTAAACAAACATGTGCCAGACAGTGGAGCCACACCGGCTCACT | 360 |
| OY | 306 | GTGTGGGGTCAAGGGCAACTACAGAACCATCGGTGTAAAGTAGAGCCGCCGCTCAATCA | 365 |
| Dp | 361 | GTGGGGGGTCAAGGGCAACTTCCAGACCAATTGGCTTAAGTGCAGCCGCCGCTTAAACA | 420 |
| OY | 366 | GTGCAACACGACACAGTGGGAAATGAGTCAAGCTGTGTATCAACCGGGCCAAAGAAAGAGG | 425 |
| Dp | 421 | GTGCAACACGACACGGCGCAACGAGGTCAATCTCGTATGAATGGGGCCAAAGAAAGAGG | 480 |
| OY | 426 | GAAAGCCGTGGGAATGTGTACACACACAGGGGTGCAGATAGCTTCCCAAGCCGGGGCTTA | 485 |
| Dp | 481 | GAAATCATGTGGAATGTGTAAACCAACAACAGTGTACACAAGCCCTGGCAGCCGGCACCTTA | 540 |
| OY | 486 | CGGCGCACACGGGTGAACGGAAACTGGTACTAGACGGCGGACCTGCTGTGATGACAGAA | 545 |
| Dp | 541 | CGCCCAACGGGTGAACCGCAACTGTGTACTGGAGCGCGGAGTGTCTTCCCTGGCCGCCCA | 600 |
| OY | 546 | GAATGAGCTGCGCAGGACATGCGCCGACAGCTGTGTCTACACATGGATTTTGAACGTGATCT | 605 |
| Dp | 601 | GGAGGGGTGCAGGACATCGGTACGCAAGCTCATCTCAACATGGACATTTGACGTGATCT | 660 |
| OY | 606 | GGGTGAGGCCGAATGTATCATGTTTTCTTGAAGGGGACCCCAAGCCCTGTAATACCAATGA | 665 |
| Dp | 661 | AGGTGGAGGCCGAATGTATCATGTTTTCCCATGGGAACCCCAAGCCCTGATGATACCAATGA | 720 |
| OY | 666 | TGCCAGTGTAAATGGAATCCGGGAAGGACAGCAAGCAACTGTGAGGAATGGCAGGCA | 725 |
| Dp | 721 | CTACAGCCAAAGTGTGGACACAGGCTGGACGGGAAGAACTGTGAGGAATGGCTGGGAA | 780 |
| OY | 726 | GCAACAGGAGACCCAGATGTGTGGAAACCGCACTGCGCTCTTCAAGCGGCGCATGATC | 785 |
| Dp | 781 | GGCGCAGGGTGGCCGGTATGTGTGGAAACCGCACTGAGCTCATGCAAGGCTTCCCTGGACC | 840 |
| OY | 786 | CAGTGTAAACAACCTCATGAGGCTCTTTTGAAGCCGGCAGACATGAATGATATGTTCA | 845 |
| Dp | 841 | GTCGTGATCCATCTCATGAGGTCTCTTTGAAGCTGGAGACATGAATAACAGATCTCACG | 900 |
| OY | 846 | AGACCAACAACGAAACCCGACCTGTGGGGAGATGACGGAAGCGGCTTGCAGATGCTGAG | 905 |
| Dp | 901 | AGACTTCAACATGGAACCCCTCCCTGATGAGATGACAGAGCTGCGCTGTGGCTGAG | 960 |
| OY | 906 | CAGGAACCCCGGGGGCTTCTACCTCTTGAGGAGGAGGCGCATTTGACACGAGTCA | 965 |
| Dp | 961 | CAGGAACCCCGGGGGCTTCTTCTCTTGTGGAGGGGTGTGCGATGACCAATGTCTATCA | 1020 |
| OY | 966 | TGACGGGAAAGTATATGGAACCTGACTGAGGCGATCATGTTGACAATGCCATCGCAA | 1025 |
| Dp | 1021 | TGAAGACAGGGCTTACCGGGGCACTGATGAGACGATCATGTTGACGACGCCCATTTGAG | 1080 |
| OY | 1026 | GGCTTAACGAGCTCATAGCGGAATGGAACAGCTGATCTTGTCACTGACACCACTTCCA | 1085 |
| Dp | 1081 | GGCGGGCACTACCCAGCAGGAGGACAGGCTGAGGCTGTCACTGCGCAACATCTCCA | 1140 |
| OY | 1086 | TGTCTTCTCTTTTGGTGGCTTACACACTGCGGTGGAACTTCATTTTGGTCTGGGCCCCGG | 1145 |
| Dp | 1141 | CGTCTTCTCTTGGAGGCTTACCCCTGCGAGGAGGTCCATCTTGGGGCTGGCCCTGG | 1200 |
| OY | 1146 | CAAGGCTTGAACAGCAAGTCTTACACTTCCTCATGTGCAATGGCCAGGCTATG | 1205 |

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Db 1201 CAAGGCCCGGAGACAGAAAGGCTTACACGGTCCATCTATACGAGAAAGGCTCAGCATATGT 1260
Qy 1206 GCTTGGCGGGGGGCTCCAGGCGCCGATGTTAATGACAGACACAGGAGAAACCTCATACCG 1265
Db 1261 GCTCAAGACGGGGCGCCGGCGGATGTACCGAGACGAGAGCGGAGCGCCCGCATATCG 1320
Qy 1266 GCAGCAGCGGCGCTGCTCCCTGGCTAGCGAGACCCACGCGGGGCGAAGACGTGGCGGTGT 1325
Db 1321 GCAGCAGTACAGATGCTCCCTGGACGAAAGACCCACGAGCGGAGACGTGGCGGTGT 1380
Qy 1326 CGCGCAGGCGCCGACGCGACCTGTGTGACGCGCGTGCAGAGAGACCTTCGTGCGCA 1385
Db 1381 CGCGCGGCGCCGACGCGACCTGTGTGACGCGCGTGCAGAGAGACCTTCATACGCA 1440
Qy 1386 CATCATGCGCTTTGGCGGGCTGCGTGAAGCCCTTACACGAGTGTGATCTGCGACGCTCCG 1445
Db 1441 CGTCAATGCGCTTTCGCGCGCTGCTGTGAGCCCTACACCGCTGCGACTGGCGCCCGC 1500
Qy 1446 CACCGCACACGATCCCGCACTAGGGTAC 1475
Db 1501 CGGCACACACGACGCGCGCACCGGGTTC 1530
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RESULT 6
US-10-053-637-15
; Sequence 15, Application US/10053637
; Publication No. US20030158132A1
; GENERAL INFORMATION:
; APPLICANT: KOVESDI, IMRE
; TITLE OF INVENTION: METHOD OF ENHANCING BONE DENSITY OR FORMATION
; FILE REFERENCE: 206211
; CURRENT APPLICATION NUMBER: US/10/053,637
; CURRENT FILING DATE: 2002-01-22
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
; LENGTH: 1777
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: SEAP HBNF fusion
; NAME/KEY: CDS
; LOCATION: (11)..(1765)
; OTHER INFORMATION:
; NAME/KEY: misc.feature
; LOCATION: (1538)..(1762)
; OTHER INFORMATION: HBNF domain
US-10-053-637-15
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Query Match 67.9%; Score 1002.8; DB 15; Length 1777;
Best Local Similarity 80.1%; Pred. No. 1.7e-285;
Matches 1178; Conservative 0; Mismatches 292; Indels 0; Gaps 0;
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Qy 6 CCTCATCCAGTGAAGAGAAACCCGCTTCTTGAAACGCGACGAGCCGAGCCCT 65
Db 61 CATCATCCAGTGAAGAGAAACCCGACTTCTTGAAACGCGAGGAGCGAGGCCCT 120
Qy 66 TGATGATGCAAGAAAGTTGCAAGCCGATCCAGACAGCTGCGAAGATGTATCTCTTCT 125
Db 121 GGGTCCCGCAAGAAAGCTGCAAGCTGCGACAGACAGCGCGCAAGAACCTCATATCTTCT 180
Qy 126 GGGGATGGATGGGGGTCTACGGTGAACAGCACTCGGATCTTAAAGGGGCAAGTGA 185
Db 181 GGGCGATGGGATGGGGGTCTTACGGTGAACAGCTGCGAGATCTTAAAGGGGCAAGTGA 240
Qy 186 TGGCAAACTGGAGCTTGAGACACCCCTGCGCATGGAACGATTCCATACGTGCTGTG 245
Db 241 GGACAAACTGGGGCTTGAGATACCCCTGCGCATGGAACGCTTCCATATGTGCTGTG 300
Qy 246 CAAGCATATCAACGTGAGACAGAGTGCACAGACGCGAGGACCTGCGACTGCTTACT 305
Db 301 CAAGCATATCAATGTAGACAAACATGTGCAGACAGTGAAGCCACAGCGGCTTACT 360
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Qy 306 GTGTGGGGTCAAGGGCAACTACAGAACCATGCGTGTAAAGTGAAGCGCCCGCTACATCA 365
Db 361 GTGTGGGGTCAAGGGCAACTTCCAGACCATGTGCTTGAAGTGAAGCGCCCGCTTAAACA 420
Qy 366 GTGCAACACGACCGTGGGAATGAGTGAACGTCTGTATCAACCGGGCCAAAGAACAG 425
Db 421 GTGCAACACGACCGGGAAAGAGTATCTCGGTATGAATTCGGGGCCAAAGAACAG 480
Qy 426 GAAAGCCGTGGAGTGTGACCAACCAAGGTTGACATGCTTCCAGCCGGGGCTTA 485
Db 481 GAAAGTGTGGAGTGTGACCAACCAAGTGTGACAGCGCTTCCAGCCGGGACCTTA 540
Qy 486 CGCGACACCGGAAACCGAAACTGGTACTGAGCGCCGACCTGCGTGAATGACAGAA 545
Db 541 CGCGACACCGGAAACCGAACTGGTACTGAGCGCCGACCGTGTGCTTCCGGCCGCA 600
Qy 546 GAATGCTGCCAGACATCGCGCACAGCTGTCTTAAACATGATGATTAATGATGATCT 605
Db 601 GGAAGGGGTCCAGACATCGCTACAGCATCTTCCAAACATGACATTTGACGTATCT 660
Qy 606 GGGTGAAGCGCAATGTATCTTTCTGAGGGGACCCCAAGCCTGAAATACCAAGTGA 665
Db 661 AGGTGAAGCGCAAGTATCATGTCTTCCATGGGAACCCAGACCTGTAGTACCAAGTGA 720
Qy 666 TGCCAGTGAATGAGTCCGGAAGACAGACAGCAACCGTGTGAGAGATGCGAGCCAA 725
Db 721 CTACAGCCAGGTGGAGACAGCTGAGCGGAAGATCTGTGCAAGATGCTGCGGAA 780
Qy 726 GCACCAAGGAGCGCAGTATGTGTGGAACCGCATGCGCTCTTCAAGCGGCGCATGATC 785
Db 781 GCGCCAGGAGTGCCTGGTATGTGTGGAACCGCATGAGCTCATGACGCTTCCCTGAGCC 840
Qy 786 CAGTGAACACACCTCATAGGCGCTTTTGAGCGCGCAACATGAATGAATGTTTACCA 845
Db 841 GTCTGTGACCATCATGAGGTCTCTTTGAGCTGTGAACATGAATGCAAGATCCACCG 900
Qy 846 AGACCAACACAAAGACCGGACCTTGGCGAGATGACGAGCGGCGCTTCAAGTCTTAG 905
Db 901 AGACTTCACACATGAGACCTCTCTGTATGAGATGACAGAGCTGCTGCGCTGCTAG 960
Qy 906 CAGGAACCCCGGGGCTTCTACCTCTTGTGTGAGGAGCGCGCATTTGAACACGATCACA 965
Db 961 CAGGAACCCCGGGGCTTCTCTCTCTGTGTGAGGAGGTGTGCAATGATGATCA 1020
Qy 966 TGACGCGAAAGTTATAGCACTGACAGGCGCATATGTTTGAACATGCGCATGCCAA 1025
Db 1021 TGAAAGCAGGGCTTACCGGGACATGACAGATCATGTTTCAAGCAGCGCATTTGAGAG 1080
Qy 1026 GAGCTAAGAGCTCACTAAGCAACTGACAGCGTGAACCTTGTCACTGACAGCACTCCCA 1085
Db 1081 GCGGGGCGAGCTCACACGAGAGAGAGACAGCTGAGCTTGTCACTGCGACACTCCCA 1140
Qy 1086 TGTCTTCTCTTTTGGTGGCTACACATGCGTGGGACCTTCATTTTGGTGTGCCCCGG 1145
Db 1141 GGTCTTCTCTTGGAGGCTACCCCTCGAGGAGTGCATCTTCCGGGCTGAGCCCCCTG 1200
Qy 1146 CAAGGCTTTAAGCAAGTCTTCACTCATCTCTATAGCAATGCGCCAGGTATGC 1205
Db 1201 CAAGGCTCGGAGACAGAAAGGCTTACAGGTCTCTCTTATAGCAAAAGGTTCAGGTATGT 1260
Qy 1206 GCTTGGCGGGGCTTGAAGCGCGCATGTTAATGAGCAACAAGAGAAACCTCTTACCG 1265
Db 1261 GCTCAAGACAGCGCGCGCGCGGATGTTTACGAGAGAGAGCGGAGACCCGAGATACG 1320
Qy 1266 GCAGCAGGCGGCGCTGCGCTTGGCTTACGAGAACCCACGCGGGCGAAGAGTGTGCGGT 1325
Db 1321 GCAGCAGTCAAGAGTGCCTTGAAGAGAACCCACGAGCGGAGAGCGTGTGCTT 1380
Qy 1326 CGCGGAGGCGCGCAGGCGCACCTGTGTGACAGGCGGTGTGAAGAGAGACCTTCTGTGCGCA 1385
Db 1381 CGCGGCGGCGCGCAGGCGCACCTGTGTGACAGGCGGTGTGAAGAGAGACCTTCTATAGCGCA 1440
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TITLE OF INVENTION: METHOD OF ENHANCING BONE DENSITY OR FORMATION
FILE REFERENCE: 206211
CURRENT APPLICATION NUMBER: US/10/053.637
CURRENT FILING DATE: 2002-01-22
NUMBER OF SEQ ID NOS: 28
SOFTWARE: PatentIn version 3.1
SEQ ID NO 27
LENGTH: 1975
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: SEAP/W/VEGF121 fusion
NAME/KEY: CDS
LOCATION: (11)..(1963)
OTHER INFORMATION:
NAME/KEY: misc feature
LOCATION: (1538)..(1591)
OTHER INFORMATION: Spacer (W) encoded by the annealed nucleotides (SEQ ID NOS: 25 and 26)
NAME/KEY: misc feature
LOCATION: (1598)..(1960)
OTHER INFORMATION: VEGF121 domain
US-10-053-637-27

Query Match 67.9%; Score 1002.8; DB 15; Length 1975;
Best Local Similarity 80.1%; Pred. No. 1.8e-285;
Matches 1178; Conservative 0; Mismatches 292; Indels 0; Gaps 0;

6 CCTCATCCCAAGTGGAGAGAAACCCCGCTTCTTGAACCCGACGAGCCAGGCCCT 65
61 CATCATCCCAAGTGGAGAGAAACCCCGCTTCTTGAACCCGAGAGCCGAGGCCCT 120
66 TGATGAGCCAAAGATTGACGCGATCCAGACAGCTGCGCAAGATGTATCTCTCTT 125
121 GGGTGGCCCAAGAGAGCTGACGCTGCAAGACGCGCCAGAACTTATCTTCTCT 180
126 GGGGAGTGGAGTGGGGGCTCTTACGCTGACAGCACTCGATCTTAAAGGGCAGATGA 185
181 GGGCGATGGAGTGGGGGCTCTTACGCTGACAGCACTCTTAAAGGGCAGATGA 240
186 TGGCAAACTGGAGCTTGAACACCCCTGGCCATGACCAAGTTCCATACGTGGCTTGT 245
241 GGAACAACTGGAGCTTGAACACCCCTGGCCATGACCAAGTTCCATACGTGGCTTGT 300
246 CAAGACATCAAGTGGAG 305
301 CAAGACATCAAGTGGAG 360
306 GTGTGGAGTCAAGAGGCACTAAGAACATCGGTGTAGTGAAGCCGCGCTTACATCA 365
361 GTGTGGAGTCAAGAGGCACTTTCAGACATTTGGCTTGAAGTGAAGCCGCGCTTAA 420
366 GTGTGGAGTCAAGAGGCACTTTCAGACATTTGGCTTGAAGTGAAGCCGCGCTTAA 425
421 GTGTGGAGTCAAGAGGCACTTTCAGACATTTGGCTTGAAGTGAAGCCGCGCTTAA 480
426 GAAGGCGGTGGAGTGGTGAACCAACAGAGTGGAGAGAGAGAGAGAGAGAGAGAG 485
481 GAAGGCGGTGGAGTGGTGAACCAACAGAGTGGAGAGAGAGAGAGAGAGAGAGAG 540
486 GCGGCAACAGTGAACCGAACTGTGTCTCAAGCGCGAGCTTGTCTGTATGACAGAA 545
541 GCGGCAACAGTGAACCGCACTGTGTCTCAAGCGCGAGCTTGTCTGTATGACAGAA 600
546 GAATGGCTGGAG 605
601 GAAGGCGGTGGAG 660
606 GGGTGGAG 665
661 AGGTGGAG 720
666 TGCCAGTGTGAATGAGTCCGGAAGAGACAAAGAACTGTGTGAGAGAGAGAGAGAG 725

721 CTACAGCCAGAGTGGAG 780
726 GCAACAG 785
781 GCGGCAAG 840
786 CAGTGAACAG 845
841 GTCTGAG 900
846 AGACCAACAG 905
901 AGACCAACAG 960
906 CAGAAACCCCGGAG 965
961 CAGAAACCCCGGAG 1020
966 TGACGCAAG 1025
1021 TGAAAG 1080
1026 GCGTACAG 1085
1081 GCGGAG 1140
1086 TGCT 1145
1141 GCT 1200
1146 CAAGGCTTTAGACAG 1205
1201 CAAGGCTTTAGACAG 1260
1206 GCTTGGAG 1265
1261 GCTTGGAG 1320
1266 GAG 1325
1321 GAG 1380
1326 GCGGAG 1385
1381 GCGGAG 1440
1386 CATCATGAG 1445
1441 GGTATGAG 1500
1446 CACGCGCAACAG 1475
1501 CCGGAG 1530

RESULT 9
US-10-053-637-5
Sequence 5, Application US/10053637
Publication No. US20030158132A1
GENERAL INFORMATION:
APPLICANT: KOVESDI, IMRE
TITLE OF INVENTION: METHOD OF ENHANCING BONE DENSITY OR FORMATION
FILE REFERENCE: 206211
CURRENT APPLICATION NUMBER: US/10/053.637
CURRENT FILING DATE: 2002-01-22
NUMBER OF SEQ ID NOS: 28
SOFTWARE: PatentIn version 3.1
SEQ ID NO 5
LENGTH: 1918
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:

QY 66 TGAATAGCCAAAGAGTGGACGCCGATCCAGACAGCTGCCAAGATGATCTCTTCTT 125
DB 111 GGGTGCCTCCAGAAAGCTGAGCTCTGACAGACAGCGCCGCAAGAACCTATCATCTTCT 170
QY 126 GGGGATTTGGGATTTGGGGGTGCTTACGGTGAACGCCACTCGGATCTTAAAGGGGACATGTA 185
DB 171 GGGCGATGGGATTTGGGGGTGCTTACGGTGAACGCCACTCGGATCTTAAAGGGGACAGAA 230
QY 186 TGGCAAACTGGGACTGAGACACCCCTGGCATGACCAATGCCATTAAGTGGCTGTG 245
DB 231 GGAACAACCTGGGGCTTGAAGATACCTTGGCATGACCCGCTTCCATTAATGTGCTGTG 290
QY 246 CAAGACATACAAAGTGGACAGACAGGTGCCAGACAGCGAGGACCTGCACTGCACTGCACT 305
DB 291 CAAGACATACAAATGTAGACAAACATGTGCAGACATGTGAGGCCACAGCCACGGCTTACCT 350
QY 306 GTGTGGGGTTCAGAGGGGCACTACAGAACCATCGGTGTAAGTGCAGCGCCCGCTTACATCA 365
DB 351 GTGCGGGGTTCAGAGGGGCACTTCCAGACCATTTGGCTTGAAGTGCAGCGCCCGCTTAAACA 410
QY 366 GTGCAACACGACACGTGGGATGAGGTCAAGTCTGTATCAACCGGGCCAAAGAACAG 425
DB 411 GTGCAACACGACACGCGGCAAGAGGTCAATCTCGTATGAATCGGGCCAAAGAACAG 470
QY 426 GAAAGCCGTGGAGTGTGTGACCAACACAGGTGCAGCATGCTCCCAAGCGGGGCTTA 485
DB 471 GAAAGTCAGTGGAGTGTGTGACCAACACAGAGTGCAGCAGCTCCGACAGCGGACCTTA 530
QY 486 CCGGACACAGGTGAAACCGAACTGGTACTCAGACCGCCGACCTGCTGTGTGATGACAGAA 545
DB 531 CCGGACACAGGTGAAACCGAACTGGTACTCAGACCGCCGACCTGCTGTGTGATGACAGAA 590
QY 546 GAATGGCTCCAGACATCGCCGACAGCTGTGTCTTCAACATGATATTAAGTGTATCT 605
DB 591 GGAAGGGTCCAGACATCGCTACAGAGTCTCATCTTCCAAATGAGCATTTGAGTATCT 650
QY 606 GGGTGGAGCCGAAATGTATCATGTCTTCTGAGGGAGCCCGACACCTGAATACCAAGATGA 665
DB 651 AGTGGAGGCGGAAAGTATCATGTCTTCCATGGGAACCCGACACCTGATACCAAGATGA 710
QY 666 TCCCATGTGAAATGAGTCCGGAAGGACAGAGAACTGTGTGAGGAATGGCAAGGCCAA 725
DB 711 CTACAGCCAAAGTGGAGCCAGGCTGACGGAAGAAATCTGTGAGGAATGGCTGCGCAA 770
QY 726 GCACCAAGGAGCCAGTATGTGTGAAACGCACTGCGCTCTTCAAGGGCGCGATGATCTC 785
DB 771 GCGCCAGGGTGCCTCGGTATGTGTGAAACGCACTGAGCTATGCAAGGCTTCCCTGAGACC 830
QY 786 CAGTGTAAACACCTCATGAGGCTCTTTGAGCCGCGACATGAATATATATGTTCAAGCA 845
DB 831 GTCTGTGACCATTCATCGATGGGTCTTTGAGCCTGGAGCATGAATATGAGATCCACCG 890
QY 846 AGACCAACACCAAGAACCCGACCTTGCAGGATGACGAGGGGCGCCCTGCAAGTGTGAG 905
DB 891 AAGCTTCACACTGAGACCCCTCCCTGATGAGATGACAGAGGCTGCGCTGCTGTGAG 950
QY 906 CAGGAACCCCGGGGCTTCTACCTCTTGTGAGGAGGCGCGCATTTGACACAGGTCAACA 965
DB 951 CAGGAACCCCGGGGCTTCTCTCTTGTGAGGAGGCGCGCATTCGACACAGGTCAACA 1010
QY 966 TGAAGCAAAAGCTTATATGCACTGACGTAGGCGATGATGTTGAACATGTCATGACCA 1025
DB 1011 TGAAGCAAGGGCTTACCGGGCACTGACGTAGACGATCATGTTGACAGAGCATTTGAGAG 1070
QY 1026 GGGTAAACAGCTCATAGGAACTGACACGCTGATCTTGTGACATGACAGACATCTCCA 1085
DB 1071 GCGGGGCAAGCTCACAGGAGAGAGACAGCTGAGCCCTGCTGACATGCGACACATCTCCA 1130
QY 1086 TGTCTTCTCTTTTGGGCTACACACTGAGTGGGACCTTCATTTTCGATGAGCCCGG 1145
DB 1131 GGTCTTCTCTCTTGGAGGCTACCCCTGCGAGGAGAGCTCATCTTTCGAGCTGAGCCCTGAG 1190
QY 1146 CAAGGCTTGAACAGCAAGTCTTACACCTCATCTTATGCAATGGCCAGGCTATGC 1205

DB 1191 CAAGGCTCCGAGACAGAAAGGCTTACACGATCTCTTATACGAAACGGTCCAGGCTATGT 1250
QY 1206 GCTTGGCGGGGCTTGAAGGCCGCAATGTTAATGACAGACAAAGCGAGAACCTCTATACC 1265
DB 1251 GCTCAAGACAGCGCGCGCGCGGATTTACAGAGACAGAGCGGAGACCCCGAGTATCG 1310
QY 1266 GCAGCAGCGGGCGCGCGCTTGAAGGAGACCAAGGAGGAGGAGAGAGTGGCGGTGT 1325
DB 1311 GCAGCAGTACAGAGTGCCTTCTGAGACGAAAGAACCAAGCAGGCGAGAGCTGTGCTGT 1370
QY 1326 CCGCGAGGCGCGCAGCGGACCTTGTGACAGCGCTGAGAGAGAGACCTTGTGCGCA 1385
DB 1371 CCGCGCGGCGCGCAGCGGACCTTGTGACAGCGCTGAGAGAGAGACCTTGTGCGCA 1430
QY 1386 CATCATGCTTCTTGGGGGCTGCTGAGAGCCCTTACACGACATCTGCAATCTGCCAGCCCGC 1445
DB 1431 GCTCATGAGCTTTCGCGCGCTGCTGAGAGCCCTTACACGCTTGCAGCTGGGCGCCCGC 1490
QY 1446 CACGCGACACAGCATCCCGAGCTAGGGTACC 1476
DB 1491 CCGCACACACGACGCGCGCACCCAGGTAC 1521

RESULT 11
US-10-071-645-4
; Sequence 4, Application US/10071645
; Publication No. US20030148389A1
; GENERAL INFORMATION:
; APPLICANT: Bihain, Bernard
; APPLICANT: Bour, Barbara
; APPLICANT: Bouqueleret, Lydie
; TITLE OF INVENTION: Schizophrenia Related Gene and Protein
; FILE REFERENCE: 92, US2, CIP
; CURRENT APPLICATION NUMBER: US/10/071, 645
; PRIOR FILING DATE: 2002-02-06
; PRIOR APPLICATION NUMBER: 60/223, 482
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: PCT/IB01/01891
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patent.pm
; SEQ ID NO: 4
; LENGTH: 1779
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-071-645-4

Query Match 67.9%; Score 1002; DB 15; Length 1779;
Best Local Similarity 80.2%; Pred. No. 3e-285;
Matches 1176; Conservative 0; Mismatches 290; Indels 0; Gaps 0;

QY 8 TCATCCAGCTGAGAGGAGAAACCCGCTTGTGAAACCGCGACGAGCCAGGCGCTTG 67
DB 215 TCATCCAGCTGAGAGGAGAAACCCGCTTGTGAAACCGCGAGGACGCGAGCGCTTG 274
QY 68 ATGTAGCAAAAGTGTGAGCGGATCCAGACAGCGTCCAAAGTATATCTCTTTGG 127
DB 215 TCATCCAGCTGAGAGGAGAAACCCGCTTGTGAAACCGCGAGGACGCGAGCGCTTG 274
QY 275 GTGCGGCAAAAGCTGAGCGCTTGTGACAGAGAGCGCCAAAGCTTATCTTCTGG 334
DB 128 GGAATGGATGGGGGTCTTACGGTGAACGCACTCGGATCTTAAAGGGGAGATGATG 187
QY 335 GGAATGGATGGGGGTGTCTACGGTGAACGCTGACAGAGAGCGCCAAAGCTTATCTTCTGG 394
DB 188 GGAATGGATGGGGGTCTTACGGTGAACGCACTCGGATCTTAAAGGGGAGATGATG 247
QY 395 ACAAACCTGGGGCTGAGATACCCCTGGCAATGAGACCGCTTCCATATGTGCTGTCCA 454
DB 248 AGACATCAAGTGTGACAGACAGTGCAGACAGCGAGGACCTGCACTGAGCTTGTCCA 307
QY 455 AGACATCAAGTGTGACAAACATGTGCAGACAGTGTGAGGCGACAGCGGCTTATCTTGT 514
DB 308 GTGGGGTCAAGGGCACTACAGAACATCGGTGTATGTGAGCGCGCGCTAATCATAGT 367

Db 515 GCGGGGCTCAAGGCACTTCACAGCATGTGGCTTGAAGCCGCGCCCTTTAAACAGT 574
Qy 368 GCACACGACACGTGGGAATGAGTCACTGTGTATCAACCGGGCCCAAGAAAGCAGGA 427
Db 575 GCAACACGACACCGGGCAAGAGTCACTTCGGTGAATCGGGCCCAAGAAAGCAGGA 634
Qy 428 AGGCGGTGGAGTGTGACACCAACGAGGTGACAGTGCCTCCCGAGCCGGGGCTTACG 487
Db 635 AGTCAGTGGAGTGTGATACCAACACAGATGACAGCGCTTGGCCAGCCGGCACTTACG 634
Qy 488 CGCACACGTGAAACCGAACTGTGACTCAGACCGCCGACCTGCTGTATGACAGAGA 547
Db 695 CCCACAGGTGAACCGCACTGGTACTCGACCGCCGAGTGGCTGCTCGGCCCGCAGG 754
Qy 548 ATGCTGTCCAGACATGTGCGGCACAGTGTCTTCAACATGATATTGATGATCTTGG 607
Db 755 AGGGGTGCGCAGACATGTGCTACAGAGCTCATCTTCAACATGACATTTGACGTATCTTAC 814
Qy 608 GTGAGGCGCGAATGTATCATGTCTTCTGAGGGGACCCCGACCTGAAATACCCAGATGATG 667
Db 815 GTGAGGCGCGAATGTATCATGTCTTCTGAGGGGACCCCGACCTGAAATACCCAGATGATG 874
Qy 668 CCAAGTGAATGAGTCCGGAAGACAGACAACTGTGTGACAGAAATGACAGCCCAAGC 727
Db 875 ACAGCCAAAGTGGAGACAGGCTGAGCGGAAGATGTGTGACAGAAATGCTGGCCAGC 934
Qy 728 ACCAGGAGCCCAAGTATGTGTGACACGCACTGCGCTCTTCAAGCGCGCCAGTATCCA 787
Db 935 GCGAGGAGTGCCTGGTATGTGTGACACGCACTGAGCTCATGACAGGCTTCCCTGGACCGGT 994
Qy 788 GTGTAAACACACTCATGAGGCTCTTGTGAGCGCGACAGCATGAATGATATATTCAGCAAG 847
Db 995 CTGTGACCATCTTCAATGAGTCTCTTGTGAGCTGTGAGACATGAATATGAGATCCAGCAG 1054
Qy 848 ACCACACCAAGACCCGACCTGTGAGAGATGACGAGGCGGCGCTGCAAGTGTCTGACGA 907
Db 1055 ACTCCACACTGACACCCCTCTGATGAGATGACAGAGGCTGCGCTGCGCTGTGACGA 1114
Qy 908 GGAACCCCGGGGCTTCACTCTTGTGTGAGGAGGCGCCATTTGACACAGTGCATCATG 967
Db 1115 GGAACCCCGGGGCTTCTTCTCTGTGTGAGGAGTGTGCTCATGACCATGTGATCATCATG 1174
Qy 968 AGGCAAGAGCTTATGAGCACTGACAGGCGATCATGTTTGAACAATGCCATGCCAAG 1027
Db 1175 AAAGCAGGCTTACCGGCACTGACGATGACATGATGATGACAGGCCATTTGAGAGG 1234
Qy 1028 CTAAAGAGCTCACTAGGCACTGACACGCTGATCTTGTCTACTGACAGACCACTCCCATG 1087
Db 1235 CGGGCAGCTCACACAGGAGAGGACACGCTGAGCTGTCTGACCTGCGGACCACTCCACG 1294
Qy 1088 TCTTCTCTTTTGTGCTTACACACTGCTGTGAGACCTTCAATTTTGTGCTTGGCCCGGCA 1147
Db 1295 TCTTCTCTTCTGAGAGGCTACCCCTGTGAGGAGCTCATCTTCTGAGGCTGGCCCTTGGCA 1354
Qy 1148 AGGCTTGAACAGAGTCTTACACCTCATCTTATGAGCAATGCGCCAGGCTATGAGCG 1207
Db 1355 AGGCTGAGGACAGAGAGCTTACAGGCTCTCTTATGAGAAACGCTGACAGGCTATGAGCG 1414
Qy 1208 TTGGCGGGGCTGAGGCGCCGATGTTAATGAGCAACAGCAGAAACCTCTCATACCGC 1267
Db 1415 TCAAGAGCGGCGCGCGCGGAGTGTACGAGAGCGAGAGCGGGAGCCCGCAGATATCGC 1474
Qy 1268 AGCAGCGGCGCTGCTGCTGTGAGAGACCAACCGGGGCGAAAGCTGTGGCTGTGG 1327
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Qy 1388 TCATGAGCTTTGCGGCGTGTGTGAGGCTTACACCGACTCAATCTTGCAGAGCCCGCGCA 1447

Db 1595 TCATGAGCTTTGCGGCGCTGTGTGAGGCGCTTACACCGCTTGTGAGCGCCCGCGCG 1654
Qy 1448 CGGCGACAGCATTCGCCGACTAGGGT 1473
Db 1655 GCACACCGAGCGCGCGCACCGGGT 1680

RESULT 12
US-10-182-094-7
; Sequence 7, Application US/10182094
; Publication No. US2004001913A1
; GENERAL INFORMATION:
; APPLICANT: Liang, Peng
; TITLE OF INVENTION: MOB-5/HMOB-5 AS A CANCER DIAGNOSTIC MARKER
; FILE REFERENCE: 22000.0091U3
; CURRENT APPLICATION NUMBER: US/10/182.094
; CURRENT FILING DATE: 2002-07-25
; PRIOR APPLICATION NUMBER: US 60/178.185
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 2051
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: /No. US2004001913A1e =
US-10-182-094-7

Query Match 67.9%; Score 1002; DB 16; Length 2051;
Best Local Similarity 80.2%; Pred. No. 3.1e-285;
Matches 1176; Conservative 0; Mismatches 290; Indels 0; Gaps 0;

Qy 8 TCATCCAGCTGAGAGAAACCCGCTTGTGAAACCGCCAGGACCCAGCCCTTG 67
Db 583 TCATCCAGCTGAGAGAAACCCGCTTGTGAAACCGCCAGGACCCAGCCCTTG 642
Qy 68 ATGTACCAAGAGTGTGAGCGGATCCAGACAGCTGCAAGATGATCTTCTTGG 127
Db 643 GTGCCCAAGAGTGTGAGCGGATCCAGACAGCTGCAAGATGATCTTCTTGG 702
Qy 128 GGGATGAGTGGGGGTGCTTACAGTGTGACAGCCACTGCGATCTTAAAGGGCAGATGATG 187
Db 703 GCGATGAGTGGGGGTGCTTACAGTGTGACAGCCACTGCGATCTTAAAGGGCAGATGATG 762
Qy 188 GCAACTGAGACCTGAGACACCCCTGTGCAATGAGCAAGTTCATAGTGTGTCCA 247
Db 763 ACAACTGAGGCGCTGAGATACCCCTGTGCAATGAGCAAGTTCATAGTGTGTCCA 822
Qy 248 AGACATACAGCTGTGACAGACAGTGTGCAAGACAGGCGCACTGCTTACTGT 307
Db 823 AGACATACAGCTGTGACAGACAGTGTGCAAGACAGGCGCACTGCTTACTGT 882
Qy 308 GTGGGTCAAGGGCACTACAGAAACCATGCTGTATGTCAGGCGCCGCTTACATCAGT 367
Db 883 GCGGGTCAAGGGCACTTCAAGCACTTGTGTGATGAGTGTGAGCGCCGCTTTAACAGT 942
Qy 368 GCAACACGACAGTGTGAAATGAGTCACTGTGTGATCAACCGGGCCAAAGAAAGCAGGA 427
Db 943 GCAACACGACAGTGTGAAATGAGTCACTGTGTGATGATGAGGCGCAAGAAAGCAGGA 1002
Qy 428 AGGCTGTGAGTGTGATCAACCAAGGCTGAGATGCTTCCAGCCGGGCTTACG 487
Db 1003 AGTCACTGAGAGTGTGATCAACCAAGGCTGAGATGCTTCCAGCCGGGCTTACG 1062
Qy 488 CGCACAGGTGAACCGAACTGTGACTCAGACGCGGACCTGCTGTGATGACAGAGA 547
Db 1063 CCACACAGGTGAACCGAACTGTGACTCAGACGCGGACCTGCTGTGATGACAGAGA 1122
Qy 548 ATGCTGTCCAGGACATGCGCGACAGCTGTCTTAAACAATGATATTGACGTGATCTGG 607
Db 1123 AGGGGTGCGAGGACATGCTGTGACAGCTCATCTTCAACATGAGCATTTGACGTATCTAG 1182

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QY 608 GTGAGAGCCGAATGATCATGTTTCTGAGGGAGCCCAAGACCTGTAAATCCAGATGATG 667
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Db 1183 GTGAGAGCCGAATGATCATGTTTCTGAGGGAGCCCAAGACCTGTAAATCCAGATGACT 1242
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QY 668 CCAAGTGTAAATGAGTCCGGAAGAGACAGACAACTGGTGCAGGAATGGCAGGCCAAGC 727
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Db 1243 ACAGCCAGAGGTGGAGCAAGCTGTGACGAGGAAGAAATGTGTGACAGGAATGGCTGGCAAGC 1302
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QY 728 ACCAGGAGACCCAGTATGTGTGGAACCGACCTGCTCCCTTACAGGCGCGCATGACTCCA 787
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Db 1303 GCCAGGGTGTCCGGATATGTGTGGAACCGACCTGACTGACAGGCTTCCCTGAGACCCGT 1362
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QY 788 GTGTAAACACACTCATGAGGCTCTTGTAGCCCGCAGACATGAATGAATGTTACAGCAAG 847
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Db 1363 CTGTGACCATCTCATGGGTCTCTTGTAGGCTGTGAGACATGAATGACGAGATCCAGC 1422
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QY 848 ACCACACCAAGAGCCGAGCTCTGTGGAGATGAACGAGGCGGCTGCAAGTGTGAGGA 907
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Db 1423 ACTCCACACTGTGACCCCTCCCTGATGAGATGACAGAGGCTGCGCTGCGCTGTGAGCA 1482
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QY 908 GGAACCCCGGGGCTTCTACCTCTTGTGAGGAGGAGCGCATTTGACACAGGTCAACATG 967
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QY 968 ACAGCAAAAGCTTATATGCACTGACTGAGGCGATCATGTTTGAATGCAATGCCATGCCAAG 1027
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Db 1543 AAAGCAAGGGCTTACCGGGCACTGACTGAGACGATCATGTTTGAACGACGCGCATTTGAAGAG 1602
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QY 1028 CTAAACAGCTCATTAACGAACTGGAACACGCTGATCTCTTGTGATGAGACACTTCCCATG 1087
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QY 1088 TCTTCTCTTGTGTGCTACACACTGTGTGAGCACTTCCATTTTGTGCTGTGGCCCGGCA 1147
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Db 1663 TCTTCTCTTGTGAGGTTATCCCTGTGAGAGGAGCTCATCTTGTGGCTGTGGCCCGGCA 1722
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QY 1148 AGGCTTGAACAGACAGTCTTCACTCCATCTCTTATGAGCAATGGCCCGGAGGTATGCGC 1207
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Db 1723 AGGCTTGAACAGAGAGGCTTCACTCCATCTCTTATGAGCAATGGCTGTGGAGGTATGCGC 1782
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QY 1208 TTGGCGGGGCTGAGGCGCGATGTTTATGAGCAGCAACGAGAGAACTCTCATACCGG 1267
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Db 1783 TCAAGAGCGGCGCGCGCGCGAGTGTACCGAGAGCAGAGCGGAGCGCGAGTATGCGC 1842
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QY 1268 AGCAGCGGCGCGCGCGCGCGCTGAGCGAGACCCACGCGGCGAGAACTGTGGCGGTTCG 1327
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Db 1843 AGCAGCTAGCAGTGTGCGCGCTGTGACGAAAGAACCCACGAGCGAGAGAGTGTGGCGGTTCG 1902
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QY 1328 CGGAGGCGCGCGAGCGGCACTGTGTGACGCGCGTGTGAGAGAGAGACCTTGTGGCGGACA 1387
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Db 1903 CGGCGCGCGCGAGAGCGGCACTGTGTGACGCGCGTGTGAGAGAGAGACCTTGTATAGCGGACG 1962
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QY 1388 TCATGAGCTTTGCGGGGTGTGCGTGTGAGGCTTACACCGACTGCAATCTGTGAGCGCGGCA 1447
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Db 1963 TCATGAGCTTTGCGGGGTGTGCGTGTGAGGCTTACACCGACTGCAATCTGTGAGCGCGGCGC 2022
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QY 1448 CCGGCAACAGCATCCCGACTAAGGT 1473
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Db 2023 GCAACCAACGAGCGCGGCAACCGGGT 2048
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RESULT 13
US-10-182-094-9
; Sequence 9, Application US/10182094
; Publication No. US20040019193A1
; GENERAL INFORMATION:
; APPLICANT: Liang, Peng
; TITLE OF INVENTION: MOB-5/HMOB-5 AS A CANCER DIAGNOSTIC MARKER
; FILE REFERENCE: 22000.0091U3
; CURRENT APPLICATION NUMBER: US/10/182.094
; CURRENT FILING DATE: 2002-07-25
; PRIOR APPLICATION NUMBER: US 60/178,185
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;; PRIOR FILING DATE: 2000-01-26
;; NUMBER OF SEQ ID NOS: 22
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO: 9
;; LENGTH: 2121
;; TYPE: DNA
;; ORGANISM: Artificial Sequence
;; FEATURE: Description of Artificial Sequence: /No. US20040019193A1e =
;; OTHER INFORMATION: Synthetic construct
US-10-182-094-9

Query Match      67.9%; Score 1002; DB 16; Length 2121;
Best Local Similarity 80.2%; Pred. No. 3.1e-285;
Matches 1176; Conservative 0; Mismatches 290; Indels 0; Gaps 0;

QY 8 TCATCCCACTGAGAGAGAAACCCGCTTTGTGAAACCGGACGAGCCAGGCCCTTGG 67
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Db 653 TCATCCCACTGAGAGAGAGAAACCCGCACTTGTGAAACCGGAGGAGAGCCGAGCCCTGG 712
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QY 68 ATGTAGCCAAAGATTGTGAGCCGATCCAGACAGTGCAGAAATGTATCTCTTTGG 127
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Db 713 GTGCGGCCAAGAGGCTGACGCTGTACAGACAGCGCCAGAACTCATCTTCTCTGG 772
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QY 128 GGGATGGATGGGGGCTCTACGGTACAGGCACTCGGATCTTAAAGGGCAGATGAATG 187
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Db 773 GCGATGGATGGGGGTCTACGGTACAGGCACTCGGATCTTAAAGGGCAGAAAGG 832
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QY 188 GCMAACTGGAGACTGTAGACACCTCTGTGATGACAGATTCCATACGTGCTCTGTCCA 247
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Db 833 ACAACTGGGGCTGTAGATACCCCTGGGCACTGAGACCGCTTCCATATGTGCTGTCCA 892
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QY 368 GCAACACGACACTGTGGAAATGAGTCACTGTGTGATCAACCGGGCCAAAGAAAGAGGGA 427
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Db 1013 GCMAACGACACACGCGGCAACGAGTCACTCGGTATATATGTGGCCAAAGAAAGAGGGA 1072
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QY 428 AGCGGTGGAGTGTGTGACACACACAGGAGTGCAGATGCTCTCCCAAGCGGGGCTTACG 487
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QY 548 ATGGCTGCTGAGACATTCGCGGACAGCTGTGTCTTAAATGATGATTTGACGATGATCTGG 607
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QY 608 GTGAGAGCCGAATGTACATGTTTCTGTAGGGGAGCCCAAGACCTGTGAATACCAATGATG 667
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Db 1253 GTGAGAGCCGAATGTACATGTTTCTGTAGGGGAGCCCAAGACCTGTGAATACCAATGACT 1312
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QY 668 CCAAGTGTAAATGAGTCCGGAAGAGACAGACAGAACTGTGTGAGAAATGGCAGGCCAAGC 727
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Db 1313 ACAGCCAAAGTGTGAGACAGGCTGTGACGCGGAAAMAATGTGTGAGAAATGGCTGGGAAAGC 1372
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QY 728 ACCAGGAGACCCAGTATGTGTGGAACCGGACTGCGCTCTTACAGGCGGCGGATGACTCCA 787
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Db 1373 GCCAGGGTGTCCGGTATGTGTGGAACCGGACTGAGGCTTCTGTGAGGCTTCCCTGAGACCCGT 1432
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QY 788 GTGTAAACACACTCATGAGGCTCTTGTGAGCCCGGACAGACATGAATGAATGTTACAGCAAG 847
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Db 1433 CTGTGACCATCTCATGGGTCTCTTGTGAGCCTGTGAGACATGAATGACGAGATCCAGCAG 1492
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QY 848 ACCACACCAAGAGACCCGACTGTGGGAGATGACGAGGCGGCTGTGCAAGTGTGAGGA 907
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1493 ACTCCACTGAGACCCCTCCCTGATGAGATGACAGAGGCTGCCTGCGCTGTGAGCA 1552
QY 908 GGAACCCCGGGGCTTACTCTTGTGAGAGGAGGCCCATTTGACAGGCTACCATG 967
Db 1553 GGAACCCCGGGGCTTACTCTTGTGAGAGGAGGCTGCATGACATGATGATCATG 1612
QY 968 ACCGCAAGCTTATATGACTGACTGAGGCGATCATGTTTGAATGATGATGAGG 1027
Db 1613 AAGCAGAGGCTTACCGGCACTGACTGAGAGCATGTTTGAATGATGATGAGG 1672
QY 1028 CTACAGAGCTCACTAGGAACTGAGACAGCTGATCTTGTCTACTGACAGACCTCCATG 1087
Db 1673 CCGGCAAGCTCACTAGGAGAGAGACAGCTGAGCTGCTGCTGACAGACCTCCATG 1732
QY 1088 TCTTCTCTTGTGCTGATACACACTGCTGAGAGAGCTTCTGCTGCTGCTGCTGCTG 1147
Db 1733 TCTTCTCTTGTGAGAGGCTGATCCCTGAGAGAGCTTCTGCTGCTGCTGCTGCTG 1792
QY 1148 AGGCTTATGACAGCAAGTCTTACCTTCTTATGAGCAATGAGGCTGATGCTGCTG 1207
Db 1793 AGGCTTATGACAGCAAGTCTTACCTTCTTATGAGCAATGAGGCTGATGCTGCTG 1852
QY 1208 TTGGCGGGGCTGAGGCGCGATGTTAATGAGCAAGCAAGCAAGCAAGCAAGCAAG 1267
Db 1853 TCAAGAGCGGCGCGCGCGCGATGTTAATGAGCAAGCAAGCAAGCAAGCAAGCAAG 1912
QY 1268 AGAGGCGCGCGCGCGCGCGCTGCTGAGAGCAAGCAAGCAAGCAAGCAAGCAAG 1327
Db 1913 AGAGGCGCGCGCGCGCGCGCTGCTGAGAGCAAGCAAGCAAGCAAGCAAGCAAG 1972
QY 1328 CGGAGAGCGCGCGCGCGCGCTGCTGAGAGCAAGCAAGCAAGCAAGCAAGCAAG 1387
Db 1973 CGGAGAGCGCGCGCGCGCGCTGCTGAGAGCAAGCAAGCAAGCAAGCAAGCAAG 2032
QY 1388 TCATGAGCTTGTGGGCTGCTGAGAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 1447
Db 2033 TCATGAGCTTGTGGGCTGCTGAGAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 2092
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Db 2093 GCACCAACAGCATCCCGCATAGGCT 2118

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RESULT 14
US-09-006-298-22
; Sequence 22, Application US/09006298
; Patent No. US2002008224A1
; GENERAL INFORMATION:
; APPLICANT: Jolly, Douglas J.
; APPLICANT: Moore, Margaret D.
; APPLICANT: Chada, Sunil
; TITLE OF INVENTION: NON-IMMUNOGENIC PRODRUGS AND SELECTABLE
; TITLE OF INVENTION: MARKERS FOR USE IN GENE THERAPY
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED AND BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/006,298
; FILING DATE: 13-JAN-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: McMaister, David D.

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; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 930049, 459
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1634 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 13..1617
; US-09-006-298-22

Query Match 67.8%; Score 1001.4; DB 9; Length 1634;
Best Local Similarity 80.2%; Pred. No. 4,4e-285;
Matches 1176; Conservative 0; Mismatches 291; Indels 0; Gaps 0;

QY 6 CCTCATCCAGCTGAGAGGAAACCCCGCTTCTGGAACCGGCAGGACGCGGCTT 65
Db 78 CATCATCCAGCTGAGAGGAAACCCCGCTTCTGGAACCGGCAGGACGCGGCTT 137
QY 66 TGATGAGCAAGAAATTCAGCCGATCCAGACAGCTGCAAGAAATGTCATCTTCTT 125
Db 138 GGGTCCCGCCAGAAACTGACGCTGCAAGACAGCAGCAGCAGCAGCAGCAGCAG 197
QY 126 GGGGATGGAGTGGGGTCTTACGCTGACAGCAAGCAAGCAAGCAAGCAAGCAAG 185
Db 198 GGGGATGGAGTGGGGTCTTACGCTGACAGCAAGCAAGCAAGCAAGCAAGCAAG 257
QY 186 TGCAAACTGGAGCTGAGACACCCCTGCGCATGAGCAAGTTCCTATAGTGGCTGTC 245
Db 258 GGAACAACTGGGGCTGAGATACCCCTGCGCATGAGCAAGTTCCTATAGTGGCTGTC 317
QY 246 CAAGACATCAAGCTGAGACAGAGTGCAGACAGGAGGAGCAAGCAAGCAAGCAAG 305
Db 318 CAAGACATCAAGCTGAGACAGAGTGCAGACAGGAGGAGCAAGCAAGCAAGCAAG 377
QY 306 GTGTGGGGTCAAGGGCACTACAGAACATCGGTGTAAGTGCAGCGCGCTTACATCA 365
Db 378 GTGTGGGGTCAAGGGCACTTCCAGACATTTGGCTTGAAGTGCAGCGCGCTTACATCA 437
QY 366 GTTCAACAGACAGACGTTGGAGATGAGTGCAGCTGTGATCAACCGGCGCAAGAAACAG 425
Db 438 GTTCAACAGACAGACGTTGGAGATGAGTGCAGCTGTGATCAACCGGCGCAAGAAACAG 497
QY 426 GAAAGCGTGGAGTGTGACCAACCAAGGAGTGCAGCATGCTCCCAAGCGGGGCTTA 485
Db 498 GAAAGCGTGGAGTGTGACCAACCAAGGAGTGCAGCATGCTCCCAAGCGGGGCTTA 557
QY 486 CGGCAACAGGTAACCGAAACTGTACTCAGACGCGGAGCTGCTGATGACAGAA 545
Db 558 CGGCAACAGGTAACCGCAACTGTACTCAGACGCGGAGCTGCTGATGACAGAA 617
QY 546 GAAATGCTCCAGAGACATGCGGACAGCTGTCTAACAATGATATTTGACGTATCT 605
Db 618 GAGAGGAGTCCAGAGACATGCGGACAGCTGTCTAACAATGATATTTGACGTATCT 677
QY 606 GGGTGAAGCCCAATTAATGATTTCTGAGGGAACCCCAAGCCCTGAATATCCCAATGA 665
Db 678 AGGTGAAGCCCAATTAATGATTTCTGAGGGAACCCCAAGCCCTGAATATCCCAATGA 737
QY 666 TGCAGTGAATGAGTCCGGAAGGACAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 725
Db 738 CTACAGCCAGAGTGGAGCAAGCTGGAACGGAAGAAATCTGTGCAAGAAATGCTGCGAA 797
QY 726 GACACAGGAGCCCAATATGTGTGAACCGCACTGCGCTCTTCAAGCGGCGAGTACT 785
Db 798 GCGCCAGGAGTCCCGATATGTGTGAACCGCACTGAGCTCATGAGAGCTTCCCTGAGACC 857
QY 786 CAGTGAACACACTCATAGGCGCTTTTGAAGCGCGGAGACATGAAGTATATATTTAGCA 845

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Db 858 GTCTGACCCACATCTCATGGGTCTTTTGAAGCTTGAGACATGAAATAGAGATTCACCG 917
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Db 918 AAGATCTCAACTGAGACCCCTCTCTGATGAGATGACAGAGGCTGCCCTCGCTGTGAG 977
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Db 978 CAGGAACCCCGGGGCTTACTCTTCGTGAGGGAGGTGTCGATGACCAAGGTACCA 1037
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Db 1098 GCGGAGCGAGCTCAACGAGAGAGGACAGCTGAGCCTGTCACCTGCGACCACTCCA 1157
Qy 1086 TGTCTTCTCTTTGATGCTACACATGAGTGGGACCTGCATTTTGGTGTGGCCCGG 1145
Db 1158 CGTCTTCTCTTGGAGGCTACCCCTGCGAGGAGCTCATCTTGGGCTGACCTTG 1217
Qy 1146 CAAGGCTTGAACAGCAAGTCTTACACTCACTCTCTATGCAATGAGCCAGCTATGC 1205
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Qy 1206 GCTTGGCGGGGCTCGAGGCGGATGTTATGACAGACAAAGCGAGAAACCTCTATACG 1265
Db 1278 GCTCAAGAGCGGGCGCGGATGTACCGAGACGAGAGCGGAGCGCCGAGATGATG 1337
Qy 1266 GCAGCAGGCGGCGGCTGCTGCTGCTAGCGAGACCCAGGGGGGAGAGAGTGGCGGTT 1325
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Db 1398 CGGCGCGGCGCGCAGAGCGCACTGTGTGACAGCGCGTGCAGAGAGACCTTGTGCGCA 1457
Qy 1386 CATCATGCGCTTGGCGGCTGCGTGTGAGAGCCCTTACACCGACTGCAATCTGCAAGCCCCG 1445
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Db 1518 CCGCACACACGAGCGCGCGCACCCG 1544

RESULT 15
US-10-332-733-26
Sequence 26, Application US/10332733
Publication No. US20040106565A1
GENERAL INFORMATION:
APPLICANT: Margarette Odenthal and Diana Jung
TITLE OF INVENTION: Gene Expression, Genome Alteration And Reporter Expression
FILE REFERENCE: 1472/68806
CURRENT APPLICATION NUMBER: US/10/332,733
NUMBER OF SEQ ID NOS: 41
SOFTWARE: Patent Ver. 2.1
SEQ ID NO 26
LENGTH: 1558
TYPE: DNA
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: Description of artificial sequence: SEAP
US-10-332-733-26

Query Match 67.8%; Score 1000.8; DB 17; Length 1558;
Best Local Similarity 80.1%; Freq. No. 6.6e-285;
Matches 1176; Conservative 0; Mismatches 292; Indels 0; Gaps 0;

Qy 6 CCTCATCCAGCTGAGAGAAAAACCCCGCTTCTGAAACCGCAGGAGCCGACCCCT 65
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Qy 66 TGAATGACCAAGAGATTGACGCGGATCCAGACAGCTGCGCAAGAAATGTCATCTTCTT 125
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Qy 306 GTGTGGGCTCAAGGCGCACTACAGAACATGCTGTATAGTGCAGCGCGCGCTCAATCA 365
Db 351 GTGCGGGGTCAAGGCGCACTTTCAGACCATGCTTGTAGTGCAGCGCGCGCTTAAACA 410
Qy 366 GTGCAACACGACAGCTGGGAAATGAGTCAAGTCTGTGATCAACCGGGCGCAAGAAAGCAG 425
Db 411 GTGCAACACGACAGCGCGCAACGAGTCACTCGGTATGAAATGGGGCGCAAGAAAGCAG 470
Qy 426 GAAAGCGGTGGAGTGTGACCAACCAAGGTGACAGATGCTTCCAGCGGGGCTTA 485
Db 471 GAAAGTCAATGGGAGTGTGACCAACCAAGGTGACAGATGCTTCCAGCGGGGCTTA 530
Qy 486 CGCGCACAGGTGAACCGAACTGGTACTCAGACGCGGACCTGGCTGCTGATGACAGAA 545
Db 531 CGCGCACAGGTGAACCGAACTGGTACTCAGACGCGGACCTGGCTGCTGATGACAGAA 590
Qy 546 GAATGCTGCGAGACATGCGCGCACAGCTGCTTACAACTGATATTTGACGTGATCT 605
Db 591 GGAAGGGTGCAGAGACATGCTGACAGCTCATCTTCCAACTGGAATTTGACGTGATCT 650
Qy 606 GGTGAGAGCGGAATGTACATGTTTCTGAGGGGAGCCCGACCTGAAATACCGAGATGA 665
Db 651 AGGTGAGGCGGAAGTACATGTTTCTGAGGGGAGCCCGACCTGAGTACCGAGATGA 710
Qy 666 TGCCAGTGTGAATGAGTCCGGAAGGACAGACAGAACTGTGACAGAAATGAGGAGCA 725
Db 711 CTACAGCCAAAGTGGGACCAAGCTGAGCGGAAGATCTGTGACAGAAATGAGGAGCA 770
Qy 726 GCACCAAGGAGCCAGTATGTGTGGAACCGCACTGCGCTCTTCAAGCGCGGATGATCT 785
Db 771 GCGCCAGGGGTGCGGATGTGTGTGGAACCGCACTGAGCTCATGAGCGCTTCCCTGAGACC 830
Qy 786 CAGTGTAAACACTCATGAGGCTTGTGAGCGCGAGACATGAAATTAATGTTACGA 845
Db 831 GTCTGTGACCATCTCAATGAGGCTTCTTGTGAGCTGTGAAACATGAAATGAGATCTCAC 890
Qy 846 AGACCAACCAAGAGCCGAGCCCTGCGGAGATGACGAGGCGGCGCTGCAAGTGTGAG 905
Db 891 AAGATCTCAACTGAGACCCCTCTCTGATGAGATGACAGAGGCTGCGCTGCTGCTAG 950
Qy 906 CAGGAACCCCGGGGCTTCTACTCTTGTGTGAGAGGAGCGCATTTGACCAAGGTACCA 965
Db 951 CAGGAACCCCGGGGCTTCTACTCTTGTGTGAGAGGAGGTGCGATGACCAATGTGATCA 1010
Qy 966 TGAAGCAAGGCTTATATGAGCACTGAGGCGCATATGTTTGAACATGCGCATGCGCA 1025
Db 1011 TGAAGCAAGGCTTATACCGGACCTGACGAGACGATCATGTTGACAGCGCATTTGAGAG 1070
Qy 1026 GCGTAAAGAGCTCACTAGCAAGCTGAGACAGCGTGTCTTGTCACTGAGACCACTCCA 1085
Db 1071 GCGGCGCAAGCTCACTACAGAGAGAGACAGCTGAGGCTTGTCACTGCGACACTCCA 1130
Qy 1086 TGTCTTCTCTTGTGCTACACACTGCGTGGGACCTCATTTTCTGGTGTGGCCCGG 1145

| | | | |
|----|------|--|------|
| Db | 1131 | CGTCTTCTCCCTTGGAGGCTACCCCTTCGAGGAGACTTCATCTTTCGGGCTGGCCCCCTGG | 1190 |
| Qy | 1146 | CAAGGCTTTAGACAGCAAGTCTTACACCTCCATCCTCTTATGGCATGGACCCAGGCTATGC | 1205 |
| Db | 1191 | CAAGGCCCCGGGACAGGAAGGCTCTACCGGTCTCTCTATACGAAACGGTCCAGGCTATGT | 1250 |
| Qy | 1206 | GCTTGGCGGGGCTTCGAGGCCGATGTTTATGGACGACAGCGCAGGAACCTTCATACG | 1265 |
| Db | 1251 | GCTCAAGACGCGCGCCCGGCGGATGTTACCGAGAGCGAGCGGGAGCCCCGAGTATCG | 1310 |
| Qy | 1266 | GCAGCAGGCGGCGCGTGCCTTCGGCTAGCGAGACCCACGGGGGCGAAGCGTGGCGGTGT | 1325 |
| Db | 1311 | GCAGAGTCACACAGTGCCTTCGGACGAAGAGACCCACGCAAGCGAGACGTGGCGGTGT | 1370 |
| Qy | 1336 | CGCGCGAAGGCCCCGAGGCGCACCTGTGTGACAGGCGGTGACAGAGAGACCTTCGTGGCGCA | 1385 |
| Db | 1371 | CGCGGCGCGGCGCGGCGCACCTGTGTCACGGGGTGACAGAGCAGACCTTCATAGCGCA | 1430 |
| Qy | 1386 | CATCATGGGCTTTGGGGCTGCGTGGAGCCCTTACCGGACCTGGCAATCTGGACGGCCCCGC | 1445 |
| Db | 1431 | CGTATGGCTTTGCGCGGCTGCTCGAGAACCTTACACGCGCTGGCAGCCTGGCGCCCCGC | 1490 |
| Qy | 1446 | CACCGCCACAGCATCCCCGACTAGGCT | 1473 |
| Db | 1491 | CGGACACACGACCGCCGCGCACCCGGGT | 1518 |

Search completed: October 19, 2004, 23:49:26
Job time : 760.5 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using BW model

Run on: October 19, 2004, 10:20:22 : Search time 5049.5 Seconds
(without alignments)
10651.558 Million cell updates/sec

Title: US-09-911-132a-1

Perfect score: 1476

Sequence: 1 gcatccatccatccagctga.....gcatcccgactaggtacc 1476

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

EST:*
1: gb_esc1:*
2: gb_esc2:*
3: gb_hlc:*
4: gb_esc3:*
5: gb_esc4:*
6: gb_esc5:*
7: gb_esc6:*
8: gb_g881:*
9: gb_g882:*

Pred. No. is the number of results predicted by a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|--------------------|
| 1 | 635.4 | 43.0 | 733 | 7 | CK956273 4096346 B |
| 2 | 603.4 | 40.9 | 1027 | 5 | BX439339 BX439339 |
| 3 | 588.2 | 39.9 | 991 | 5 | BX379970 BX379970 |
| 4 | 582.6 | 39.5 | 950 | 5 | BX458398 BX458398 |
| 5 | 574.8 | 38.9 | 984 | 1 | AL552555 AL552555 |
| 6 | 561 | 38.0 | 1593 | 9 | AY404253 Homo sapi |
| 7 | 557.6 | 37.8 | 772 | 7 | CK453205 908900 MA |
| 8 | 537.6 | 36.4 | 1587 | 9 | AY404255 Mus muscu |
| 9 | 526.2 | 35.7 | 1125 | 5 | BX343739 BX343739 |
| 10 | 522 | 35.4 | 2459 | 3 | AK076459 Mus muscu |
| 11 | 517.4 | 35.1 | 902 | 1 | AL553521 AL553521 |
| 12 | 516.6 | 35.0 | 936 | 5 | BX417625 BX417625 |
| 13 | 511.2 | 34.6 | 681 | 7 | CK834465 4058791 B |
| 14 | 492.8 | 33.4 | 905 | 1 | AL540746 AL540746 |
| 15 | 476.6 | 32.3 | 929 | 1 | AL551653 AL551653 |
| 16 | 476.2 | 32.3 | 636 | 7 | CN792609 4127499 B |
| 17 | 476 | 32.2 | 992 | 1 | AL548705 AL548705 |
| 18 | 475.4 | 32.2 | 1083 | 1 | AL545591 AL545591 |
| 19 | 470.2 | 31.9 | 998 | 1 | AL549703 AL549703 |
| 20 | 469 | 31.8 | 1593 | 9 | AY404254 Pan trogl |
| 21 | 457.6 | 31.0 | 625 | 9 | AY416259 Homo sapi |
| 22 | 439 | 29.7 | 616 | 6 | CP176922 E0856C01- |
| 23 | 438.6 | 29.7 | 724 | 6 | BY732148 BY732148 |
| 24 | 437.6 | 29.6 | 890 | 4 | BT161220 602865678 |

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|----|-------|------|------|---|--------------------|
| 25 | 425.2 | 28.8 | 550 | 9 | AY416260 Pan trogl |
| 26 | 421.6 | 28.6 | 625 | 9 | AY416261 Mus muscu |
| 27 | 421.2 | 28.5 | 782 | 6 | CB989365 AGENCOURT |
| 28 | 421 | 28.5 | 653 | 7 | CN788352 4122694 B |
| 29 | 418.8 | 28.4 | 935 | 4 | BG832086 602765105 |
| 30 | 400.8 | 27.2 | 2084 | 3 | CR681888 Telraodon |
| 31 | 398.6 | 27.0 | 855 | 6 | CB998271 AGENCOURT |
| 32 | 397.4 | 26.9 | 1422 | 3 | AK008000 Mus muscu |
| 33 | 397.2 | 26.9 | 799 | 4 | BG480361 602529434 |
| 34 | 397 | 26.9 | 740 | 6 | CB959579 AGENCOURT |
| 35 | 384.8 | 26.1 | 722 | 6 | BY732151 BY732151 |
| 36 | 375.6 | 25.4 | 535 | 2 | AW450908 UT-H-B13- |
| 37 | 365.4 | 24.8 | 700 | 7 | CN793186 4128172 B |
| 38 | 364.2 | 24.7 | 596 | 4 | BM742455 K-EST0015 |
| 39 | 362 | 24.5 | 821 | 6 | CB996560 AGENCOURT |
| 40 | 361.4 | 24.5 | 809 | 6 | CB995228 AGENCOURT |
| 41 | 360.4 | 24.4 | 799 | 6 | CB994156 AGENCOURT |
| 42 | 359.8 | 24.4 | 590 | 4 | BM742176 K-EST0014 |
| 43 | 358.8 | 24.3 | 650 | 7 | CN723202 E0856C01- |
| 44 | 354.2 | 24.0 | 607 | 7 | CN721228 E0818D06- |
| 45 | 350.4 | 23.7 | 685 | 6 | BY736065 BY736065 |

ALIGNMENTS

RESULT 1
CK956273 733 bp mRNA linear EST 15-MAR-2004
LOCUS 4096346 BARC 10BOV Bos taurus cDNA clone 10BOV35_H01 5', mRNA
DEFINITION sequence.

ACCESSION CK956273 GI:45470653
VERSION CK956273.1
KEYWORDS EST.
SOURCE Bos taurus (cow)
ORGANISM Bos taurus

REFERENCE 1 (bases 1 to 733)
Sonstegard, T.S., Van Tassel, C.P., Matukumalli, L.K., Harhay, G.P., Bosak, S., Rubenfield, M. and Gasbarre, L.C.
Production of EST from cDNA libraries derived from immunologically activated bovine gut

JOURNAL Unpublished (2004)
COMMENT Contact: Tad S. Sonstegard
Bovine Functional Genomics Laboratory
Animal and Natural Resources Institute
Bldg. 200 Rm2a BARC-East, Beltsville, MD 20705, USA
Tel: 3015048416
Fax: 3015048414
Email: tads@anri.barc.usda.gov

Single pass sequencing. Bases called and trimmed with phred
0.000925 using options -trim alt -trim fasta. Vector identified
by cross match using options -mismatch 12 -mismatch 18
Place: 35 row: H column: 01
Seq primer: CCCAGTCACGACGTGTAAACG
High quality sequence stop: 733.
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/strain="Holstein"
/db_xref="taxon:9913"
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/sex="Male"
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/dev_stage="Multiple"
/lab_host="PH10B T1 phage resistant"
/clone_lib="BARC 10BOV"
/note="Organ: Small Intestine; Vector: pagen-1; Site: 1:
ECORV; Site 2: NotI; Equimolar amounts of mRNA extracted
from proximal jejunum of 18 and 21 wk old steers, and

FEATURES

source

distal ileums of 14 day old calves. proximal jejunum
exposed to C. oncophora for 3 and 6 weeks, and distal
ileum exposed to C. parvum for 7 days"

ORIGIN

Query Match 43.0%; Score 635.4; DB 7; Length 733;
Best Local Similarity 96.2%; Pred. No. 3.4e-144;
Matches 651; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY 791 TAAACACCTCATGGGCTCTTTGAGCCGGGAGACATGAAGTAAATGTTACAGAACCC 850
DB 12 TAAACACCTCATGGGCTCTTTGAGCCGGGAGACATGAAGTAAATGTTACAGAACCC 71
QY 851 AACACCAAGAACCCGAGCTGGGAGAGATGACGAGGAGGCGCCCTGCAAGTGGCTGAGAGGA 910
DB 72 AACACCAAGAACCCGAGCTGGGAGAGATGACGAGGAGGCGCCCTGCAAGTGGCTGAGAGGA 131
QY 911 ACCCCGAGGAGCTTCTAATCTTCTGTGAGAGGAGCCGCAATTGACACGGTCAACATGAGC 970
DB 132 ACCCCGAGGAGCTTCTAATCTTCTGTGAGAGGAGCCGCAATTGACACGGTCAACATGAGC 191
QY 971 GCAAGCTTATATGGCACTGACTGAGGCGATCATGTTTGAACAATGCCATGCGCAAGGCTA 1030
DB 192 ACAAGCTTATATGGCACTGACTGAGGCGATCATGTTTGAACAATGCCATGCGCAAGGCTA 251
QY 1031 ACGAGCTACTAGCGAAGTGAACAGAGCTGATCTTGTCACTGAGACACCTCCCATGCT 1090
DB 252 ATGAGCTACTAGCGAAGTGAACAGAGCTGATCTTGTCACTGAGACACCTCCCATGCT 311
QY 1091 TCTCTTTTGGTGGCTACACACTGCGTGGAGACCTTCATTTTCGCTGCGCCCGGAGAG 1150
DB 312 TCTCTTTTGGTGGCTACACACTGCGTGGAGACCTTCATTTTCGCTGCGCCCGGAGAG 371
QY 1151 CCTTAGACAGCAAGTCTTACCTCATCTCTATATGGCAATGGCCAGGCTATGCGCTTG 1210
DB 372 CCTTAGACAGCAAGTCTTACCTCATCTCTATATGGCAATGGCCAGGCTATGCGCTTG 431
QY 1211 GCGGGGCTCGAGAGCCCGATGTTAATGGAGCAACAAGGAGAAACCTCATATCCGGCAGC 1270
DB 432 GCGGGGCTCGAGAGCCCGATGTTAATGGAGCAACAAGGAGAAACCTCATATCCGGCAGC 491
QY 1271 AGCGGGCTCGAGAGCCCGATGTTAATGGAGCAACAAGGAGAAACCTCATATCCGGCAGC 1330
DB 492 AGCGGGCTCGAGAGCCCGATGTTAATGGAGCAACAAGGAGAAACCTCATATCCGGCAGC 551
QY 1331 GAGGCGCGGAGGCGACCTGTGTGACAGCGGTGAGAGAGACCTTGTGTGGGCGACATCA 1390
DB 552 GCGGGCGCGGAGGCGACCTGTGTGACAGCGGTGAGAGAGACCTTGTGTGGGCGACATCA 611
QY 1391 TGGGCTTTGCGGGCTGTGAGAGCCCTACACGCACTGCAATGCGCAGGCGCGGCGACAG 1450
DB 612 TGGGCTTTGCGGGCTGTGAGAGCCCTACACGCACTGCAATGCGCAGGCGCGGCGACAG 671
QY 1451 CCACGACGATCCCGGAC 1467
DB 672 CCACGACGATCCCGGAC 688

RESULT 2
LOCUS BX439339 1027 bp mRNA linear EST 05-MAY-2004
DEFINITION BX439339 Homo sapiens PLACENTA Homo sapiens cDNA clone CS0DE009YD10
5-PRIME mRNA sequence.
ACCESSION BX439339
VERSION BX439339.2 GI:47036618
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE 1 (bases 1 to 1027)
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization

JOURNAL Unpublished (2001)
COMMENT On May 15, 2003 this sequence version replaced gi:30789748.

Contact: Genoscope - Centre National de Sequencage
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
was not normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
This sequence belongs to sequence cluster 1699.f
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?c=CS0DE009YD10&plc=1699.f.

FEATURES

source

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/db_xref="taxon:9606"
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/clone_lib="Homo sapiens PLACENTA"
/note="Vector: pCMVSPORT 6; 1st strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and EcoRV sites of the
pCMVSPORT 6 vector.
Library was not normalized."

ORIGIN

Query Match 40.9%; Score 603.4; DB 5; Length 1027;
Best Local Similarity 79.9%; Pred. No. 2.4e-136;
Matches 739; Conservative 6; Mismatches 177; Indels 3; Gaps 3;

QY 6 CCTATCCCAAGCTTGAAGAGAGAAACCCGCTTCTGTGAACCGCCAGGAGCCGCT 65
DB 104 CATCATCCCAAGTGTGAGAGAGAAACCCGACTTCTGGAACCGCGAGGAGCGGAGCCCT 163
QY 66 TGAATGAGCAAGAGTTGAGCGGATCCAGACAGCTGCAAGAGTGCATCTCTTCTT 125
DB 164 GGGTCCGCAAGAGTGTGACAGCTGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 223
QY 126 GGGGAGTGGAGTGGGGGTGTGCTTACCGGTGAGAGAGAGAGAGAGAGAGAGAGAGAG 185
DB 224 GGGGAGTGGAGTGGGGGTGTGCTTACCGGTGAGAGAGAGAGAGAGAGAGAGAGAGAG 283
QY 186 TGGCAAACTGGGAGCTGAGACACCCCTGGCCATGAGACCAATGCCATACGTGCTGTG 245
DB 284 GAGCAAACTGGGAGCTGAGAGACCCCTGGCCATGAGACCAATGCCATACGTGCTGTG 343
QY 246 CAAGCATTAACAAGTGGAG 305
DB 344 CAAGCATTAACAAGTGGAG 403
QY 306 GTGTGGGTCAAGGCACTACAGAACCATGCTGTAAGTGAAGCGGCGCGCTTACATCA 365
DB 404 GTGTGGGTCAAGGCACTTCCAGACATTGGCTTGAAGTGAAGCGGCGCGCTTAAACA 463
QY 366 GTGCAACAGACAGCTGGGAATGAGTCAAGTCTGTATCAACGGGCGCAAGAAAGCAG 425
DB 464 GTGCAACAGACAGCTGGGCAAGTGAATGATGATGATGATGATGATGATGATGATGAT 523
QY 426 GAAAGCGGTGGAGTGGAG 485
DB 524 GAAAGTGAAGTGGAGTGGAG 583
QY 486 CGCGCAGACAGTGAACCGAACTGGTACTAGACGCGCACTGCTGTGATGACAGAA 545
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QY 546 GAATGCTGCGAGAGATCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 605
DB 644 GAGAGGTTGCGAGAGATCGCTACGACAGCTCATCTCCAAATGAGCATTTGACGTGATCT 703

| | | | | |
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| OY | | 606 | GGGTGTGAGCCCGAATGTCATGTTTCTTGAGGGAGCCCACACCCTGAATTGCCAGATGA | 665 |
| OY | | 704 | AGGTGTGAGCCCGAAGTACATGTTTT-GCATA GTGGAA CCGAACCTTGATGCCAGATGA | 762 |
| OY | | 666 | TGCCAGTGTGAATGAGATGTCGGGAMGAGAACAGAACTGGTGTGCAGTAATGGACGCCAA | 725 |
| Db | | 763 | CTACAGCCGAAGTGTG- GACAGGCTGTGAGCGGGAAGAATTGGTGTGCAAGAAATGGCTGGCGAM | 821 |
| OY | | 726 | GCACGAGGAGGCCAGTATGTGTGGAA CCGCATGCGCTCTTCAGGCGGCCGATGACTC | 785 |
| Db | | 822 | GCCCCGAGGGGTGCCCGGTACGTGTGGAA CCGCATGTAGCTCATGTACAGGCTTCCCTGACACC | 881 |
| OY | | 786 | CAGGTACAACACCTCATGGGCGCTTTGTAGACCCGCGACAA CANTGAAGTATTAATGTCA -GC | 844 |
| Db | | 882 | GTCGTGTGACCATCTCATGGGTCTCTTTGTAGCTGTGAA CATTGA AAMMGATATCCACC | 941 |
| OY | | 845 | AAGACCAACCAAGAGACCCGACCCCTGTGCGGAGATGACGAGAGCGGCCCTTGAGATGTCTGA | 904 |
| Db | | 942 | GAGACTCCMCAC TGTGRCCTCTCTTGATGTGAGRTGACAGAGGCTGCCCTGTGCTGTA | 1001 |
| OY | | 905 | GCAGGAACCCCCCGGGGCTTTTCACTT 929 | |
| Db | | 1002 | GCAGGAACCCGCGGCTTTTCTCTT 1026 | |
| RESULT 3 | | | | |
| BX379970 | | | | |
| LOCUS | | | | |
| DEFINITION | | BX379970 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA | 991 bp mRNA linear EST 26-APR-2004 | |
| ACCESSION | | BX379970 | | |
| VERSION | | BX379970.2 GI:46573405 | | |
| KEYWORDS | | EST. | | |
| SOURCE | | Homo sapiens (human) | | |
| ORGANISM | | Homo sapiens | | |
| REFERENCE | | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | |
| AUTHORS | | Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. | | |
| TITLE | | Li, W.B., Gruber, C., Jesssee, J. and Polayes, D. | | |
| JOURNAL | | Full-length cDNA libraries and normalization | | |
| COMMENT | | On May 8, 2003 this sequence version replaced gi:30448940. | | |
| | | Contact: Genoscope Genoscope - Centre National de Sequencage BP 191 91006 Evry cedex - France Email: seque@genoscope.cns.fr, Web : www.genoscope.cns.fr 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five primers end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by life technologies, a division of Invitrogen. This sequence belongs to sequence cluster 1699.f | | |
| | | For more information about this cluster, see http://www.genoscope.cns.fr/cdna?c=CS0D104ZAD05QPl&c=1699.f . | | |
| FEATURES | | Location/Qualifiers | | |
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| | | /mol_type="mRNA" | | |
| | | /db_xref="taxon:9606" | | |
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| | | /clone_1lb="Homo sapiens PLACENTA COT 25-NORMALIZED" | | |
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| Query Match | | 39.9% | Score 588.2 | DB 5; Length 991; |
| Best Local Similarity | | 80.2% | Pred. No. 1,2e-132; | |
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| | | | |
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| Qy | 126 | GGGGGATGGGATGGGGGGTGCCTACGGTGTACAGGCCACTTCGGATCTCTAAAGGGGAGATGAA | 185 |
| Db | 226 | GGGGGATGGGATGGGGGGTGTCTTAAAGTGACAGCTCGCAGAGATCTCTAAAGGGGAGAA | 285 |
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| Db | 286 | GGACAACTGGGGGCTTGAGTTTACCTCTGGCATGACCGCTTCCCATATGTGGCTCTGTCTC | 345 |
| Qy | 246 | CAGAATATCAACCTGGAACAGACAGGTGCCAGACAGCGCAGGCACTGCCATGCTTACTT | 305 |
| Db | 346 | CAAGCATATCAATGTAGCAAAACATGTGCCAGACAGTGTAGCCACAGCTACGGGCTTACTT | 405 |
| Qy | 306 | GTGTGGGGGTCAAGGGCACTTACAGAACCTTGGTGTGTAAATGTACAGCCGCGCTCTCAATCA | 365 |
| Db | 406 | GTGGGGGGTCAAGGGCAACTTCCAGAACATTTGGCTTTAGTGTACAGCCGCGCTTTAACCA | 465 |
| Qy | 366 | GTGCACAACGACAGTGGGAAATGAGGTCAACGCTGTGTATCAACCGGGGCAAGAAAGCAGG | 425 |
| Db | 466 | GTGCACAACGACAGCGCGCAACGAGGTCTATCTCCGTATGATGTGGGCGCAAGAAAGCAGG | 525 |
| Qy | 426 | GAAAGCCCTGGAGATGTGTGACCAACACAGGGGTGACAGATGCTTCCCAAGCCGGGGCTTA | 485 |
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| Qy | 545 | AGAAATGCTGTCAAGAGACATCGCCGACAGCGTGTCTCAACATGGAATTTAGAGTGTATCC | 604 |
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| Qy | 725 | AGCACAGAGGAGCCCATGATGTGTGTGAAACCGCAATGGGCTTCCCTCAGCGGCCGATGACT | 784 |
| Db | 826 | CGC-CAAGGGGCGCCGGTACGTGTGAAACCGCATGAGCTCATATGCAGGCTTCCCTGACCC | 884 |
| Qy | 785 | CCAGTGTAAACACCTCATGGGCTCTTTTGAAGCCGGGAGACATGAAATTAATTTTCAGC | 844 |
| Db | 885 | CGTCTGTGATCCCATCTCATGGGCTCTTTTGAAGCTTGAGAAATATAATTCAGATTCACCC | 944 |
| Qy | 845 | AAGACCAACCCAGAACCCGACCTCTGGCGGAGATGACGAGGCGGCC | 891 |
| Db | 945 | GAGACTCCACACTGGAMCCCTCCTGTATGGAGATGACABAGCTGCC | 991 |
| RESULT 4 | | | |
| LOCUS | BX458398 | 50 bp | linear |
| DEFINITION | BX458398 Homo sapiens PLACENTA Homo sapiens cDNA clone CS0DB002YN21 | EST 05-MAY-2004 | |
| ACCESSION | BX458398 | | |
| VERSION | BX458398.2 | GI:47053565 | |
| KEYWORDS | EST. | | |
| SOURCE | Homo sapiens (human) | | |
| ORGANISM | Homo sapiens | | |
| REFERENCE | 1 | (bases 1 to 950) | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. |

AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
 TITLE Full-length cDNA libraries and normalization
 JOURNAL Unpublished (2001)
 COMMENT On May 22, 2003 this sequence version replaced gi:3102309.

CONTACT: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 EVRY cedex - France
 Email: segreg@genoscope.cns.fr, Web : www.genoscope.cns.fr
 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
 end enriched, double-strand cDNA was digested with Not I and cloned
 into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
 was not normalized. Library was constructed by Life Technologies, a
 division of Invitrogen.
 This sequence belongs to sequence cluster 1699.f
 For more information about this cluster, see
<http://www.genoscope.cns.fr/cdna?b=CS0DE002CG110P1&c=1699.f>.

FEATURES

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 /clone="CS0DE002YNN21"
 /issue_type="PLACENTA"
 /clone_lib="Homo sapiens PLACENTA"
 /note="Vector: pCMVSPORT 6; 1st strand cDNA was primed
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 double-strand cDNA was digested with Not I and cloned into
 the Not I and EcoRV sites of the pCMVSPORT 6 vector.
 Library was not normalized."

ORIGIN

Query Match 39.5%; Score 582.6; DB 5; Length 950;
 Best Local Similarity 80.8%; Pred. No. 2,8e-131;
 Matches 678; Conservative 1; Mismatches 160; Indels 0; Gaps 0;

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DB 222 GGGCCATGGAGATGGGGGTCCTACGCTGACAGCACTCGGATCTTAAAGGGCAGATGAA 291
QY 186 TGGCAAACTGGGACCTGAGACACCCCTGGCCATGACCACTTCCATACGTGGCTCTGTC 245
DB 292 GGACAAACTGGGGGCTGAGATTAACCCCTGGCCATGACCACTTCCATACGTGGCTCTGTC 351
QY 246 CAAGACATCAACGTTGACAGACAGAGTGCAGACAGCGAGGACAGCTGCGACCTGACCT 305
DB 352 CAAGACATCAACGTTGACAGACAGAGTGCAGACAGCGAGGACAGCTGCGACCTGACCT 411
QY 306 GTGTGGGGTCAAGGGCACTACAGAACATCGATGTAGTGCAGCGCCCGCTACATCA 365
DB 412 GTGTGGGGTCAAGGGCACTTCCAGACATTTGGCTTGAATGACAGCGCCCGCTTAAACA 471
QY 366 GTTGAACACGACAGCTGGGATGAGGTCACTGTGTGATCAACCGGGCCAAAGAAAGCAG 425
DB 472 GTTGAACACGACAGCTGGGATGAGGTCACTGTGTGATCAACCGGGCCAAAGAAAGCAG 531
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DB 532 GAAGTCAAGTGGAGTGTGATGACACACAGGAGTGCAGATGCTCCCGAGCGGGGCTTA 591
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DB 592 CGCGGACAGCGGTGAACCGGAACTGTGTATCAGACCGCGGACTTGCCTGTGATGACAGAA 651
QY 546 GAATGCTGCGGACATGCGCGACAGCTGGTCTTAAACATGATATTGACGTGATCTT 605

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DB 652 GGAGGGGTGCGCAGACATCGCTACCGACGCTCATCTCCAACATGACATGACGTGCTCT 711
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DB 712 AGGTGAGGCGCAATGATCATGTTTCTGAGGGGAGCCCAAGACCTTGAATACCGAGTCA 771
QY 666 TCCAGTGTGATGAGTCCGGAAGACAGACAGAACTGTGTGAGAGTGGCAGAGCCCA 725
DB 772 CTACAGCCAGGTGGAGACAGCTGACGGGAAGATCTGTGCAAGATGGCTGGCGAM 831
QY 726 GCACCAAGAGCCAGTATGTGTGACACCGACCTGCTCTTACGCGGCGGATGACTC 785
DB 832 GGCACAGGGGTGCCGCTAGTGTGACACCGACCTGCTCTTACGCGGCGGATGACTC 891
QY 786 CAGTGTACACCTCATGAGGCTCTTTGAGCCCGACACATGATGATGTTGACG 844
DB 892 GTCTGTGACCATCTCATGAGGCTCTTTGAGCCCGACACATGATGATGTTGACG 950

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RESULT 5
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 LOCUS AL552555 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
 DEFINITION Clone CS0D1067YC24 5-PRIME, mRNA sequence.
 ACCESSION AL552555
 VERSION AL552555.3 GI:45857340
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 984)
 AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
 TITLE Full-length cDNA libraries and normalization
 JOURNAL Unpublished (2001)
 COMMENT On Feb 15, 2001 this sequence version replaced gi:31274370.

CONTACT: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 EVRY cedex - France
 Email: segreg@genoscope.cns.fr, Web : www.genoscope.cns.fr
 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
 end enriched, double-strand cDNA was digested with Not I and cloned
 into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
 was not normalized. Library was constructed by Life Technologies, a
 division of Invitrogen. This sequence belongs to sequence cluster
 1699.f
 For more information about this cluster, see
<http://www.genoscope.cns.fr/cdna?b=CS0D1067B120P1&c=1699.f>.

FEATURES

source
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 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
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 /issue_type="PLACENTA COT 25-NORMALIZED"
 /clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
 /note="1st strand cDNA was primed with a NotI-oligo(dT)
 primer. Five prime end enriched, double-strand cDNA was
 digested with Not I and cloned into the Not I and EcoRV
 sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Query Match 38.9%; Score 574.8; DB 1; Length 984;
 Best Local Similarity 80.5%; Pred. No. 2.3e-129;
 Matches 708; Conservative 1; Mismatches 168; Indels 3; Gaps 3;

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QY 6 CCTATCCAGCTGAGAGAGAAACCCGCCCTTTGAAACCGCAGCGAGCCGAGCCCT 65
DB 106 CATATCCAGCTGAGAGAGAAACCCGCCCTTTGAAACCGCAGCGAGCCGAGCCCT 165
QY 66 TGATGTAGCCAGAGAGTTGACAGCGGATTCAGACAGCTGCGCAAGATGATCTCTTCTT 125
DB 166 GGGTGGCCGCAAGAGAGTTGACAGCGGATTCAGACAGCTGCGCAAGATGATCTCTTCTT 225

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| | | | | |
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| Oy | | 126 | GGGGGATGGAGTGGGGGGTGCCCTACGGGTGACAGCACACTCGAATCCGAAGAAGGGGCAGATGAA | 185 |
| Db | | 226 | GGGGCATGGAGTTGGGGGGTGTCTTAAGGTGACAGCTGCCAGAGATCTCTMAAAGGGCAGAGAAA | 285 |
| Oy | | 186 | TGGCAAACTGGGAGCTGTGAGACACCCTTCGGCCATGGAACGATTGCCATACGTGGCTCTGTC | 245 |
| Db | | 286 | GGAACAACTGGGGGCTTGAGTTAACCTTCGGCCATGGAACCGCTTCCATATGTGGCTCTGTC | 345 |
| Oy | | 246 | CAAACATATCAAAGTGGACAGACAGAGTGTCCAGACAGCCAGGACACTGCTCACTGCTTACT | 305 |
| Db | | 346 | CAAGCATATCAATGTATGACAAACATGTGCCAGACAGTGGAGCCACAGCCAGGCGCTTACT | 405 |
| Oy | | 306 | GTGTGGGGGTCAAGGGCACTACAGAAACATGGGTGTAAAGTGAGCGCGCCGCTCAATCA | 365 |
| Oy | | 406 | GTGCGGGGTCAAGGGCACTTCCAGAACATTTGGCTTTAGGTGACGCGCCGCTTTMACCA | 465 |
| Db | | 466 | GTGCACACGACACGCGGCCAACGAGGTCACTCCGTGATGAAATGGGCGCAAGAAAGCAGG | 525 |
| Oy | | 426 | GAAAGCCCTGGGAGTGTGTGACCAACACAGAGGTGTAGCATGTCTTCCCAGCCGGGCGCTTA | 485 |
| Db | | 526 | GAAGTCAATGGGAGTGTATCACCAACACAGTGTAGACACGCTTCGACAGCGCGGACCTTA | 585 |
| Oy | | 486 | CGCGCACACGGTGAACCGAAACTGGTACTCAGACGCGGACCTGCTGTGATGAC-AGA | 544 |
| Db | | 586 | CGCCACACGGTGAACCGCAACTGTACTTCGAGCGCCGACGCTGCTCGGCGCCGCA | 645 |
| Oy | | 545 | AGAAATGGCTGCAGAGACATGCGCCGACAGCTGTGTATCAACATGAGATAATTGACGTATCC | 604 |
| Db | | 646 | GAGGGGGGTGCAGAGACATCGCTACGACGCTCATCTTCCACATGGAATTTGACGTGATCS | 705 |
| Oy | | 605 | TGGGTGGAGGCGCGAATGTATCATGTTTTCTGAGGGGAGCCCCAGACCTCTGAATPACCAATG | 664 |
| Db | | 706 | TAGGTGGAGGGCGCAAGTATGTTTCCCATGTGGAAACCCACAGACCTTAGTAPCCACAGATG | 765 |
| Oy | | 665 | ATGCCAGTGTGAATGAGTGTCCGGAAAGACAAGCAGAACCTGATGAGAAATGACAGGCA | 724 |
| Db | | 766 | ACTACAGCCCAAGTGGAGACAGAGCTGTGACGGGAAGAACTGTGTGACAGAAATGCTGCGGA | 825 |
| Oy | | 725 | AGCACCAAGGAGGCCCATGTATGTGTGAAACCGCATCTGCGCTCTTACGCGGCGCATGACT | 784 |
| Db | | 826 | CGC-CAGGGGTGCGCGGTATCGTGTGAAACCCGACATGACCTATGACAGGCTTCCCTGAGCC | 884 |
| Oy | | 785 | CCAAGTCT-AAACACACTATGAGGCGCTCTTTAGCCGGAGACATCAATATTAATGTTAG | 843 |
| Db | | 885 | CGTGTATAACCCATCTCATGTAGGTCTCTTTGAGCTGTGAGACATGAATAACGATATCAC | 944 |
| Oy | | 844 | CAAGACCAACCAAGAACCCGACCTGTGCGGAGATGACGG | 883 |
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| AY404253 | | 1593 bp | DNA | linear GSS 15-DEC-2003 |
| LOCUS | | | | |
| DEFINITION | | | Homo sapiens ALPL2 gene, VIRUTAL TRANSCRIPT, partial sequence, | |
| VERSION | | | AY404253 | |
| ACCESSION | | | AY404253.1 | GI:39760230 |
| KEYWORDS | | | GSS. | |
| SOURCE | | | Homo sapiens (human) | |
| ORGANISM | | | Homo sapiens | |
| REFERENCE | | | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | |
| AUTHORS | | | Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. | |
| | | | 1 (baaes 1 to 1593) | |
| | | | Clark,A.G., Gianoweki,S., Nielson,R., Thomas,P., Kejarawal,A., | |
| | | | Todd,M.A., Tanenbaum,D.M., Ciavella,D.R., Lu,F., Murphy,B., | |
| | | | Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Shtinsky,J.J., | |
| | | | Adams,M.D. and Cargill,M. | |
| TITLE | | | Infering nonneutral evolution from human-chimp-mouse orthologous | |
| | | | gene tfiles | |

| JOURNAL | PUBMED | REFERENCE | AUTHORS | TITLE | JOURNAL | COMMENT | FEATURES | ORIGIN |
|--------------------------------------|---|---------------------|--|-------------------|-------------------------|---|--|--|
| Science 302 (5652), 1960-1963 (2003) | 14671302 | 2 (bases 1 to 1593) | Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarival, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferreira, S., Mang, G., Zheng, X.H., White, T.J., Slutsky, J.J., Adams, M.D. and Cargill, M. | Direct Submission | Submitted (16-NOV-2003) | Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA | This sequence was made by sequencing genomic exons and ordering them based on alignment. | Location/Qualifiers 1. 1593 /organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="Lacxon:9606" <1..>1593 /gene="ALPPL2" /locus_tag="HCM1829" |
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| 57 | CATCATCCCACTTGAAGAGAGAAACCCGAGCTTCTGAAACCGCCAGCGAGCCGCTT | 116 | | | | | | |
| 66 | TGATGTAGCCAAAGAGTTGTCAGCCCGATCCAGACAGTGTCCAAAGATGTATCTTCTT | 125 | | | | | | |
| 117 | GAGTGCCGCCAAGAGAGCTGACGCTTGCACACAGACGCGCCAAAGACCTATCATCTTCTT | 176 | | | | | | |
| 126 | GGGGGATGGAGTGGGGGGTGGCTTACGCTGACAGCCACTGAGATCTTAAAGGGGACATGTA | 185 | | | | | | |
| 177 | GGG-----GATGGGGGTGTCTTACGGTGAACAGTCCAGAGATCTTAAAGGGGACAGAA | 230 | | | | | | |
| 186 | TGGCAACTGGGACCTGAGACACCCCTTGGCCATGAGACCAAGTTCCATACGTGGCTGTG | 245 | | | | | | |
| 211 | GAGCAAACTGGGGCTTGAAGACCTTCTTGGCCATGAGACCGCTTCCGTACGTGGCTGTG | 290 | | | | | | |
| 246 | CAAGACATACACGTGGAACAGACAGTGTCCAGACAGCGCAGGCAATGCACTGCTTACT | 305 | | | | | | |
| 291 | CAAGACATACAGTGTGAACAGACAGTGTCCAGACAGTGAAGCCAGCGCCTTACT | 350 | | | | | | |
| 306 | GTGTGGGGTCAAGGGCACTACAGAACCATGCTGTATGATGAGCGAGCGCCGCTTCAATCA | 365 | | | | | | |
| 351 | GTTCGGGGGTCAAGGGCACTTCTCAGACCATTTGGCTTGAATGACGCCGCCCTTTAACCA | 410 | | | | | | |
| 366 | GTGCAACACGACACGTGGGAATGAGGTACGCTTGTGTATCAACCGGGCCAAAGAACAG | 425 | | | | | | |
| 411 | GTGCAACACGACACCGCGGCAAGAGGTATCTCGGTATGATGGGGCCAAAGAACAG | 470 | | | | | | |
| 426 | GAAGCGCTGGGAGTGTGACCAACACAGGCTGACAGATGCTTCCCAAGCCGGGCTTA | 485 | | | | | | |
| 471 | AAAGTCAGTGGGAAGTGTATACACACACCGGGTGAAGCATGCTTCCAGCGCGGCTTA | 530 | | | | | | |
| 486 | CGCGCACACGCTGAACCGAACTGGTACTTCAAGCGCGGACCTGCTGTCATGACAGAA | 545 | | | | | | |
| 531 | CGCCACACGGGTGAACCGCAACTGGTACTCGGATGCGGACGTCCTCGGCGCCGCA | 590 | | | | | | |
| 546 | GAATGGCTGACAGACATCGCCGACACAGCTGGTCTTACAAACATGATATGACGTGCT | 605 | | | | | | |
| 591 | GGAGGGGTGCCAGACATCGCCGACAGCACTCATCTCAACATGACATTTGATNNNNNNNN | 650 | | | | | | |
| 606 | GGGTGAGGCGGAATGTATCATGTTTCTGAAGGGGACCCAGACCTGTAATACCCAGATGA | 665 | | | | | | |
| 651 | NN | 710 | | | | | | |
| 666 | TGCCAGTGTGAATGAGATCGCGAAGAGACAAGACAGAACTGGTGCAGATGGCAGGCCAA | 725 | | | | | | |
| 711 | NN | 770 | | | | | | |

QY 726 GCACGAGGAGCCAGTATGTGGAACCGACTGGCTCTTCAGGCGCGATGATCTC 785
 Db 771 NNN 830
 QY 766 CAGTGTAAACACCTCATGAGGCTCTTTGAGCCGAGCAGATGAAATATATGTTGAGA 845
 Db 831 NNN 890
 QY 846 AGACCAACCAAGAACCCGACCTGGCGAGATGACGAGGCGCCCTCAACTGTGAG 905
 Db 891 NNN 950
 QY 906 CAGGAACCCCGGAGCTTCTACCTCTTCTGAGGAGGCGCATTTGACCAAGCTACCA 965
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 QY 1026 GGCTAACGAGCTCATAGGAACCTGACACGCTGATCTTGTCTGACGACCACTCCCA 1085
 Db 1071 NNN 1130
 QY 1086 TGTCTTCTCTTTGCTGCTACACACTGCGGAGCTCATTTTCTGCTGCGCCCGG 1145
 Db 1131 NNN 1190
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 Db 1191 NNN 1250
 QY 1206 GCTTGGCGGGGCTGAGGCGCGATGTTATGCGACAGCAAGCGAACCCTCATACCG 1265
 Db 1251 NNN 1310
 QY 1266 GCAGAGGCGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1325
 Db 1311 GCAGAGTGTAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1370
 QY 1366 CGCGGAGGCGCGACGAGCGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1385
 Db 1371 CGCGGCGGCGCGACGAGCGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1430
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 Db 1431 GGTCAATGCTTGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1490
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 Db 1491 CGGCAACCAAGCGCGCGCACCGCGG 1517

RESULT 7
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 DEFINITION CK453205
 ACCESSION CK453205.1 GI:40800419
 VERSION EST.
 KEYWORDS
 SOURCE Sus scrofa (pig)
 ORGANISM Sus scrofa
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

REFERENCE 1 (bases 1 to 772)
 Smith,T.P.L., Fieking,B.A., Ford,J.J., Vallet,J.L., Wise,T.A.,
 Noneman,D.J., Wray,J.E. and Keeler,J.W.
 Porcine EST collection using a normalized library constructed from
 embryos representing early developmental stages
 Unpublished (2003)
 JOURNAL Contact: Smith TPL
 COMMENT USDA, ARS, US Meat Animal Research Center

PO Box 166, Clay Center, NE 68933-0166, USA
 Tel: 402 762 4366
 Fax: 402 762 4390
 Email: smith@email.marc.usda.gov
 Single pass sequencing. Bases called with phred v0.020425.c and
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 cross_match v0.990329.
 Plates: TMW8024 row: H column: 10
 Seq primer: GPATACGCTCATATAGG.
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 /ligase_type="pooled"
 /lab_host="DH10B"
 /clone_lib="MARC 4Pig"
 /note="Vector: pCDNA3.1; Site 1: EcoRI; Site 2: NotI;
 library made with combined RNA from day-10, day-13,
 day-15, day-25, and day-30 whole embryos."

ORIGIN

Query Match 37.8%; Score 557.6; DB 7; Length 772;
 Best Local Similarity 82.6%; Pred. No. 3,5e-125;
 Matches 638; Conservative 0; Mismatches 134; Indels 0; Gaps 0;
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 Db 1 GTTTCCTGAGGAGTCCCGAGCTTGAATPACCCAGATATGCTGATGAGTCCG 60
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 Db 61 GAAGACAAGGAGAACTGTGTCAGAAATGGCAGCCCAAGCAGGAGCCCGTATGT 120
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 Db 121 GTGAAACCGCACTGCGCTCTTCAAGCGCGCGATATCTTCACTGTAACACACTCATGG 180
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 QY 1287 GGCTAGCAGAACCCAGCGGGGCGAAGAGCTGCGGCTGTTCCGCGAGGCGCGAGCGCA 1346
 Db 661 GGTGTCGAGAACCCAGCGGGGCGAGAGCTGCGGCTGTTCCGCGAGGCGCGCTGCGCGCA 720

QY 1347 CCTGTGACAGCGCGTGCAGAGAGACCTTGTGGCGCACATCATGGCCCTTT 1398
DB 721 CCTGTGACAGCGCGTGCAGAGAGACCTTGTGGCGCACATCATGGCCCTTT 772

RESULT 8
AY404255
LOCUS
DEFINITION
MUS musculus ALPPL2 gene, VIRTUAL TRANSCRIPT, partial sequence.
AY404255
VERSION
KEYWORDS
SOURCE
ORGANISM
MUS musculus (house mouse)

REFERENCE
AUTHORS
1 (bases 1 to 1587)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
Todd, M.A., Tanenbaum, D.M., Civeello, D.R., Lu, F., Murphy, B.,
Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Smitsky, J.J.,
Adams, M.D. and Cargill, M.
Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
Science 302 (5652), 1960-1963 (2003)

TITLE
JOURNAL
PUBMED
REFERENCE
AUTHORS
2 (bases 1 to 1587)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
Todd, M.A., Tanenbaum, D.M., Civeello, D.R., Lu, F., Murphy, B.,
Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Smitsky, J.J.,
Adams, M.D. and Cargill, M.
Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering
them based on alignment.
Location/Qualifiers
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/mol_type="genomic DNA"
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ORIGIN
Query Match 36.4%; Score 537.6; DB 9; Length 1587;
Best Local Similarity 44.3%; Pred. No. 3,1e-120;
Matches 643; Conservative 0; Mismatches 801; Indels 6; Gaps 1;

QY 8 TCATCCAGCTGAGAGAAACCCCGCTTGTGAACCGCAGGACGCCAGGCCCTTG 67
DB 59 TCATCCAGCTGAGAGAAACCCCGCTTGTGAACCGCAGGACGCCAGGCCCTTG 118
QY 68 ANTATCCAGAGATTGCGACCCGATCCAGACAGCTGCGAAGATGTCATCTTCTTG 127
DB 119 ATGCTCCAGAGATTGCGACCCGATCCAGACAGCTGCGAAGATGTCATCTTCTTG 178
QY 128 GGGATGGAGTGGGGGCTGCTGACGATGACGACGATCGATCTAAAGGGCAGATGATG 187
DB 179 G-----GATGGGGGTACCCACAGTACAGCCACAGATCTTAAAGGGCAGTGGAG 232
QY 188 GCAAACTGGAGCTGAGACACCCCTGCGCATGAGACAGTTCCCATAGCTGTGCA 247
DB 233 GCCATCTAGGACCGGAGACACCCCTGCGCATGAGACAGTTCCCATAGCTGTGCA 292
QY 248 AGCATATCAACCTGAGACAGAGTGGCAGACAGCGGACATGCGCATCTTACTCTGT 307
DB 293 AGCATATCAACCTGAGACAGAGTGGCAGACAGCGGACATGCGCATCTTACTCTGT 352
QY 308 GTGGGCTCAAGGGCACTACAGAACCATCGGTAAAGTGCAGCGCCGCTACATCATGT 367

DB 353 GTGGGCTCAAGCACTACAGACCATCGGCTGAGCGGACCGGAGATTGACCATG 412
QY 368 GCAACAGCAACAGTGGGAATGAGGTGACGCTGTGTATCAACGGGGCCAAAGAGAGGA 427
DB 413 GCAACAGCAACATTTGGCAATGAGGTGACGCTGTGTATCAACGGGGCCAAAGAGAGGA 472
QY 428 AGCGCTGGAGAGTGTGACACACAGGAGTGCAGATGCTCCAGCGGGCCCTAGC 487
DB 473 AGCTGTGGAGAGTGTGACACAGGAGTGCAGATGCTCCAGCGGGCCCTAGC 532
QY 488 CGCACACGTTGAACCGAACTGTGACTCAGAGCCGACCTGCTGTATGACAGAGA 547
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QY 548 ATGGCTGCAGAGCATGTCGCGCACAGCTGTGTCAACATGATATTTGACGTATCTGG 607
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DB 653 NNN 712
QY 668 CCAAGTGAATGAGAGTCCGGAAGACAGACAGAACTGTGTGACAGATGCGACCAAGC 727
DB 713 NNN 772
QY 728 ACCAGGAGCCAGATGTGTGGAACCGGACCTGCGCTTCCAGGGCCGATGACTCCA 787
DB 773 NNN 832
QY 788 GTGTACACACCTCATGAGGCTCTTTGAGCCGCGACAGATGAGTAAATGTTCAAGAG 847
DB 833 NNN 892
QY 848 ACCACACCAAGACCCGACCTGCGAGATGACGAGCGCGCTGCAAGTGTCTAGCA 907
DB 893 NNN 952
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QY 1328 CGGAGCGCGGAGGCGACTGTGTGACAGGCGTGAAGAGAGGAGGAGGAGGAGGAGGAGG 1387
DB 1373 CGGAGCGCGGAGGCGACTGTGTGACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1432
QY 1388 TCATGCGCTTTTGGGAGCTGCTGAGACCTTACACCGATCTGCAATCTGCGAGCCCGGCA 1447
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QY 1448 CCGCCACGAG 1457
DB 1493 GCCAGAGCAG 1502

RESULT 9
BX343739 1125 bp mRNA linear EST 07-APR-2004
LOCUS BX343739 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
DEFINITION clone CS0D1017YB14 5-PRIME, mRNA sequence.

ACCESSION BX343739
VERSION BX343739.2 GI:46270510
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
TITLE Li, W.B., Gruber, C., Jessee, J., and Polayes, D.
JOURNAL Full-length cDNA libraries and normalization
COMMENT On May 2, 2003 this sequence version replaced gi:30336211.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seque@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by life technologies, a
division of invitrogen. This sequence belongs to sequence cluster
1699.f

For more information about this cluster, see
http://www.genoscope.cns.fr/cda?c=CS1A10052B0P1ec=1699.f.

FEATURES
source
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Location/Qualifiers

/organism="Homo sapiens"
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/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Query Match 35.7%; Score 526.2; DB 5; Length 1125;
Best Local Similarity 80.6%; Pred. No. 1.8e-117;
Matches 662; Conservative 1; Mismatches 154; Indels 4; Gaps 4;

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DB |||||
271 GGTGCGCGCAAGAGCTGACCTGCGACAGACGCGCAAGACCTTATATCTTCT 330
QY 126 GGGGATGAGATGGGGTCTCTACGCTGACAGCACTCGATCTTAAAGGCGAGATGA 185
DB |||||
331 GGGCGATGGGATGGGGTCTCTACGCTGACAGCACTCGAAGATCTTAAAGGCGAGATGA 390
QY 186 TGGCAAACTGGGACCTGAGACACCCCTGGCCATGACGAGTTCCATACGTGCTCTGT 245
DB |||||
391 GGACAAAACTGGGCGCTGAGTTACCCCTGGCCATGAGACCGCTTCCATATGTGCTCTGTC 450
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DB |||||
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QY 306 GTGTGGGGGTCAAGGGCAACTACAGAACCATCGGTGAATGTGAGCGCCGCTTACATCA 365
DB |||||
511 GTGGGGGGTCAAGGGCAACTTCCAGACCATTTGCTTGAATGTGAGCGCCGCTTTAACCA 570
QY 366 GTGCAACACGACAGTGGGATGAGTCACTCTGTATCAACCGGGCCAGAAAGCAGG 425
DB |||||
571 GTGCAACACGACAGCGGGACGAGAGTCACTCTGTATGATCCGGGCGAAGAAAGCAGG 630
QY 426 GAAAGCGGTGGAGTGTGACACACAGAGGGTGGAGATGCTCCGACGCGGGGCGCTA 485
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QY 545 AGAATGCTGCGACGACATGCGCGACAGCTGCTTACACATGATATTTGACGATTC 604
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QY 605 TGGGTGAGGGCGGAATGTAATGTTCTCTGAGGGGAGACCCGACCTGAATCCGAGATG 664
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DB |||||
930 ACGCCAAAGGGGGCCCGGTACGCTGTGAGACGCGACATGAGCTTCAATGACAGGCTTCCCTGTGAC 989
QY 784 TCCAGTGTACACACCTCATGGGCTCTTTAGACCGCGAG 824
DB |||||
990 CGTCTGTGAC-CATCTCATAGGTCTCTTTAGCTTGAGAA 1029

RESULT 10
AK076459 2459 bp mRNA linear HTC 03-APR-2004
LOCUS AK076459
DEFINITION Mus musculus 0 day neonate head cDNA, RIKEN full-length enriched
library, clone:4833407E05 product:alkaline phosphatase 2, liver,
full insert sequence.

ACCESSION AK076459
VERSION AK076459.1 GI:26096820
KEYWORDS HTC, CAP trapper.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
TITLE Carninci, P. and Hayashizaki, Y.
JOURNAL High-efficiency full-length cDNA cloning
METH. Enzymol. 303, 19-44 (1999)
PUBMED 99279253
REFERENCE 10349636

AUTHORS
TITLE Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
JOURNAL Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)
PUBMED 20499374
REFERENCE 11042159

AUTHORS
TITLE Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
Kono, H., Akiyama, J., Nishi, K., Kitazuma, T., Tashiro, H., Itoh, M.,
Sun, N., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, A.,
Yamanoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kaibiwagi, K.,
Fujiwara, S., Inoue, K., Togawa, Y., Iwata, M., Ohara, E., Watanabe, M.,
Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, K., Matsuda, S., Kawai, J.,
Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system--384-format

sequencing pipeline with 384 multicapillary sequencer
 JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
 MEDLINE 20530913
 PUBMED 11076861
 REFERENCE 4
 The RIKEN Genome Exploration Research Group Phase II Team and the
 PANTOM Consortium.
 TITLE Functional annotation of a full-length mouse cDNA collection
 JOURNAL Nature 409, 685-690 (2001)
 REFERENCE 5
 The PANTOM Consortium and the RIKEN Genome Exploration Research
 Group Phase I & II Team.
 TITLE Analysis of the mouse transcriptome based on functional annotation
 of 60,770 full-length cDNAs
 JOURNAL Nature 420, 563-573 (2002)
 REFERENCE 6 (bases 1 to 2459)
 Aochi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,
 Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W.,
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 Hori, P., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T.,
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 Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,
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 Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T.,
 Sugabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaki-Akahira, S.,
 Takeda, Y., Tanaka, T., Tomaru, A., Toyota, T., Yasunishi, A.,
 Muramatsu, M. and Hayashizaki, Y.
 TITLE Direct Submission
 JOURNAL Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of
 Physical and Chemical Research (RIKEN), Laboratory for Genome
 Exploration and Chemical Research (RIKEN), Laboratory for Genome
 Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
 RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-Ku, Yokohama,
 Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.jp,
 URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222,
 Fax: 81-45-503-9216)
 COMMENT cDNA library was prepared and sequenced in Mouse Genome
 Encyclopedia Project of Genome Exploration Research Group in Riken
 Genomic Sciences Center and Genome Science Laboratory in RIKEN.
 Division of Experimental Animal Research in Riken contributed to
 prepare mouse tissues.
 Please visit our web site for further details.
 URL: http://genome.gsc.riken.jp/
 URL: http://fantom.gsc.riken.jp/.
 FEATURES
 Location/Qualifiers
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 GBNM_007431, evidence: BLASTN, 98%, match=2451)
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 Best local Similarity 63.2%; Pred. No. 2,2e-116;
 Matches 907; Conservative 0; Mismatches 505; Indels 22; Gaps 6;
 Db 11 TCCACGTGAGAGAAACCCGCTTCTGGAACCGCCAGCAGCCAGCCCTTGATG 70
 234 TGCCAGAGAAAG 293

Qy 71 TAGCCAGAAGTTGACAGCCGATCCAGAC--AGCTGCCAAGAAATGATCTCTCTGG 127
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 Qy 188 GCAACTGGGACCTGAGACACCCCTGGCCATGAGACAGTTCCATAGTGGCTGTGCA 247
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 Qy 248 AGACATTAACATGTGACAGACAGTGTCCAGACAGCCAGGACCTGCCATGCTTACCTGT 307
 Db 474 AGACATTAACATGACCAACGCTCAGTCTCCCTGACAGCCGGGACATGCTCCTACTTGT 533
 Qy 308 GTGGGGTCAAGGGCACTACAGAACCATGCTGTAAAGTGAAGCCGCCCTTACATCAGT 367
 Db 534 GTGGCGTGAAGGCCAAGAGGAGCAGAGTGGAGTGAAGCGGACAGACGACGCGAT 593
 Qy 368 GCAACACGACAGCTGGGATGAGTCACTGCTGTGATCAACCGGGCCAGAAAGACAGGA 427
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 Qy 605 TGGGTGAGAGCCGAATGTACATGTTCTGAGGGAGACCCGACCCCTGAATACCGATG 664
 Db 834 TGGGTGGCGGCGGAATATCATGTTACCCGAAACGAACTGATGTGGAATACGAATCG 893
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 Qy 776 CGGATGATCCAGTGTGAACACACCTCATGGGCGCTTTGAGCGGGAGACATGAAGTATA 835
 Db 1011 TTGACCCCTTCAGGGTGAACCTCTTGAAGTCTTTGAGCCCGGGAGATGACAGTATG 1070
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 Db 1071 AATTGAATGGAACCAACCTGACCTGCTTCCTCCAGATGTGTGAGTGGCTCC 1130
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 Qy 1016 CCATGCGCAAGGCTTAACGACTCACTAGGAACTGACAGCTGATCTTGTCACTGACG 1075
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Qy 1372 ACCTTGCTGGCGACATCATATGCGCTTGGCGGGTGGTGGAGAGCCCTACACCGAC 1425
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RESULT 11
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LOCUS AL553521 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
DEFINITION clone CS0D1076YD24 5-PRIME, mRNA sequence.
ACCESSION AL553521
VERSION AL553521.3 GI:45858290
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 902)
Li W.B., Gruber C., Jessee J. and Polyes D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On Feb 15, 2001 this sequence version replaced gi:3127535.
COMMENT

Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
1699.f

For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?c=CS0D1076YD24Plec=1699.f.

FEATURES
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Location/Qualifiers
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primer. Five prime end enriched, double-strand cDNA was
digested with Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Query Match 35.1%; Score 517.4; DB 1; Length 902;
Best Local Similarity 81.0%; Pred. No. 2,4e-115;
Matches 626; Conservative 9; Mismatches 135; Indels 3; Gaps 3;

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Db 106 CATCATCCAGTGTGAGAGAGAAACCCGACTTCTGAAACCGGAGGACCGAGCCCT 165
Qy 66 TGAATGAGCAAGAACTTGCAGCGATCCAGACAGCTGCGCAAGATGTCATCTCTT 125

Db 166 GGGTCCCGCAAGAACTGACCTGACACAGACCGCCCAAGAACTTCATCATCTTCT 225
Qy 126 GGGGATGGGATGGGGGTGGCTTACGGTGAACAGCACTCGATCTTAAAGGGCAGATGA 185
Db 226 GGGCGATGGGATGGGGGTGTCTTACGGTGAACAGCACTCGATCTTAAAGGGCAGATGA 285
Qy 186 TGGCAAACTGGGACCTGAGACACCCCTGGCCATGAGACGATTCCCATAGTGGCTGTGC 245
Db 286 GGACAAACTGGGGCTGTAGATACCCCTGGCCATGAGACCGCTTCCCATATATGTGGCTGTGC 345
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Qy 306 GTGTGGGGTCAAGGGCACTACAGAACCATGCTGTATAGTGAAGCGCCCGCTTACATCA 365
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RESULT 12
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LOCUS BX417625 Homo sapiens PLACENTA Homo sapiens cDNA clone CS0DE011YC17
DEFINITION 5-PRIME, mRNA sequence.
ACCESSION BX417625
VERSION BX417625.2 GI:46955936
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 936)
Li W.B., Gruber C., Jessee J. and Polyes D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On May 15, 2003 this sequence version replaced gi:30767760.
COMMENT

Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was constructed by Life Technologies, a
division of Invitrogen.

This sequence belongs to sequence cluster 1699.f
 For more information about this cluster, see
<http://www.genoscope.cns.fr/cdna?c=CS0DE011AB09QP1ac=1699.f>.
 Location/Qualifiers

FEATURES

source

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Library was not normalized."

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ORIGIN

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Query Match      35.0%; Score 516.6; DB 5; Length 936;
Best Local Similarity 80.0%; Pred. No. 3.8e-115;
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QY 66 TGAATAGCCAAAGTTGAGCGGATCCAGACAGCTGCCAAGATGTCATCTCTTCTT 125
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QY 126 GGGGAGTGGGATGGGGGTGCTTACGCTGACAGCAGCTCGAGTCTTAAAGGGAGATGA 185
DB 262 GGGCGATGGATGGGGGTGCTTACGCTGACAGCAGCTCGAGATCTTAAAGGGAGATGA 321
QY 186 TGGCAACTGGGACTTGAGACACCCCTGGGCTGATGACAGCTTCCATACGTGCTCTG 245
DB 322 GGACAAACTGGGGCTGAGTTACCCCTGGGCTGATGACAGCTTCCATACGTGCTCTG 381
QY 246 CAAGACATCAAGTGGACAGACAGTGGCCAGACAGCGGAGCTGGCCATCTTCACTT 305
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QY 306 GTGTGGGGTCAAGGGGCACTACAGAAACATCGGTGTAGTGACCGCGGCTCAATCA 365
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DB 502 GTGCAACACGACAGCTGGGAATGAGTCACTGTGTATCAACCGGGCCAAAGAGCAG 561
QY 426 GAAGGCGGTGGAGTGTGACACACAGGCTGACAGATGCTCCCGAGCGGGGCTT 485
DB 562 GAAGTCAAGTGGAGTGTGACACACAGGCTGACAGATGCTCCCGAGCGGGGCTT 621
QY 486 CGGACACAGGTAACCGAAACTGTGTCTGAGACGCGGAGCTGCTGTATGACAGAA 545
DB 622 CGGACACAGGTAACCGAAACTGTGTCTGAGACGCGGAGCTGCTGTATGACAGAA 681
QY 546 GAATGGCTGCAGAGACATCCCGACAGCTGTCTCAACATGATGATTTAGACGTGAT 605
DB 682 GGAAGGGGTGCAGAGACATCCCGACAGCTGTCTCAACATGATGATTTAGACGTGAT 741
QY 606 GGGTGGAGGCGGAATGTATCATGTTTCTTGAGGGAGCCCGAGCCCTGATATCCAG 665
DB 742 AGGTGGAGGCGGAATGTATCATGTTTCTTGAGGGAGCCCGAGCCCTGATATCCAG 801
QY 666 TGCAGTGTGAATGAGAGTCCGGAAGACAGCAAGCAAGCTGTGAGGAGAAATGGAG 725
DB 802 CTTCAGCAGCAAGTGGAGACAGGCTGAGCGGAAAGAACTTGTGTGAGGAAATGGAG 861
QY 726 GCAACAGGAGAGCCAGTATGTGTGAAACCGCACTGCGCTCTTCAAGCGGCGAGTAC 785
DB 862 GC-CAGGGGTGCCGAGTGTGTGAA-CGCACTGAGCTCATGAGGCTTCTGTGAGCCT 919

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QY 786 CAGTG 790
 DB 920 CTGTG 924

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RESULT 13
CK834465
LOCUS
DEFINITION
4058791 BARC BBOV Bos taurus cDNA clone BBOV_6303 5', mRNA
sequence.
ACCESSION
CK834465
VERSION
CK834465.1 GI:45064951
KEYWORDS
EST.
SOURCE
Bos taurus (cow)
ORGANISM
Bos taurus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.

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REFERENCE
1 (bases 1 to 681)
AUTHORS
Baumann,R.G., Baldwin,R.L., Sonstegard,T.S., Van Tassel,C.P. and
Matukumalli,L.K.
TITLE
Construction and Analysis of a cDNA Library Generated From
Intestinal Muscle and Epithelial Tissues of Holstein Cattle
JOURNAL
Unpublished (2004)
COMMENT
Contact: Richard G. Baumann
Bovine Functional Genomics Lab
ANRI
BLDG 162: BARC-EAST, Beltsville, MD 20705, USA
Tel: 3015048604
Fax: 3015048744
Email: rbaumann@anri.barc.usda.gov

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Single pass sequencing. Bases called and trimmed with phred
 0.000925 using options -trim_alt -trim_fasta. Vector identified
 by cross match using options -mismatch 12 -mismatch 18
 Plate: 6 row: J column: 03
 Seq primer: CCTATTGAGTGCACACTATAGAAC
 High quality sequence stop: 681.

FEATURES

source

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/lab_host="DH10B TON"
/clone_lib="BARC BBOV"
/note="Organ: Intestine; Vector: pCMVSPORT6.1. Site 1:
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pools derived from 5 sources, 4 lactating intestinal, 1
neonatal intestinal 4/5 Lactating, Proximal Duodenum,
Jejunum, Distal Ileum, Colon, 1/5 Neonatal, Proximal
Duodenum, Jejunum, Distal Ileum"

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ORIGIN

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Query Match      34.6%; Score 511.2; DB 7; Length 681;
Best Local Similarity 96.7%; Pred. No. 7.4e-114;
Matches 522; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

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DB 61 CTGACCGAGGCGGTATGTTTGAATGCAATGCGCAAGGCTTATATGCA 120
QY 1048 CTGACCGGCTGATCTTGTCACTGACAGCACTCCCATGCTTCTTTTGGTGCTAC 1107

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Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France

Email: sequef@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
1699.f

For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?c=CS0DI063AG030P1&c=1699.f.

FEATURES

source

1..929

Location/Qualifiers

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/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Query Match 32.3%; Score 476.6; DB 1; Length 929;

Best Local Similarity 81.9%; Pred. No. 2,2e-105; Mismatches 125; Indels 3; Gaps 3;

Matches 584; Conservative 1; Mismatches 125; Indels 3; Gaps 3;

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DB 140 CATCATCCAGCTGAGGAGGAGAAACCGGACTTCTGGACCGGACGAGCCGAGCCCT 199
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DB 200 GGGTGC CGCCAGAGAGCTGACGCTGCA CAGACAGCCGCGCAAGAACTCATCTTCTT 259
OY 126 GGGGAGTGGATGGGGTGGCTACGGTGAGAG--CAACTCGGATCTTAAAGGGCAGATGA 184
DB 260 GGGCGAGTGGATGGGGTGGCTACGGTGAGAGCTTGCAGAGTCTTAAAGGGCAGAGGA 319
OY 185 ATGGCAAACTGGGACTGAGACACCCCTGGCCATGACAGCTTCCATAGTGGCTGT 244
DB 320 AGGACAAACTGGGGCTGAGTACCTCTGGCCATGACCCGCTTCCATATGTGGCTGT 379
OY 245 CCAAGACATCAACGTGAGACAGAGTGCAGACAGCCAGCGACTGCCATGCTTACC 304
DB 380 CCAAGACATCAACGTGAGACAGAGTGCAGACAGTGGAGCCACAGCCAGGCTTACC 439
OY 305 TGTGTGGGCTCAAGGGCACTACAGAACCATCGGTGTAAGTGACCGCCCGCTTACATC 364
DB 440 TGTGTGGGCTCAAGGGCACTTCCAGACCATGTGGCTTGAAGTGACCGCCCGCTTACC 499
OY 365 AGTCAACACGACACGTGGGATGAGGTCAAGTCTGTGATCAACCGGGCCAGAAAGCAG 424
DB 500 AGTCAACACGACACGTGGGATGAGGTCAAGTCTGTGATCAACCGGGCCAGAAAGCAG 559
OY 425 GGAAGCCGTGGAGTGTGACCAACCAAGGTCAGATGCTTCCAGCCGGGGCT 484
DB 560 GGAAGTCAGTGGAGTGTGACCAACCAAGGTCAGATGCTTCCAGCCGGGGCT 619
OY 485 ACGCGCACAGGTGGAACCGAACTGTGATCAGACCGGACCTGCTGTGATGACAGAGA 544
DB 620 ACGCGCACAGGTGGAACCGAACTGTGATCAGACCGGACCTGCTGTGATGACAGAGA 679
OY 545 AGAATGGCTCCAGAGCATGCGCCAGAGCTGTGCTCAACATGATATTGACGTATCC 604
DB 680 AGAAGGGGTCCAGAGCATGCGCTAGAGCTCATCTCCAATGACATGACGTATCC 739
OY 605 TGGGTGAGGCGCCAGATGATGTTTCTTGAAGGGGACCCAGAG--CCCTGAATACCCAGAT 663
DB 740 TAGGTGAGGCGCCAGATGATGTTTCTTGAAGGGGACCCAGAG--CCCTGAATACCCAGAT 799
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OY 664 GATGCCAGTGTGATGATGAGTCCGGAAGACACAGCAGAACTGTGTGAGGATG 716
DB 800 GACTACAGCCTAAGGTGGAGCCAGGCTGAC--GGGAATCTGTGTGACAGATG 851
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Search completed: October 19, 2004, 17:33:05
Job time : 5060.5 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 19, 2004, 07:43:22 : Search time 6521 Seconds
(without alignments)
10703.818 Million cell updates/sec

Title: US-09-911-132A-5

Perfect score: 1476

Sequence: 1 gattcttcgattccagctga.....gtattccagattaagttacc 1476

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 2364849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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2: gb_hcg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
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11: gb_sta:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| 2 | 1476 | 100.0 | 1476 | 6 | AX356649 | AX356649 Sequence |
| 3 | 1476 | 100.0 | 1476 | 6 | AX840886 | AX840886 Sequence |
| 4 | 1474.4 | 99.9 | 1476 | 6 | AX840891 | AX840891 Sequence |
| 5 | 1472.8 | 99.8 | 1476 | 6 | AX840892 | AX840892 Sequence |
| 6 | 1471.2 | 99.7 | 1476 | 6 | AX840893 | AX840893 Sequence |
| 7 | 1469.6 | 99.6 | 1476 | 6 | AX840894 | AX840894 Sequence |
| 8 | 845.6 | 57.3 | 1476 | 6 | BD175591 | BD175591 Expressio |
| 9 | 845.6 | 57.3 | 1476 | 6 | AX356645 | AX356645 Sequence |
| 10 | 834.8 | 56.6 | 1476 | 6 | AX840884 | AX840884 Sequence |
| 11 | 833.8 | 56.5 | 1798 | 6 | ES9950 | ES9950 Highly acti |
| 12 | 833.8 | 56.5 | 1798 | 6 | AR214214 | AR214214 Sequence |
| 13 | 833.8 | 56.5 | 1798 | 6 | AX012341 | AX012341 Sequence |
| 14 | 831.6 | 56.3 | 1650 | 6 | AX741748 | AX741748 Sequence |
| 15 | 777 | 52.6 | 2460 | 4 | AF052226 | AF052226 Bos tauru |
| 16 | 777 | 52.6 | 2460 | 6 | ES9951 | ES9951 Highly acti |
| 17 | 777 | 52.6 | 2460 | 6 | AR214215 | AR214215 Sequence |
| 18 | 777 | 52.6 | 2460 | 6 | AX012343 | AX012343 Sequence |
| 19 | 772.2 | 52.3 | 2536 | 4 | AF052227 | AF052227 Bos tauru |

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| 21 | 772.2 | 52.3 | 2542 | 6 | AR214216 | AR214216 Sequence |
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| 24 | 613.8 | 41.6 | 1813 | 9 | HUMALP11 | M31008 Human Inter |
| 25 | 611.2 | 41.4 | 1587 | 6 | E08258 | E08258 cDNA encodi |
| 26 | 611.2 | 41.4 | 1587 | 6 | E10970 | E10970 Base sequen |
| 27 | 611.2 | 41.4 | 1587 | 9 | HUMALPHB | M15694 Human adult |
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| 30 | 606 | 41.1 | 2225 | 10 | RSMAAP | X17611 Rat mRNA fo |
| 31 | 603 | 40.9 | 2372 | 6 | E10979 | E10979 Intron-inc1 |
| 32 | 603 | 40.9 | 2484 | 6 | E10972 | E10972 Intron-inc1 |
| 33 | 603 | 40.9 | 3022 | 6 | E10976 | E10976 Intron and |
| 34 | 603 | 40.9 | 3147 | 6 | E10975 | E10975 Intron-inc1 |
| 35 | 584 | 39.6 | 2602 | 10 | S66545 | S66545 putative al |
| 36 | 583.6 | 39.5 | 2445 | 6 | E10973 | E10973 Intron-inc1 |
| 37 | 583.6 | 39.5 | 3108 | 6 | E10974 | E10974 Intron-inc1 |
| 38 | 573.8 | 38.9 | 1539 | 10 | AY054302 | AY054302 Mus muscu |
| 39 | 573 | 38.8 | 1649 | 6 | AX741749 | AX741749 Sequence |
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| 41 | 572.8 | 38.8 | 1637 | 9 | HUMALPFC1 | M13077 Human plac |
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| 43 | 572.8 | 38.8 | 1956 | 6 | A37554 | A37554 Sequence 20 |
| 44 | 572.8 | 38.8 | 7469 | 6 | AX209896 | AX209896 Sequence |
| 45 | 572.8 | 38.8 | 13910 | 6 | AR165934 | AR165934 Sequence |

ALIGNMENTS

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LOCUS BD175594
DEFINITION Expression of alkaline phosphatase in yeast.
ACCESSION BD175594
VERSION BD175594.1 GI:29121292
KEYWORDS JP 2002253269-A/4
SOURCE JP 2002253269-A/4
ORGANISM synthetic construct
synthetic construct
artificial sequences.
1 (bases 1 to 1476)
REFERENCE
AUTHORS Mueller,R., Thalhofer,J.P., Geipel,F., Hoelke,W., Glaeser,S.,
Eckstein,H., Kirschbaum,T. and Riebel,B.B.N.
JOURNAL Expression of alkaline phosphatase in yeast
PATENT: JP 2002253269-A 4 10-SEP-2002;
F HOFFMANN LA ROCHE AG
COMMENT
OS Artificial Sequence
PN JP 2002253269-A/4
PD 10-SEP-2002 JP 2001222153
PF 23-JUL-2001 JP 2001222153
PR 25-JUL-2000 DE 10036491.8
PI RAINER MUELLER,JOHANN PETER THALHOFFER,FRANK GEIPEL,WERNER PI
HOELKE,
PI STEPHAN GLASER,HELMUT ECKSTEIN,THOMAS KIRSCHBAUM, PI
BETTINA BOMMARTUS,NEB RIEBEL
PC C12N15/09,C12N1/19,C12N9/16//C12N1/19,C12R1:645),(C12N1/19,
PC C12R1:78),
PC (C12N9/16,C12R1:645),(C12N9/16,C12R1:78),C12N15/00 CC
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Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 1.3e-266;
Matches 1476; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 ACCESSION AX356649.1 GI:18673989
 VERSION AX356649.1
 KEYWORDS
 SOURCE
 ORGANISM
 synthetic construct
 artificial sequence.

REFERENCE
 1 Mueller, R., Thalhofer, J. P., Geipel, F., Hoelke, W., Glaser, S.,
 Eckstein, H., Kirschbaum, T., and Bommali, B.
 Expression of alkaline phosphatase in yeast
 Patent: EP 1176205-A 5 30-JAN-2002;
 Roche Diagnostics GmbH (DE) ; F. HOFFMANN-LA ROCHE AG (CH)

FEATURES
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 Best Local Similarity 100.0%; Pred. No. 1.3e-26;
 Matches 1476; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAATCTTGATTCAGCTGAAGAGAAATCCAGCTTTTGAATAGACAAGCTGCTCA 60
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[illegible]

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| LOCUS | Sequence 3 | from Patent | EPI348760. |
| DEFINITION | AX840886 | | |
| VERSION | AX840886.1 | GI:3979033 | |
| KEYWORDS | | | |
| SOURCE | | | |
| ORGANISM | | | |
| REFERENCE | | | |
| AUTHORS | 1 | Mueller, R., Thalhofer, J.P., Geipel, P., Hoelke, W., and Kirschbaum, T. | |
| TITLE | | Production of inactive mutants or mutants with a low activity of an alkaline phosphatase and their expression in yeast | |
| JOURNAL | | Patent: EP 1348760-A 3 01-Oct-2003; | |
| FEATURES | | Roche Diagnostics GmbH (DE) ; F. HOFMANN-LA ROCHE AG (CH) | |
| Source | | location/Qualifiers | |
| ORIGIN | | 1. 1476 | |
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| | | /mol_type="unassigned DNA" | |
| | | /db_xref="taxon:32630" | |
| | | /note="Nucleic acid" | |
| Query Match | 100.0%; | Score 1476; | DB 6; |
| Best Local Similarity | 100.0%; | Pred. No. 1,3e-266; | Length 1476; |
| Matches 1476; | Conservative 0; | Mismatches 0; | Indels 0; |
| | | Gaps 0; | |
| Qy | 1 | GAATTCCTGATTCAGCTGAAGAAAGAAATCCAGCTTTTGGAAATAGACAAGCTGCTCAA | 60 |
| Db | 1 | GAATTCCTGATTCAGCTGAAGAAAGAAATCCAGCTTTTGGAAATAGACAAGCTGCTCAA | 60 |
| Qy | 61 | GCTTGGATGTTGCTGAAGAGTTGCCAACCAATTCAACTGCTGTAAGAAATGTTATTTTG | 120 |
| Db | 61 | GCTTGGATGTTGCTGAAGAGTTGCCAACCAATTCAACTGCTGTAAGAAATGTTATTTTG | 120 |
| Qy | 121 | TTTTTGGGTAGTGTATGGGTGTTCCAACTGTTACTGCTACTAGAAATTTTGAAGGGTCAA | 180 |
| Db | 121 | TTTTTGGGTAGTGTATGGGTGTTCCAACTGTTACTGCTACTAGAAATTTTGAAGGGTCAA | 180 |
| Qy | 181 | ATGAATGGTAAGTGGGTCCAGAAACCCAAATGGCTATGGATTCATTTTCCATAGTGGCT | 240 |
| Db | 181 | ATGAATGGTAAGTGGGTCCAGAAACCCAAATGGCTATGGATTCATTTTCCATAGTGGCT | 240 |
| Qy | 241 | TTGTCTAAGACTTCAATGTTGATAGACAAGTTCCAGATTCTGCTGTAAGTCTACTGCT | 300 |
| Db | 241 | TTGTCTAAGACTTCAATGTTGATAGACAAGTTCCAGATTCTGCTGTAAGTCTACTGCT | 300 |
| Qy | 301 | TACTTGTGTGTGTTAAGGGTAATTACAGAACTATTGGTGTTCGCTGCTGCTAGATAC | 360 |
| Db | 301 | TACTTGTGTGTGTTAAGGGTAATTACAGAACTATTGGTGTTCGCTGCTGCTAGATAC | 360 |
| Qy | 361 | AATCAATGTAACTACTAGAGGTAATGAAGTTACTCTGTATTAATTAAGAGCTAAGAG | 420 |
| Db | 361 | AATCAATGTAACTACTAGAGGTAATGAAGTTACTCTGTATTAATTAAGAGCTAAGAG | 420 |
| Qy | 421 | GCTGGTAAGCGTGTGTGTTGTTACTACTAGATGATCAACATGCTTCTCCAGCTGCT | 480 |
| Db | 421 | GCTGGTAAGCGTGTGTGTTGTTACTACTAGATGATCAACATGCTTCTCCAGCTGCT | 480 |
| Qy | 481 | GCTTACGCTCACTATTGTAADGAAATTTGGTACTCTGATGCTGATTTGCCAGCTGATGCT | 540 |

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Db 481 GCTTAGGCTCATCTGTATATAGAAATGGTACTGATGCTGATTTGGCAGCTGATGCT 540
QY 541 CAAAAGATGGTGTCAAGATATTTGCTGCTCAATGGTTTACAAATATGATATGATTTGTT 600
Db 541 CAAAAGATGGTGTCAAGATATTTGCTGCTCAATGGTTTACAAATATGATATGATTTGTT 600
QY 601 ATTTGGGTGGTGTAGAAATGTACATGTTTCCAGAGGTACTCCAGATCCAGATATCCCA 660
Db 601 ATTTGGGTGGTGTAGAAATGTACATGTTTCCAGAGGTACTCCAGATCCAGATATCCCA 660
QY 661 GATGATGCTTCTGTATATGTTGTTAGAAAGATTAACCAAAATTTGGTTCAGAAATGCGCA 720
Db 661 GATGATGCTTCTGTATATGTTGTTAGAAAGATTAACCAAAATTTGGTTCAGAAATGCGCA 720
QY 721 GCTAAGCATCAAGAGTCTCAATATGTTTGGAAATGAAAGTCTTGTTCAGAGTCTGAT 780
Db 721 GCTAAGCATCAAGAGTCTCAATATGTTTGGAAATGAAAGTCTTGTTCAGAGTCTGAT 780
QY 781 GATTCAGTGTACTCATTTGATGAGTGTGTTGTTGAACCAAGTATATGAAATATATGTT 840
Db 781 GATTCAGTGTACTCATTTGATGAGTGTGTTGTTGAACCAAGTATATGAAATATATGTT 840
QY 841 CAAAGATCATCTAAGATCCACTTTGGCTGAATATGATGAGCTGCTTGGCAAGTT 900
Db 841 CAAAGATCATCTAAGATCCACTTTGGCTGAATATGATGAGCTGCTTGGCAAGTT 900
QY 901 TTGTCTAGAAATCCAGAGGTTTTTACTTGTGTTGTAAGGTTGTAATGATGATGAT 960
Db 901 TTGTCTAGAAATCCAGAGGTTTTTACTTGTGTTGTAAGGTTGTAATGATGATGAT 960
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QY 1021 GCTAAGGCTTAATGAATTTGATCTTCTGAAATTTGATCTTGTATCTGCTATCAT 1080
Db 1021 GCTAAGGCTTAATGAATTTGATCTTCTGAAATTTGATCTTGTATCTGCTATCAT 1080
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Db 1081 AGTCATGTTTTTCTTTTGGTGTACACTTTGAGAGGTAATCTTATTTTGGTTGGCT 1140
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Db 1141 CCAGGTAAGGCTTTGGATAGTACCTTCACTTATTTTGTATGTAATGATGCTCCAGCT 1200
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Db 1201 TATGCTTTGGGTGGTGTCTAGACCAATGTTAATGTAATGTAATGTAATGTAATGTA 1260
QY 1261 TACAGACAAAGCTGCTGTTCCATTTGCTAGTGAAGTCAATGGTGGTGAAGTGTGCT 1320
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QY 1321 GTTTTGTCTAGAGGTCCACAAAGCTCATTTGTTGATGATGTTCAAGAAATCTTTGTT 1380
Db 1321 GTTTTGTCTAGAGGTCCACAAAGCTCATTTGTTGATGATGTTCAAGAAATCTTTGTT 1380
QY 1381 GCTCATATTAATGGCTTTTGTGCTGTTGTGTTGAACCATATACATGATTTGTAATTTGCCAGCT 1440
Db 1381 GCTCATATTAATGGCTTTTGTGCTGTTGTGTTGAACCATATACATGATTTGTAATTTGCCAGCT 1440
QY 1441 CCAGCTACTGCTACTAGTATTCAGATTAAGGTACC 1476
Db 1441 CCAGCTACTGCTACTAGTATTCAGATTAAGGTACC 1476

RESULT 4
LOCUS AX840891 1476 bp DNA linear PAT 16-DEC-2003
DEFINITION Sequence 8 from Patent EP1348760.
ACCESSION AX840891

VERSION AX840891.1 GI:39979034
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Nucleic acid"

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Query Match 99.9%; Score 1474.4; DB 6; Length 1476;
Best Local Similarity 99.9%; Pred No. 2.6e-266;
Matches 1475; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAATTCCTGATTCACGCTGAAGAGAGAAATCCAGCTTTTGGATATGACAAAGCTGCTCA 60
Db 1 GAATTCCTGATTCACGCTGAAGAGAGAAATCCAGCTTTTGGATATGACAAAGCTGCTCA 60
QY 61 GCTTTGATGTTGCTTAAGAGTTCACCAATTCAACTGCTGCTTAAGATATATTTTG 120
Db 61 GCTTTGATGTTGCTTAAGAGTTCACCAATTCAACTGCTGCTTAAGATATATTTTG 120
QY 121 TTTTGGGTGATGATGGGTGTTTCCACTGTTACTGCTACTAGAAATTTTGAAGGGTCAA 180
Db 121 TTTTGGGTGATGATGGGTGTTTCCACTGTTACTGCTACTAGAAATTTTGAAGGGTCAA 180
QY 181 ATGAATGGTAAGTGGTCCAGAAATCCATTTGCTATGATCAATTTCCATACGTTGCT 240
Db 181 ATGAATGGTAAGTGGTCCAGAAATCCATTTGCTATGATCAATTTCCATACGTTGCT 240
QY 241 TTGCTAGACCTTCAATGTTGATGACAAAGTTCAGATTTCTGCTGTAATGCTACCT 300
Db 241 TTGCTAGACCTTCAATGTTGATGACAAAGTTCAGATTTCTGCTGTAATGCTACCT 300
QY 301 TACTTGTGTGGTGAAGGTAATTAACAGAACTATTTGTTCTGCTGCTGCTAGATAC 360
Db 301 TACTTGTGTGGTGAAGGTAATTAACAGAACTATTTGTTCTGCTGCTGCTAGATAC 360
QY 361 AATCAATGTAATCTACTAGAGGTATGAAAGTTACTTCTGTTATTAATAGACTAAGAG 420
Db 361 AATCAATGTAATCTACTAGAGGTATGAAAGTTACTTCTGTTATTAATAGACTAAGAG 420
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Db 421 GCTGTGAAGGCTTTGGTGTGTTACTACTTCACTAGAGTTCAAATGCTTCTCCAGCTGGT 480
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Db 541 CAAAAGATGGTGTCAAGATATTTGCTGCTCAATTTGTTTCAATATGATATGATGTT 600
QY 601 ATTTGGGTGGTGTAGAAATGTAATGTTTCCAGAGTACTCCAGATCCAGATATCCCA 660
Db 601 ATTTGGGTGGTGTAGAAATGTAATGTTTCCAGAGTACTCCAGATCCAGATATCCCA 660
QY 661 GATGATGCTTCTGTATATGTTGTTAGAAAGATAGCAAAATTTGTTCAAGAAATGCGCA 720
Db 661 GATGATGCTTCTGTATATGTTGTTAGAAAGATAGCAAAATTTGTTCAAGAAATGCGCA 720
QY 721 GCTAAGCATCAAGGCTCAATATGTTTGGAAATGAACTGCTTGTTCAGAGCTGCTGAT 780
Db 721 GCTAAGCATCAAGGCTCAATATGTTTGGAAATGAACTGCTTGTTCAGAGCTGCTGAT 780

Db 721 GCTAAGCATCAAGTGTCTAATATGTTGGAAATGAAGCTGTTGTGCAAGCTGCTGAT 780
 Qy 781 GATTAGTGTCTAATTTGATGCGTTTGTGTAACCACTGATATGAATGATTAATGTT 840
 Db 781 GATTCTAGTGTCTAATTTGATGCGTTTGTGTAACCACTGATATGAATGATTAATGTT 840
 Qy 841 CAACAAGATCATCTAAGATCCAACTTTGGCTGAATGACTGAAGCTGCTTGGCAAGTT 900
 Db 841 CAACAAGATCATCTAAGATCCAACTTTGGCTGAATGACTGAAGCTGCTTGGCAAGTT 900
 Qy 901 TTGCTAGAAATCCAAAGAGTTTCTTGTGTTGTAAGGTGTGAATGATGATGAT 960
 Db 901 TTGCTAGAAATCCAAAGAGTTTCTTGTGTTGTAAGGTGTGAATGATGATGAT 960
 Qy 961 CATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1020
 Db 961 CATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1020
 Qy 1021 GCTAAGGCTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1080
 Db 1021 GCTAAGGCTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1080
 Qy 1081 AGTCATGTTTTTCTTTGGTGTGTTACCTTTGAGAGTACTTCTATTTTGGTTGGCT 1140
 Db 1081 AGTCATGTTTTTCTTTGGTGTGTTACCTTTGAGAGTACTTCTATTTTGGTTGGCT 1140
 Qy 1141 CCGAGTAAAGCTTTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1200
 Db 1141 CCGAGTAAAGCTTTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1200
 Qy 1201 TATGCTTTGGGTTGGTGTGTTAGACGATGATTAATGATGATGATGATGATGATGAT 1260
 Db 1201 TATGCTTTGGGTTGGTGTGTTAGACGATGATTAATGATGATGATGATGATGATGAT 1260
 Qy 1261 TACAGACAAACAGCTGCTGTTCCATTGGCTAGTGAACCTCATGGTGTGAAGATGTTGCT 1320
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 Qy 1321 GTTTTTGTCTAGAGTCCACAAGCTCATTTGGTTCATGTTGTTCAAGAAAGAACTTTTGT 1380
 Db 1321 GTTTTTGTCTAGAGTCCACAAGCTCATTTGGTTCATGTTGTTCAAGAAAGAACTTTTGT 1380
 Qy 1381 GCTCATATTAATGCTTTTGTGCTGTTGTTGTTGAACCATACCTGATTTAATTTGCCAGCT 1440
 Db 1381 GCTCATATTAATGCTTTTGTGCTGTTGTTGTTGAACCATACCTGATTTAATTTGCCAGCT 1440
 Qy 1441 CCAGCTACTGCTACTAGTATTCAGATTAAAGTACC 1476
 Db 1441 CCAGCTACTGCTACTAGTATTCAGATTAAAGTACC 1476

RESULT 5
 AX840892 1476 bp DNA linear PAT 16-DEC-2003
 LOCUS Sequence 9 from Patent EP1348760.
 DEFINITION AX840892
 ACCESSION AX840892
 VERSION AX840892.1 GI:39979035
 KEYWORDS
 SOURCE
 ORGANISM
 synthetic construct
 synthetic construct
 artificial sequences.
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 Roche Diagnostics GmbH (DE) ; F.HOFFMANN-LA ROCHE AG (CH)
 Location/Qualifiers
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 /organism="synthetic construct"
 /mol_type="unassigned DNA"
 /db_xref="taxon:32630"
 /note="Nucleic acid"

ORIGIN
 Query Match 99.8%; Score 1472.8; DB 6; Length 1476;
 Best Local Similarity 99.9%; Pred. No. 5.3e-266;
 Matches 1474; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 1 GAATTTCTTGAATTCACCTGAGAAAGAAATCCAGCTTTTGTGAATGACACAGCTGCTCA 60
 Db 1 GAATTTCTTGAATTCACCTGAGAAAGAAATCCAGCTTTTGTGAATGACACAGCTGCTCA 60
 Qy 61 GCTTTGATGTTGCTAAGAAAGTTGCAACCAATTCACCTGCTAAGAAAGTTATTTTG 120
 Db 61 GCTTTGATGTTGCTAAGAAAGTTGCAACCAATTCACCTGCTAAGAAAGTTATTTTG 120
 Qy 121 TTTTGGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 180
 Db 121 TTTTGGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 180
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 Db 181 ATGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 240
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 Qy 361 AATCAATGATTAATCTAAGAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAA 420
 Db 361 AATCAATGATTAATCTAAGAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAA 420
 Qy 421 GCTGTAAGGCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 480
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 Db 481 GCTTACGCTCATACCTGTTAATGAAATTTGGTACTGTAAGCTGATGATGCT 540
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 Db 661 GATGATGCTTCTGTTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 720
 Qy 721 GCTAAGCATCAAGGCTCCTAATGTTGTTGAATGAAGCTGTTGTTGCAAGCTGCTGAT 780
 Db 721 GCTAAGCATCAAGGCTCCTAATGTTGTTGAATGAAGCTGTTGTTGCAAGCTGCTGAT 780
 Qy 781 GATTCTAGTGTACTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 840
 Db 781 GATTCTAGTGTACTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 840
 Qy 841 CAACAAGATCATCTAAGATCCAACTTTGGCTGAATGACTGAAGCTGCTTGGCAAGTT 900
 Db 841 CAACAAGATCATCTAAGATCCAACTTTGGCTGAATGACTGAAGCTGCTTGGCAAGTT 900
 Qy 901 TTGCTAGAAATCCAAAGAGTTTCTTGTGTTGTAAGGTGTGAATGATGATGATGAT 960
 Db 901 TTGCTAGAAATCCAAAGAGTTTCTTGTGTTGTAAGGTGTGAATGATGATGATGAT 960
 Qy 961 CATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1020
 Db 961 CATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1020

QY 1021 GCTAAGGCTAATGAATTCGATTGATGATCTTTGATTTGGTACTGCTGATCAT 1080
DB 1021 GCTAAGGCTAATGAATTCGATTGATGATCTTTGATTTGGTACTGCTGATCAT 1080
QY 1081 AGTCATGTTTTCTTTTGGTGGTTACACTTTGAGAGGTAATTCTATTTTGGTTGGCT 1140
DB 1081 AGTCATGTTTTCTTTTGGTGGTTACACTTTGAGAGGTAATTCTATTTTGGTTGGCT 1140
QY 1141 CCAGGTAAGGCTTTGGATAGTACTTTCACCTTATTTTGGATAGTATGGTCCAGGT 1200
DB 1141 CCAGGTAAGGCTTTGGATAGTACTTTCACCTTATTTTGGATAGTATGGTCCAGGT 1200
QY 1201 TATGCTTTGGGTGGTCTCTAGACCAAGATGTTATGATGATCTAGTGAAGAACATCT 1260
DB 1201 TATGCTTTGGGTGGTCTCTAGACCAAGATGTTATGATGATCTAGTGAAGAACATCT 1260
QY 1261 TACAGACCAAGCTGCTGTTCCATTGGCTAGTGAAGTCACTGCTGATGAAGATGTTGCT 1320
DB 1261 TACAGACCAAGCTGCTGTTCCATTGGCTAGTGAAGTCACTGCTGATGAAGATGTTGCT 1320
QY 1321 GTTTTGTCTAGAGGTCCACAGCTCATTTGGTTCATGCTGTTCCAGAAAGAACTTTTGT 1380
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QY 1381 GCTCATATTATGAGCTTTTCTGGTGTGTTGAACCATACACTGATTTGATTTGCCAGCT 1440
DB 1381 GCTCATATTATGAGCTTTTCTGGTGTGTTGAACCATACACTGATTTGATTTGCCAGCT 1440
QY 1441 CCAGCTACTGCTACTAGTATTCAGATTAAAGGTACC 1476
DB 1441 CCAGCTACTGCTACTAGTATTCAGATTAAAGGTACC 1476

RESULT 6
AX840893 1476 bp DNA linear part 16-DEC-2003
LOCUS AX840893
DEFINITION Sequence 10 from Patent EP1348760.
ACCESSION AX840893
VERSION AX840893.1 GI:39979036

KEYWORDS
SOURCE
ORGANISM
REFERENCE

AUTHORS
TITLE
JOURNAL
Roche Diagnostics GmbH (DE) / F.HOFFMANN-LA ROCHE AG (CH)
Location/Qualifiers
1. 1476

FEATURES
Source
1. 1476
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Nucleic acid"

ORIGIN

Query Match 99.7%; Score 1471.2; DB 6; Length 1476;
Best Local Similarity 99.8%; Pred. No. 1e-265;
Matches 1473; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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DB 1 GAATCTTGATTCAGCTGAGAGAAATCCAGCTTTTGGATAGCAAGCTGCTCA 60
QY 61 GCTTGGATGTTGCTAGAGAGTTGCAACCAATTCAACTGCTCTAGAGATGTTATTTG 120
DB 61 GCTTGGATGTTGCTAGAGAGTTGCAACCAATTCAACTGCTCTAGAGATGTTATTTG 120
QY 121 TTTTGGGATGATGATGGGTGTTCCAACTGTTACTGCTACTAGAAATTTGAAAGGCTCA 180
DB 121 TTTTGGGATGATGATGGGTGTTCCAACTGTTACTGCTACTAGAAATTTGAAAGGCTCA 180

QY 181 ATGAATGGATAGTGGGTCCAGAACTCCATTGGCTATGATGATCAATTTCCATAGCTTGT 240
DB 181 ATGAATGGATAGTGGGTCCAGAACTCCATTGGCTATGATGATCAATTTCCATAGCTTGT 240
QY 241 TTGCTAAGACTTACCAATGTTGATAGACAGGTTCCAGATTCTGCTGATCTGCTACTGCT 300
DB 241 TTGCTAAGACTTACCAATGTTGATAGACAGGTTCCAGATTCTGCTGATCTGCTACTGCT 300
QY 301 TACTGTGTGCTTAAAGGATTAATACAGAACTATTGGTGTCTGCTGCTGCTAGATAC 360
DB 301 TACTGTGTGCTTAAAGGATTAATACAGAACTATTGGTGTCTGCTGCTGCTAGATAC 360
QY 361 AATCAATGAATTAATCACTAGAGGTAATGAAGTACTTCTGTTATTAATAGAGCTAAG 420
DB 361 AATCAATGAATTAATCACTAGAGGTAATGAAGTACTTCTGTTATTAATAGAGCTAAG 420
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QY 1021 GCTAAGGCTAATGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1080
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QY 1201 TATGCTTTGGGTGGTGTCTCTAGACCAAGATGTTATGATGATCTAGTGAAGAACATCT 1260
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 DB 1321 GTTTTGCTAGAGGCTCACAAGCTCATTGGTTCATGCTGTTCAAGAAACCTTTGTT 1380
 QY 1381 GCTCATATTATGCTTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1440
 DB 1381 GCTCATATTATGCTTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1440
 QY 1441 CCAGCTACTGCTACTAGTATTCAGATTAGTACC 1476
 DB 1441 CCAGCTACTGCTACTAGTATTCAGATTAGTACC 1476
 RESULT 7
 AX840894 1476 bp DNA linear PAT 16-DEC-2003
 LOCUS AX840894
 DEFINITION Sequence 11 from Patent EP1348760.
 ACCESSION AX840894
 VERSION AX840894.1 GI:39979037
 KEYWORDS
 SOURCE synthetic construct
 ORGANISM synthetic construct
 REFERENCE
 1 Mueller, R., Thelhofer, J.P., Geipel, F., Hoelke, W. and Kirschbaum, T.
 AUTHORS Production of inactive mutants or mutants with a low activity of an
 TITLE alkaline phosphatase and their expression in yeast
 JOURNAL Patent: EP 1348760-A 11 01-OCT-2003;
 Roche Diagnostics GmbH (DE) ; F.HOFFMANN-LA ROCHE AG (CH)
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 1. 1476
 Location/Qualifiers
 /organism="synthetic construct"
 /mol_type="unassigned DNA"
 /db_xref="taxon:32630"
 /note="Nucleic acid"
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 Query Match 99.6%; Score 1469.6; DB 6; Length 1476;
 Best Local Similarity 99.7%; Pred. No. 2.1e-265;
 Matches 1472; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 1 GAATCTTGATTCAGCTGAAGAAATCCAGCTTTTGGAAATGACAAGCTGCTCA 60
 DB 1 GAATCTTGATTCAGCTGAAGAAATCCAGCTTTTGGAAATGACAAGCTGCTCA 60
 QY 61 GCTTGGAGTCTTGAAGAGTTCGCAACCAATTCAGCTGCTGCTGAAGATGTTATTTTG 120
 DB 61 GCTTGGAGTCTTGAAGAGTTCGCAACCAATTCAGCTGCTGCTGAAGATGTTATTTTG 120
 QY 121 TTTTGGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 180
 DB 121 TTTTGGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 180
 QY 121 TTTTGGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 180
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 QY 181 ATGAATGTAAGTGGGCTCAGAACTCCATTGGCTATGATCAATTCATAGTTGCT 240
 DB 181 ATGAATGTAAGTGGGCTCAGAACTCCATTGGCTATGATCAATTCATAGTTGCT 240
 QY 241 TTGCTTAAGCTTAACAATGTTGATGACCAAGTTCGATGCTGCTGCTGCTGCTGCTGCT 300
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 QY 301 TACTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
 DB 301 TACTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
 QY 361 AATCATATGTAATCTACTAGAGGTAATGAAGTACTCTGTTATTAATAGAGCTAAGAG 420
 DB 361 AATCATATGTAATCTACTAGAGGTAATGAAGTACTCTGTTATTAATAGAGCTAAGAG 420

QY 421 GCTGTAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
 DB 421 GCTGTAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
 QY 481 GCTTACGCTCATACTGTTAATAGAAATGGTACTGCTGATGCTGATTTGCCAGCTGCT 540
 DB 481 GCTTACGCTCATACTGTTAATAGAAATGGTACTGCTGATGCTGATTTGCCAGCTGCT 540
 QY 541 CAAATAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
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| BD175591 | BD175591 | 1476 bp | DNA | linear | PAT 18-MAR-2003 |
| LOCUS | Expression of alkaline phosphatase in yeast. | | | | |
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| ACCESSION | BD175591.1 | GI:29121289 | | | |
| VERSION | JP 2002253269-A/1. | | | | |
| KEYWORDS | Boe sp. | | | | |
| SOURCE | Boe sp. | | | | |
| ORGANISM | | | | | |

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| REFERENCE | 1 (bases 1 to 1476) |
| AUTHORS | Mueller, R., Thalhofer, J. P., Geipel, F., Hoelke, W., Glaser, S., Eckstein, H., Kirchbaum, T., and Riebel, B. B. N. |
| TITLE | Expression of alkaline phosphatase in yeast |
| JOURNAL | Patent: JP 2002253269-A 1 10-SEP-2002, |
| COMMENT | F. HOFFMANN LA ROCHE AG Bos sp. (bovine) |

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PF 23-JUL-2001 JP 2001222153
PR 25-JUL-2000 DE 10036491.8
PI RAINER MUELLER, JOHANN PETER THALHOEFFER, FRANK GEIPEL, WERNER
PI HOEIKE,
PI STEPHAN GLASER, HELMUT ECKSTEIN, THOMAS KIRSCHBAUM, PI
BETTINA BOMMARIUS NEE RIEBEL.
PC C12N15/09, C12N1/19, C12N9/16// (C12N1/19, C12R1:645), (C12N1/19,
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PC C12N9/16, C12R1:645), (C12N9/16, C12R1:78), C12N15/00 CC
Expression of alkaline phosphatase in yeast
FH Key Location/Qualifiers
FT Source 1.1476
/organism='Bos sp. (bovine)'.

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| FEATURES | Location/Qualifiers |
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| Qy | 181 | ATGAATGATGAATGGGTGTCAGAAATCCATTTGGTATGATCAATTTCCATAGTGGCT | 240 |
| Db | 181 | ATGAATGGCAAACTGGGACTTAGACACCCCTGGCCATGACAGATTTCCATAGTGGCT | 240 |
| Qy | 241 | TTGCTCAAGACTTACATATTTGATGACAAAGTTCCAGATTCGGCTGGATCGTACTGCT | 300 |
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| Db | 301 | TACCTGTGTGGGTCAAGGGCAATCAAGAACATCGGTGTAATGTGACAGCCGCCGTAC | 360 |
| Qy | 361 | AATCAATGTAAATCTAATAGAGTAATGAAGTAATCTTGTAATTAATAGACTAAGAG | 420 |
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| Qy | 541 | CAAAAGATGCTGTTCAGATATTGCTGCTCAATTGGTTACATATGATATTGATGTT | 600 |
| Db | 541 | CAGAAATAGGCTGCCAGACATCCGCCACAGCTGGTCTACAACTAGATATTGACGTG | 600 |
| Qy | 601 | ATTTGGGTGGTGAAGATGATCAATGTTTCAGAAAGTACTCCAGATCCAGAAATACCA | 660 |
| Db | 601 | ATCTGGGTGGAGGCCGAATGTACATGTTTCTGAGGGAACTCCAGACCTTGAATACCA | 660 |
| Qy | 661 | GATGATGCTCTTGTTAATGAGTTAGAAAGATAGCAAAATTGGTTCAAGATGGCAA | 720 |
| Db | 661 | GATGATGCCAGTGTGATAGATGCCGAAGCAAGCAAGAACCTGTGTGACGAATGGCAG | 720 |
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| Db | 721 | GCCAAACACAGAGAGCCCAATGTGTGAAACCGCACTGGCTCTTCAGCGGCCGAT | 780 |
| Qy | 781 | GATTCTAGTGTACTCATTTGATGGGTTTGGTTGAACAGCTGATATGAAATATGTT | 840 |
| Db | 781 | GATCCAGTGAACAACACTATGGGCTCTTTAAGCCGAGACATAGMATATATGTT | 840 |
| Qy | 841 | CAACAGATCATACTAAGATCCAACTTGGCTGAATGACTGAACTGCTTTGCCAAGTT | 900 |
| Db | 841 | CAGCAAGACCAACCAAGAACCCGACCTTGCGGAGATGACGAGGCGGCCCTTGCAAGTG | 900 |
| Qy | 901 | TGTCTAGAATATCCAAAGGTTTAACTGTTTGTGTGAAGTGGTATGAATGATCATGCT | 960 |
| Db | 901 | CTGAGCAGAACCCCGGGCTTCTAAGCTTCTGTGAGGAGGCCGATATGACACAGCT | 960 |
| Qy | 961 | CATCATGATGTGAAGGCTTATATGCTTTGACTGAAGCTATATGTTGATTAATGCTATT | 1020 |
| Db | 961 | CACCATGACGGCAAAAGCTTATATGGCACTGACTGAAGCGATCATGTTGACAAATGCCATC | 1020 |
| Qy | 1021 | GCTAAGGCTAATGAATTAAGCTTCGGAATGGATACCTTGAATTTGGTACTGCTGATCAT | 1080 |
| Db | 1021 | GCCAAAGCTTAAGAACTCACTAGCGAATGGACAGCGCTGATCCTTGCACCTGACAGACAC | 1080 |
| Qy | 1081 | AGTCATGTTTTTCTTTTGGTGGTACACTTTGAGAGGTACTTCTATTTTGGTTGGCT | 1140 |
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| Db | 1141 | CCCGGAAAGGCTTATGACAGCAAGTCTTCAACCTCCTATATGGCAATGGCCCAAGGC | 1200 |
| Qy | 1201 | TATGCTTTGGGTGGTGTCTTAGACAGATTTAAATGTAATGTAAGTAAGAACATGCT | 1260 |
| Db | 1201 | TATGGCTTTGGCGGGGGCTCGAGGCCGATTTAATAGCAGACACAGACGAGAACCTCA | 1260 |
| Qy | 1261 | TACAGCAACAAGCTGCTGTTCCATTGGCTAGTGAACCTATGCTGTGTGAAGTGTGCT | 1320 |
| Db | 1261 | TACCGGCAAGAGCGGCGGTGCCCTGTGACGAGACCAACGGGGGCGAAGACGTGGCG | 1320 |
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| Qy | 1381 | GCTCATATTATGCTTTTGTGCTGTGTGTGTAACATATACCTGATTTTGGCAGCT | 1440 |
| Db | 1381 | GGGCAATCATGCTTTTGGCGGGCGGTGTGAGGCCCTTACACCGAGCTGCAATCTGGCAGCC | 1440 |
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RESULT 9
 AX356645 1476 bp DNA linear PAT 13-FEB-2002
 LOCUS Sequence 1 from Patent EP1176205.
 DEFINITION AX356645
 VERSION AX356645.1 GI:18673986
 KEYWORDS
 SOURCE
 ORGANISM
 Bos taurus (cow)
 Bos taurus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 Bovinae; Bos.
 REFERENCE
 AUTHORS
 1 Mueller, R., Thalhofer, J.P., Geipel, F., Hoelke, W., Glaeser, S.,
 Eckstein, H., Kirschbaum, T. and Bommarius, B.
 TITLE Expression of alkaline phosphatase in yeast
 JOURNAL Patent: EP 1176205-A 1 30-JAN-2002;
 Roche Diagnostics GmbH (DE) ; F. HOFMANN-LA ROCHE AG (CH)
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 Query Match 57.3%; Score 845.6; DB 6; Length 1476;
 Best Local Similarity 73.3%; Pred. No. 1.7e-148;
 Matches 1082; Conservative 0; Mismatches 394; Indels 0; Gaps 0;
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 VERSION AX840884.1 GI:39979031
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 Bos taurus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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 Bovinae; Bos.
 REFERENCE
 AUTHORS
 1 Mueller, R., Thalhofer, J.P., Geipel, F., Hoelke, W. and Kirschbaum, T.
 TITLE Production of inactive mutants or mutants with a low activity of an
 alkaline phosphatase and their expression in yeast

JOURNAL Patent: EP 1348760-A 1 01-OCT-2003;
Roche Diagnostics GmbH (DE) ; F. HOFMANN-LA ROCHE AG (CH)
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ORIGIN

Query Match 56.6%; Score 834.8; DB 6; Length 1464;
Best Local Similarity 73.2%; Pred. No. 1.8e-146;
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QY 788 GTGTTACTATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 847
DB 782 GTGTAACACCTCATGAGGCTCTTTGAGCCGAGACATGATGATGATGATGATGATGATG 841
QY 848 ATCAATCAAGGCTTTTACTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 907
DB 842 ACCACACCAAGGACCCGACCCCTGCGAGATGACGAGAGGCGCCCTGCAAGTGTGACGA 901
QY 908 GAAATCCAAAGGCTTTTACTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 967
DB 902 GGAACCCCGGGGCTTCACTCTTCTGAGAGGAGGCGCATTCACACGCTCACATG 961
QY 968 ATGTAAGGCTTAATGCTTTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1027
DB 962 ACCGAAAGCTTAATGCTTTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1021
QY 1028 CTAATGAATGATCTTGAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1087
DB 1022 CTAAGAGCTCACTAGCAAGCTGACAGCTGATCTTGTACATGCAAGCACTCCATG 1081
QY 1088 TTTTCTTTTGGTGTGATCACTTTGAGAGGATCTTCAATTTTGGCTTGGCTCCAGGTA 1147
DB 1082 TCTTCTTTTGGTGTGATCACTTTGAGAGGATCTTCAATTTTGGCTTGGCTCCAGGTA 1141
QY 1148 AGGCTTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1207
DB 1142 AGGCTTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1201
QY 1208 TGGGTGTTGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1267
DB 1202 TTTGCGGGGGCTCGAGGCGCCATGTTAATGATGATGATGATGATGATGATGATGATG 1261
QY 1268 AACAGCTGTTGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1327
DB 1262 AGCAGGCGGCGTGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1321
QY 1328 CTAGAGTCCCAAGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1387
DB 1322 CGGAGGCGCGGAGGCGGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1381
QY 1388 TTAATGCTTTTGGTGTGTTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1447
DB 1382 TCATGCTTTTGGGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1441
QY 1448 CTGCTACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1469
DB 1442 CCGCACCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1463

RESULT 11
E59950 1798 bp DNA linear PAT 13-AUG-2002
LOCUS E59950
DEFINITION Highly active alkaline phosphatase.
ACCESSION E59950.1 GI:13017720
VERSION E59950.1
KEYWORDS JP 1999332586-A/1.
SOURCE Bos taurus (cow)
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
REFERENCE 1 (bases 1 to 1798)
AUTHORS Wernert, H., Reina, M., Herumuto, B. and Jose, L. M.
TITLE Highly active alkaline phosphatase
JOURNAL Patent: JP 1999332586-A 1 07-DEC-1999;
COMMENT OS Bovidae

PN JP 1999332586-A/1
 PD 07-DEC-1999
 PR 06-MAY-1999 JP 1999126494
 PR 05-MAY-1998 DE 19819962:7
 PI WERNER HOERUKU, REINA MÜLLER, HERUMUTTO BURKOTOSHA, PI JOSE
 LOUIS MILAN
 PC C12N15/09, C12N1/15, C12N1/19, C12N1/21, C12N5/10, C12N9/16, PC
 C12N15/00, C12N5/00
 CC
 FH Key Location/Qualifiers
 FT source 1.1798
 FT /Organism="Bovidae".
 Location/Qualifiers
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 /organism="Bos taurus"
 /mol_type="genomic DNA"
 /db_xref="taxon:9913"

ORIGIN

Query Match 56.5%; Score 833.8; DB 6; Length 1798;
 Best Local Similarity 73.2%; Pred. No. 2.7e-146;
 Matches 1069; Conservative 0; Mismatches 392; Indels 0; Gaps 0;

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 107 CTCATCCAGCTGAGGAGAAAACCCGCTTCTGAAACCGCAGGCAAGCCAGCCCT 166
 66 GATGTTCTAAGAGTTCACCAATTCATGCTGCTGTAAGATTTATTTTCTT 125
 167 TGATGAGCCAGAGTTCAGCCGATCCAGACAGCTGCGCAGATGTCATCTCTT 226
 126 GGTGATGATGAGGCTTCACTGTTACTGCTACAGAAATTTGAAGGCTCAAAATGA 185
 227 GGGGAGTGGATGGGCTGCTACGAGACACCTCGAATCTTAAGGAGGAGATGAA 286
 186 TGTAAAGTGGCTCAAGAAATCCATTTGCTATGATCAATTTCCATAGCTTGTGTC 245
 287 TGCAAACTGGAGCTGAGACACCCCTGCTGAGACAGATTCCTTAAGGAGGAGATGAA 346
 246 TAAGACTTACAAAGTTCAGCAAGTTCAGATTTCTGCTGTAAGTCTGCTTACT 305
 347 CAAGACATACAAAGTTCAGCAAGTTCAGATTTCTGCTGTAAGTCTGCTTACT 406
 306 GTGAGGTTAAGGTTAATTAAGAACTATTTGCTGCTGCTGCTGCTGCTGCTGCTGCT 365
 407 GTGAGGTTAAGGTTAATTAAGAACTATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 466
 366 ATGTAATTAAGTTCAGCAAGTTCAGATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 425
 467 GTGCAACACGACAGTGGAGTGAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 526
 426 TAAGCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 485
 527 GAAGCGCTGGAGTGGTGAACACACAGGAGTGAAGTTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 586
 486 CGCTCATCTGTTAATGAAGTTCAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 545
 587 CGGCAACAGCGTGAACCGAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 646
 546 GAATGTTGCTCAAGATTTGCTGCTCAATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 605
 647 GAATGCTGCTGAGACATCCCGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 706
 606 GGGTGTGTTAAGTTCAGTTCCTGCAAGAGTTCAGATTCAGATTCAGATTCAGATTCAGATTCAGATTC 665
 707 GGGTGTGAGCGGAGTTCAGTTCCTGCAAGAGTTCAGATTCAGATTCAGATTCAGATTCAGATTCAGATTC 766
 666 TGCTTCTGTTAAGTTCAGTTCAGATTCAGATTCAGATTCAGATTCAGATTCAGATTCAGATTCAGATTC 725
 767 TGCAAGTGAAGTTCAGATTCAGATTCAGATTCAGATTCAGATTCAGATTCAGATTCAGATTCAGATTC 826
 726 GCATCAAGTGTCTCAATATGTTGAAATAGAACTGCTTTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCT 785

827 GCACAGGAGCCAGATGATGTGAACCGCACTGCGCTCTTCAAGCGGCCAGATGATC 886
 786 TAGGTTCATCTATGATGAGCTTTGTTGAACAGGCTGATGATGATGATGATGATGATGATGATGATGATGAT 845
 887 CAGTGAACACACCTATGAGCTCTTGAAGCGGAGACATGATGATGATGATGATGATGATGATGATGATGATGAT 946
 846 AGATCATCTAAGATTCACATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 905
 947 AGACACACACAGAGCCCACTGCGGAGATGAGAGGAGCGGCCCTGCAATGCTGAG 1006
 906 TAGAAATCCAGAGTTCATCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 965
 1007 CAGGAACCCCGGCTTCTACCTCTGCTGAGGAGGCGCATTTGACCAAGCTGACCA 1066
 966 TGATGTAAGCTTATAGCTTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1025
 1067 TGACGCAAGCTTATAGCTGCTGAGGAGTTCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1126
 1026 GGTAAATGAATGATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1085
 1127 GGTAAAGAGCTACATGAGCACTGAGACAGCTGATCTTGTACATGACAGACATCCCA 1186
 1187 TGCTTCTCTTTGTT 1246
 1146 TAAGCTTGAATGAT 1205
 1247 CAGGCTTGAAGAGAGTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1306
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 1307 GCTTGGCGGGGCTCGAGGCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1366
 1266 ACAACAGCTGCTGTTCAATGCTAGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1325
 1367 GCAGCAGGCGGCGCT 1426
 1326 TGTAAAGTTCACAGCTGAT 1385
 1427 CGGCGAGGCGCGCAGGCGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1486
 1386 TATTATGCTTTGCT 1445
 1487 CATCATGCTTTGCGGCT 1546
 1446 TACTGCTACTGATTCAGA 1466
 1547 CACGCGCACAGCATCCCGA 1567

RESULT 12

AR214214 1798 bp DNA linear PAT 25-SEP-2002
 LOCUS AR214214
 DEFINITION Sequence 1 from patent US 6406899.
 ACCESSION AR214214
 VERSION AR214214.1 GI:23311768
 KEYWORDS

SOURCE

Unknown.
 Unknown.
 Unclassified.
 1 (bases 1 to 1798)
 AUTHORS Hoele, W., Muller, R., Burtcher, H. and Mullan, J. L.
 TITLE Highly active alkaline phosphatase
 JOURNAL Patent: US 6406899-A 1 18-JUN-2002;
 FEATURES Location/Qualifiers
 1.1798
 /organism="unknown"
 /mol_type="genomic DNA"

ORIGIN

Query Match 56.5%; Score 833.8; DB 6; Length 1798;
 Best Local Similarity 73.2%; Pred. No. 2.7e-146;

| Matches 1069; Conservative 0; Mismatches 392; Indels 0; Gaps 0; | | | |
|---|------|---|------|
| QY | 6 | CTGATTCACGATGAGAAAGAAATCCAGCTTTTGGAAATAGACAAGCTGCTCAAGCTT | 65 |
| DB | 107 | CTCATCCCGAGTGAAGAGAAAACCCGCTTCTGGAAACCGCAGGACCAAGCCCT | 166 |
| QY | 66 | GGATGTTGCTAAGAAAGTTGCAACCAATTCCTGCTGCTAGAAATGTTATTTTGT | 125 |
| DB | 167 | TGATGTAGCCAGAAAGTTGACGCGATCCAGACAGCTGCGCAAGAAATGTCCTCT | 226 |
| QY | 126 | GGGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG | 185 |
| DB | 227 | GGGGATGGGATGGGATGGGATGGGATGGGATGGGATGGGATGGGATGGGATGG | 286 |
| QY | 186 | TGTAAGTTGGGATCCAGAACTCCATTTGCTATGATGATGATGATGATGATGAT | 245 |
| DB | 287 | TGGCAAACTGGGATCCAGAACCCCTGGCATGACAGATTCCTCATGCTGCTGTC | 346 |
| QY | 246 | TAAAGCTTCAATGTTGATAGCAAGTTCCAGATTCTGCTGATGCTGATGCTTACT | 305 |
| DB | 347 | CAGACATACAGATGGAGACAGAGTGCCAGACAGGAGGACAGGACAGGACAGG | 406 |
| QY | 306 | GTGTGTTGTTAAGGATTTACAGAACTATGTTGTTGCTGCTGCTGATGATGATCA | 365 |
| DB | 407 | GTGTGGGTTCAAGGGCACTACAGAACTATGTTGTTGCTGCTGCTGATGATGATCA | 466 |
| QY | 366 | ATGTAATCTACTAGAGTAAATGAAATTTCTGTTATTAATAGAGTAAAGAGCTG | 425 |
| DB | 467 | GTGCAACAGACAGATGGGATGAGTACGTTGATGATGATGATGATGATGATGATG | 526 |
| QY | 426 | TAAAGCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG | 485 |
| DB | 527 | GAAAGCGGTGGAGTGTGATCCACACAGGGTGACAGTGTCTCCACGCGGGCTTA | 586 |
| QY | 486 | CGCTCATCTGTTAATAGAAATTTGATCTGATGCTGATGCTGCTGATGCTGCTG | 545 |
| DB | 587 | CGGCAACAGTGTGATCCGAACTGTGATCTAGCGCGACCTGCTGCTGATGATGATG | 646 |
| QY | 546 | GATGTTGTCAAGATATGCTGCTCAATGTTGTTCAATATGATGATGATGATGATG | 605 |
| DB | 647 | GATGTTGTCAAGATATGCTGCTCAATGTTGTTCAATATGATGATGATGATGATG | 706 |
| QY | 606 | GGTGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG | 665 |
| DB | 707 | GGTGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG | 766 |
| QY | 666 | TGCTTCTGTTAATGTTGTTAAGAAATTTGTTGTTGTTGTTGTTGTTGTTGTTG | 725 |
| DB | 767 | TGCTTCTGTTAATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG | 826 |
| QY | 726 | GCATCAAGTGTCTCATATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG | 785 |
| DB | 827 | GCATCAAGTGTCTCATATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG | 886 |
| QY | 786 | TAGTTTACTCATTTGATGGGTTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTG | 845 |
| DB | 887 | CAGTTTAAACACCTCATGAGGCTCTTTGAGCGCGGACATGATGATGATGATGATG | 946 |
| QY | 846 | AGATCATCTAAGATCCAACTTTGCTGTTGTTGTTGTTGTTGTTGTTGTTGTTG | 905 |
| DB | 947 | AGATCATCTAAGATCCAACTTTGCTGTTGTTGTTGTTGTTGTTGTTGTTGTTG | 1006 |
| QY | 906 | TAGAAATCCMAAGGTTTTTACTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTG | 965 |
| DB | 1007 | CAGGAACCCCGGGGTTTCTACTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG | 1066 |
| QY | 966 | TGATGTAAAGGCTTATATGCTTTTGAAGCTTATGTTGTTGTTGTTGTTGTTG | 1025 |
| DB | 1067 | TGACGGCAAAAGCTTATATGCTTGAAGCTTATGTTGTTGTTGTTGTTGTTG | 1126 |
| QY | 1026 | GGCTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG | 1085 |
| DB | 1127 | GGCTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG | 1186 |

| | | | |
|----|------|---|------|
| QY | 1086 | TGTTTTTCTTTTGGGTTTACCTTGAGAGGTACTTCTATTTTGGTTGGCTCAAG | 1145 |
| DB | 1187 | TGTTCTTCTTTTGGGTTTACCTTGAGAGGTACTTCTATTTTGGTTGGCTCAAG | 1246 |
| QY | 1146 | TAAAGCTTGTAGTAAGTCTTACCTTCTATTTTGTATGTTAAATGTTGCTGATG | 1205 |
| DB | 1247 | CAAGGCTTGTAGACAGAAAGTCTTACCTTCATCTCTTATGGAATGGCCAGCTATGC | 1306 |
| QY | 1206 | TTTGGGTGTGTGTTCTTACCAACATGTTTAAATGTGTATGTAAGTAAGAACCATTTACAG | 1265 |
| DB | 1307 | GCTTGGGGGGGGCTCGAGGCCCATGTGTAATGTGCAGACAAAGCAGAGAACCTCATACCG | 1366 |
| QY | 1266 | ACAACAAGCTCTGTTCATTTGGCTAGTGAACATCATGTGTGTGAATGTGTGTTT | 1325 |
| DB | 1367 | GCAGCAGGCGGCGCTGCCCCCTGGTTACGAGAACCCAGCGGGGCGAGACGTGGCGTGT | 1426 |
| QY | 1326 | TGCTAAGAGTCCACAGACTATTGTGTTCAATGTGTTCAGAGAAACCTTTTGTGTCA | 1385 |
| DB | 1427 | CGCGCGAGGGCCGAGGCGGACCTCGTGTGCAAGGGGTGCAGAGAGAGACCTTCGTGGCGCA | 1486 |
| QY | 1386 | TATTATGGCTTTTGTCTGTGTGTGTGAACATACATGATTTGTATTTTGCAGCTCCAGC | 1445 |
| DB | 1487 | CATCATGGCCCTTGTGGGGCTGCGGTGAGCCCTTACACGACATGCAATCTGCAGCCCCGCG | 1546 |
| QY | 1446 | TACTGCTACTAGTATTCAG | 1466 |
| DB | 1547 | CACCGCCACACGATCCCCGA | 1567 |

RESULT 13

AX012341

LOCUS

AX012341

1798 bp

DNA

linear

PAT 06-SEP-2000

DEFINITION

Sequence 1 from Patent EP0955369.

ACCESSION

AX012341

VERSION

AX012341.1

GI:9998390

KEYWORDS

SOURCE

ORGANISM

Bos taurus (cow)

Bos taurus

Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.

REFERENCE

1

AUTHORS

Burtcher, H.D., Mueller, R.D., Hoelke, W.D. and Millan, J.L.

TITLE

High active alkaline phosphatase

JOURNAL

Patent: EP 0955369-A.1 10-NOV-1999;

FEATURES

ROCHE DIAGNOSTICS GmbH (DE)

source

Location/Qualifiers

1..1798

/organism="Bos taurus"

/mol_type="unassigned DNA"

/db_xref="taxon:9913"

ORIGIN

Query Match

56.5%; Score 833.8; DB 6; Length 1798;

Best Local Similarity

73.2%; Pred. No. 2.7e-146;

Matches 1069; Conservative

0; Mismatches 392; Indels

0; Gaps

0;

QY

6

CTTGATTCACGATGAGAAAGAAATCCAGCTTTTGGAAATAGACAAGCTGCTCAAGCTTT

65

DB

107

CCTCATCCCGAGTGAAGAGAAAACCCGCTTCTGGAAACCGCAGGACCAAGCCCT

166

QY

66

GGATGTTGCTAAGAAAGTTGCAACCAATTCAACTGCTGCTAAGAAATGTTATTTTGT

125

DB

167

TGATGTAGCCAGAAAGTTGACGCCGATCCAGACAGCTGCCAAGATGTCATCTCTTCT

226

QY

126

GGGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG

185

DB

227

GGGGATGGGATGGGGGTGCTTACGTGACAGCACTCGATTCCTAAAGGGCAGATGAA

286

QY

186

TGTAAGTTGGGATCCAGAACTCCATTTGCTATGATGATGATGATGATGATGATG

245

DB

287

TGGCAAACTGGGATCCAGAACCCCTGGCATGACAGATTCCTCATGCTGCTGTC

346

| | | | |
|----|------|---|------|
| Qy | 489 | TCATACGTGTTAAATGAGAAATTTGGTAACCTGATGTCGTAATTTGGCCAGCTCGATATGCTCAAAA | 548 |
| Db | 638 | GCACACGGTGAACCCGAAATCTGTACTCAGACGCCGACCTGCTCGATGATCAACAAGAA | 697 |
| Qy | 549 | TGGTTGTCAAGATATTTGCTGCTCAATTTGGTTTAAATATGATATATGATTTATTTTGGG | 608 |
| Db | 698 | TGGCTCCACAGACATGCGCGACAGCTGGTCTTCAACATGATATTTGACATGATCTCGGG | 757 |
| Qy | 609 | TGGTGTAGAAATTTACATGTTTCCAGAAAGGTACTCCAGATCCGAATATCCGATATGATGC | 668 |
| Db | 758 | TGGAGGCCGAATTTACATGTTTCTTAGGGGAACTCCAGACCTCGAATATCCGAATGATGC | 817 |
| Qy | 669 | TTCTGTTAATGCTGTTAGAAAGGATAAGCAAAATTTGGTTCAGAAATGGCAACTAAGCA | 728 |
| Db | 818 | CAGTGTGAATGGAGTCCGAGAGGACAAGCAAGAACTGTGTGACGAATATGGCAGCCAAAGCA | 877 |
| Qy | 729 | TCAAGGTGCTCAATATGTTTGGAAATGAACTGCTTTTGTTCAGACGTCTGATATATCTAG | 788 |
| Db | 878 | CCAGGAGCCCAATATATGTGTGAACCGCACTGGCTCTTCAGGGCGCGATATATCTCCAG | 937 |
| Qy | 789 | TGTTACTCAATTTGATGGGTTTGTGTTGAACCAAGCTGATATGAAGTATATATGTTCAACAAG | 848 |
| Db | 938 | TGTACACACCTCATGTGGCCCTCTTTAGCCGGCAGACATGAAGTATATATGTTCAACAAG | 997 |
| Qy | 849 | TCATATAGAGATCCCAATCTTGGCTGTAATATGACTGAAGCTGCTTGTGCAAGTTTGTCTAG | 908 |
| Db | 998 | CCACACCAAGAACCCGACCTCGCGAATGACGAGGGCGGCCCTCAAGTGTGTGACAG | 105 |
| Qy | 909 | AAATCCAAAGGTTTTTACTTTGTTGTTGTAAGGTGTGTAGAAATTTGATCATGTCATCATGA | 968 |
| Db | 1058 | GAACCCCCGGGCTTCTACCTCTTGGTGAAGGAGGCCGACATTTGACACAGTCAACATGA | 111 |
| Qy | 969 | TGGTAAGGCTTATATATGGCTTTTACACTGAACCTATATGTTTGTATATATGCTATATGGC | 102 |
| Db | 1118 | CGGCAAGCTTATATATGGCACTGACTGAGCGATCATATGTTTGAACAAATGCCATGCCAAGCC | 117 |
| Qy | 1029 | TAATGAATTAAGCTCTGAATTTGATATCTTTGATATTTGGTTACTGCTGATCATATGTCATGT | 1081 |
| Db | 1178 | TAAAGAGCTCATTAAGGAAGTGGACACGCTGATCTTGTCACTGACAGACCATCCCATGT | 123 |
| Qy | 1089 | TTTTCTTTTGGTGTATACCTTGTAGAGTACTTCTATATTTTGGTTTGGCTCCAGGTAA | 1144 |
| Db | 1238 | CTTCTCTTTGGTGTGTACACACTGGTGTGGACCTTCATATTTTGGTGTGGTCCGCCGCA | 129 |
| Qy | 1149 | GGCCTTGTGATAGTACTTACACTCTCTATTTTGTATGTGTAATGGTCCAGGTATGCTTT | 1201 |
| Db | 1298 | GGCCTTGAACAGCAAGTCTTACACCTCCATCTCTATATGCAATATGGCCAGGGCATATGCGT | 135 |
| Qy | 1209 | GGGTGTGTGTTCTTAACCAAGATGTTTAAATGTATGTACTATGTGAAGAACATCTTTACAGACA | 1266 |
| Db | 1358 | TGGCGGGGGCTGAGAGCCCGAATGTTAATGTGCAGCAACACGAGGAACCTCTGTATCCGGA | 141 |
| Qy | 1269 | ACAACTCTGTTTCCATTTGGCTAGTGAACATCATGATGTGTGAAGATGTTGCTGTTTTC | 1322 |
| Db | 1418 | GCAGGCGGCGCGTGGCCCTGTAGGGAAGCAACGAGGGCGAAGACGTGGCGGTGTCC | 147 |
| Qy | 1329 | TAGAGTCCACAAGCTCATTTGGTTCATGTGTCTCAAGAAGAACTTTTGTGCTCATAT | 1381 |
| Db | 1478 | GCGAGGCCCGCAGGGGCACTGTGTSCACGCGCTGTGAGGAGAGACCTTGTGTGCGCACAT | 153 |
| Qy | 1389 | TATGCTTTTGTGTTGTGTGGAACATATCACTGATTTAATTTTGGCAGCTCCAGCTAC | 1441 |
| Db | 1538 | CATGGCTTTTGGGGCTGGGTGAGACCCCTTACACGACCTGCATCTGTCCAGCCCTCCAC | 159 |
| Qy | 1449 | TGCTATCTATGATTTCCAGATTTAA | 1470 |
| Db | 1598 | CGCACCGACATCCCGACTGA | 1619 |

| | |
|-----------|-----------------|
| RESULT 15 | |
| AF052226 | |
| LOCUS | AF052226 |
| | 2460 bp |
| | mRNA |
| | linear |
| | MAM 03-SEP-1998 |

| DEFINITION | Bos taurus intestinal alkaline phosphatase III mRNA, complete cds. |
|----------------------------|--|
| ACCESSION | AF052226 |
| VERSION | AF052226.1 GI:3510650 |
| KEYWORDS | |
| SOURCE | Bos taurus (cow) |
| ORGANISM | Bos taurus |
| REFERENCE | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos. |
| AUTHORS | Manes,F., Hoylaerts,M.F., Muller,R., Lottspeich,F., Hoelke,W. and Millan,J.L. |
| TITLE | Bovine alkaline phosphatases |
| JOURNAL | Unpublished |
| REFERENCE | 2 (bases 1 to 2460) |
| AUTHORS | Manes,T., Hoylaerts,M.F., Muller,R., Lottspeich,F., Hoelke,W. and Millan,J.L. |
| TITLE | Direct Submission |
| JOURNAL | Submitted (05-MAR-1998) Medical Genetics, Umea University, S-901 85 Umea, Sweden |
| FEATURES | Location/Qualifiers |
| source | 1..2460 |
| | /organism="Bos taurus" |
| | /mol_type="mRNA" |
| | /db_xref="taxon:9913" |
| | 66..1658 |
| | /EC_number="3.1.3.1" |
| | /note="IAP IIF" |
| | /codon_start=1 |
| | /product="intestinal alkaline phosphatase IIF" |
| | /protein_id="AAC33853.1" |
| | /db_xref="GI:3510651" |
| | /translation="MQGACVLLLLGLWQLSLAFIPVEEDPAPFMRNQAQALDVARKK LQPIQAKAKVILFLGDGMGPVTATRIILKQNNDLGEPETPLAMQFPVALSKTYS NVDPQVDSAGTATAYLCGVKGNKRTIGVSAANVYNCNTRTGREVTSVMMRAKAG SVGVTTTRVOHASPAGVAHYATVRMDVNSADIPADQOTGCOIALQVLNNMIDIVY LGGRKATMPEEGPTDPEPRPHDASVNGRKRKNTVQEMQKHQAQIVNRTLLQANA NDSSVTHLMKLFEPADMKRYNVQDDPTQDPTLBEETALQVLSNPGQFYLVEGGRT DHGHDSKATMDLAEVFNALAKANELTSELDTLILVTADSHSVSPFGYTLRGTSI I FGLAPSKATMKSYSITLILANGNGVYLGGGSRDNDVDSISEPDSQAAPVLSSTRT HGGEDVAVFARGPDQHLVHGVEETFFVAHYMAFAGVCEVPEPTDNLPAPSGLSDAHLDA ASAPSLALLGAMULLLAPALY" |
| ORIGIN | |
| Query Match | 52.6%; Score 777; DB 4; Length 2460; |
| Best Local Similarity | 71.2%; Pred. No. 1,1e-115; |
| Matches 1026; Conservative | 0; Mismatch 415; Indels 0; Gaps 0; |
| Qy | 6 CTTGATTCGAGCTAAGAGAAATCCAGCTTTTGGATATGACACAGCTGCTCAAGCTT 65 |
| Db | 122 CTTGATCCGAGTTGAGAGAAAGCCCGCTTCTGGAACCGCAGGACAGCCCGCCT 181 |
| Qy | 66 GGATGTTGCTAAGAGTTGCAACCAATTCAACTGCTGTAAGATGTTATTTGTTTT 125 |
| Db | 182 TGATGTGGCTAAGAGCTGCGAGCCCAACGAAAGCCGCAAGATGTCACTCCCTTT 241 |
| Qy | 126 GGGGATGGTATGGGSGTTCGCACTGTCTACTGCTACTAGAAATTTTGAAGGCTCAAAGAA 185 |
| Db | 242 GGGAGATGGGATGGGGGTGCTACGGTGACACGACACTCGGATACTGAAGGGGACAGATGAA 301 |
| Qy | 186 TGGTATTTGGGATCCAGAAATCCATTTGGCTATGATGCAATTTTCCATACGTTGCTTTGTC 245 |
| Db | 302 TGACAACTGGGACTTGACACCCCTGGCCATGGACCAATTCGCAATACGTGGTCTGTC 361 |
| Qy | 246 TTAAGCTTAAAGTTGATAGACAAGTTCCAGATTCGCTGTAATCTGCTTACTT 305 |
| Db | 362 CAAGACATTAACAAGCTGGACAGAGGCGCAAGCAGGCACTGCCACTGCTTAACT 421 |
| Qy | 306 GTATGGCTTAAAGGGTAAATTACAGAACTATTGGTGTTCCTGCTGCTGCTGATTAACAATCA 365 |
| Db | 422 GTGTGGGGTAAAGGGCACTTACAGAACATCGGTGTATAGTCGACCGCCGCTTAAATCA 481 |
| Qy | 366 ATGTAACTACTAGAGGTATGAACTTACTTCTGTATTATAGAGCTAAGAGCGTGG 425 |

Db 482 GTGCAACACGACGATGGAGATGAGTCAGCTGTGTATGAACCGGGCCAAAGAACGAG 541
QY 426 TAAGGCTGTGGTGTGTCTACTACTAGTAAGTTCAACATGCTTCTCCAGCTGTGTTA 485
Db 542 GAAGTCAGTGGAGTGTGACCAACACAGGTCGACAGCCCTCCACCGGTGTTA 601
QY 486 CGCTCACTACTGTAAATAGAAATGTGTACTGTAGTGTGATTTGGCCAGCTGATGTCAAA 545
Db 602 TGCACACACCGGTGACCTGTACTGTGTACTGAGACCGGACCTGTGCTGCCATGACAGAC 661
QY 546 GAATGTTGTCAAGATATTGCTGCTCAATTGTTTACATATGAGATATTGATGTTATTT 605
Db 662 GTATGGCTGCAGAGACATGCGCACACACATGTCATCAACATGATATTGACGTGATCCT 721
QY 606 GGGTGTGTAGTAATGTACATGTTTCCAGAGGTACTCCAGATCCAGATACCCAGATGA 665
Db 722 GGGTGAAGGCGAAAGTACATGTTTCTGTAGGGGACCCGAGCCCTGMAATACCCACAG 781
QY 666 TGCTTCGTTAATGTTAGTGTAGAAAGATAGCAAAATTTGTTCAAGATGGCAAGCTA 725
Db 782 TGCCAGTGTAAATGAGTCCGAAAGACAGCCGAAATCTGTGACAGAGTGGCAGGCTCA 841
QY 726 GCATCAAGGTGCTCAATATGTTTGAATAGAACTGTTTGTGCAAGCTGTGATGATTC 785
Db 842 GCACCAAGGAGCCAGATGTGTGAAACGACGAGGCTCCTCAAGCAGCCATGATGCTC 901
QY 786 TAGTGTACTCAATTGATGGGTTGTTTGAACCACTGATATGATATATGTTCACA 845
Db 902 CAGTGTACACATCTCATGGGCTCTTTGAGCCGCGACATGATATATGTTCAGCA 961
QY 846 AGATCAATCTAAAGATCCACTTGTGCTGAATGACTGAAGCTGTTGCAAGTTTGTTC 905
Db 962 AGACCCACCAAGAGACCCGACCTGTGAGGATGACGAGCGGCGCTGCAAGTGTGAG 1021
QY 906 TAGAAATCCAAAGAGTTTACTTGTGTTTGAAGGTGTAGAAATGATCATGTCATCA 965
Db 1022 CAGGAACCCCAAGGCTTCTACTCTTGTGAGGAGGAGCGCATTTGACACAGGTACCA 1081
QY 966 TGATGTAAAGCTTATATGAGCTTGTACTGAAGCTATATGTTGATATATGCTAA 1025
Db 1082 TGATACCAAGCTTATATGCGCTGACTGAGGCGTATGTGTGACATGCTCATCCCA 1141
QY 1026 GGTAAATGAAATGACTTGTGAATGATGATTTGTGTTACTGTGATCATATGTC 1085
Db 1142 GGTAAAGAGCTACTAGCACTGACAGCTGATCTTGTCACTGCAGACCACTCCCA 1201
QY 1086 TGTCTTTTCTTTTGTGTGTACACTTGAAGGTACTTCAATTTTGTGCTCCAGG 1145
Db 1202 TGTCTTCTCTTTGTGTGTACACACTGCGTGGGACCTCATTTTGTGCTCCAGG 1261
QY 1146 TAAAGCTTTGATAGTAAAGTCTTACACTTGTATTTTGTATGTATGTTCAGGTTATGC 1205
Db 1262 CAAAGGCTCAGACAAAGAGTCTTACACTTCATCTCTATGCAATGGCCCTGCTACGT 1321
QY 1206 TTTGGGTGTGTGTCTAGACCAATGTTAATGTAATGTAAGAAACATCTTACAG 1265
Db 1322 GCTTGTGTGGGCTCAAGGCGCATGTATATGACATTAAGCAGAGAACCCCTCATACCG 1381
QY 1266 ACAACAGCTGCTGTTCATTTGCTAGTAACTCAATGCTGAGAGATGTTGCTGTTT 1325
Db 1382 GCAAGCAGGCGGCTGTGCTGTACAGAGACCAAGGCGGAGACGTGGCGGTGTT 1441
QY 1326 TGTAGAGTCAACAAAGCTCATTTGTTCAATGTTTCAAGAAACATTTGTTGCTCA 1385
Db 1442 CGGCGAGGCGCCGACAGCGCACTGTGTGACCGGCTGACAGAGAGACCTTGTGGCGCA 1501
QY 1386 TATTAAGCTTTGTGTGTGTGTGTGAACCATACATGATTTGATTTGCTCAGCTCAGC 1445
Db 1502 CGTATGCGCTTGTGGGCTGTGTGAGCCCTTACACGAGCTGCAATCTGCCGCGCCCTTC 1561
QY 1446 T 1446

Db 1562 T 1562

Search completed: October 19, 2004, 14:44:36
Job time #: 6527.869

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 20, 2004, 00:09:03 : Search time 768 Seconds
(without alignments)
10088.731 Million cell updates/sec

Title: US-09-911-132A-5
Perfect score: 1476
Sequence: 1 gattcttcgattccagctga.....gattccagattcaagttacc 1476

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 413486 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 1: geneseqn1980s:*
- 2: geneseqn1980s:*
- 3: geneseqn2000s:*
- 4: geneseqn2001as:*
- 5: geneseqn2001bs:*
- 6: geneseqn2002as:*
- 7: geneseqn2002bs:*
- 8: geneseqn2003as:*
- 9: geneseqn2003bs:*
- 10: geneseqn2003cs:*
- 11: geneseqn2003ds:*
- 12: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|--------|-------------|--------|-------------|---------------------|
| 1 | 1476 | 100.0 | 1476 | 6 ADI26515 | ADI26515 Optimised |
| 2 | 1476 | 100.0 | 1476 | 10 ADE53386 | Ades53386 Bovine al |
| 3 | 1474.4 | 99.9 | 1476 | 10 ADE53391 | Ades53391 Bovine al |
| 4 | 1472.8 | 99.8 | 1476 | 10 ADE53392 | Ades53392 Bovine al |
| 5 | 1471.2 | 99.7 | 1476 | 10 ADE53393 | Ades53393 Bovine al |
| 6 | 1469.6 | 99.6 | 1476 | 10 ADE53394 | Ades53394 Bovine al |
| 7 | 1465.6 | 97.3 | 1476 | 6 ADI26549 | ADI26549 Bovine bi |
| 8 | 834.8 | 56.6 | 1464 | 10 ADE53384 | Ades53384 Bovine al |
| 9 | 831.6 | 56.3 | 1650 | 8 AB227773 | Ab227773 Calf inte |
| 10 | 616 | 41.7 | 2523 | 4 AAK51495 | Aak51495 Human pol |
| 11 | 613.8 | 41.6 | 1702 | 12 ADN43057 | Adn43057 Human sec |
| 12 | 611.2 | 41.4 | 1587 | 2 AAQ78135 | Aaq78135 Human ent |
| 13 | 611.2 | 41.4 | 1587 | 2 AAT27384 | Aat27384 Human alk |
| 14 | 611.2 | 41.4 | 2516 | 12 ADP45468 | Adp45468 Human vas |
| 15 | 611.2 | 41.4 | 2516 | 12 ADO38592 | Ado38592 Human ppb |
| 16 | 610.2 | 41.3 | 1491 | 2 AAQ90640 | Aaq90640 Human ent |
| 17 | 609.2 | 41.3 | 3076 | 2 AAT27391 | Aat27391 Human Igg |
| 18 | 609.2 | 41.3 | 3127 | 2 AAT27392 | Aat27392 Human Igg |
| 19 | 603.4 | 40.9 | 1966 | 4 AAK52479 | Aak52479 Human pol |
| 20 | 603 | 40.9 | 2372 | 2 AAT27393 | Aat27393 Human Igg |
| 21 | 603 | 40.9 | 2484 | 2 AAT27386 | Aat27386 Human Igg |

| | | | | | |
|----|-------|------|------|-------------|--------------------|
| 22 | 603 | 40.9 | 3022 | 2 AAT27390 | Aat27390 Human Igg |
| 23 | 603 | 40.9 | 3147 | 2 AAT27389 | Aat27389 Human Igg |
| 24 | 602.2 | 40.8 | 1464 | 2 AAQ90639 | Aaq90639 Human ent |
| 25 | 583.6 | 39.5 | 2445 | 2 AAT27387 | Aat27387 Human Igg |
| 26 | 583.6 | 39.5 | 3108 | 2 AAT27388 | Aat27388 Human Igg |
| 27 | 582.8 | 39.5 | 1422 | 2 AAQ90638 | Aaq90638 Human ent |
| 28 | 573 | 38.8 | 1649 | 8 AB222774 | Ab222774 Human pla |
| 29 | 572.8 | 38.8 | 1515 | 12 ADO80224 | Ado80224 Human gen |
| 30 | 572.8 | 38.8 | 1597 | 10 ADH10077 | Adh10077 Human SEA |
| 31 | 572.8 | 38.8 | 1534 | 2 AA42729 | Aa42729 Human pla |
| 32 | 572.8 | 38.8 | 1675 | 10 ADH10079 | Adh10079 Human SEA |
| 33 | 572.8 | 38.8 | 1697 | 12 ADO80223 | Ado80223 Human gen |
| 34 | 572.8 | 38.8 | 1928 | 6 ABL49916 | Ab149916 SEAP, ins |
| 35 | 572.8 | 38.8 | 1748 | 10 ADH10087 | Adh10087 Human SEA |
| 36 | 572.8 | 38.8 | 1777 | 10 ADH10083 | Adh10083 Human SEA |
| 37 | 572.8 | 38.8 | 1904 | 12 ADO80225 | Ado80225 Human gen |
| 38 | 572.8 | 38.8 | 1915 | 10 ADH10091 | Adh10091 Human SEA |
| 39 | 572.8 | 38.8 | 1918 | 10 ADH10073 | Adh10073 Human sec |
| 40 | 572.8 | 38.8 | 1975 | 10 ADH10095 | Adh10095 Human SEA |
| 41 | 572.8 | 38.8 | 2239 | 10 ADD67946 | Add67946 HIV-secre |
| 42 | 572.8 | 38.8 | 2239 | 10 ABX10618 | Abx10618 HIV-secre |
| 43 | 572.8 | 38.8 | 5264 | 8 ACC43141 | Acc43141 Nucleotid |
| 44 | 572.8 | 38.8 | 5408 | 8 ACC43140 | Acc43140 Nucleotid |
| 45 | 572.8 | 38.8 | 7469 | 4 AA47042 | Aa47042 Nucleotid |

ALIGNMENTS

| | | |
|----------|----------|---|
| RESULT 1 | ADI26515 | ADI26515 standard; DNA; 1476 BP. |
| XX | AC | ADI26515; |
| XX | AD | 22-APR-2004 (first entry) |
| XX | DE | Optimised bovine BIAPIT DNA. |
| XX | KW | alkaline phosphatase; resistance gene; zeomycin; G418; heat stability; |
| XX | KW | bovine; BIAPIT; yeast; gene; ds. |
| XX | OS | Bos taurus. |
| XX | OS | Synthetic. |
| XX | FT | Key |
| XX | FT | CDS |
| XX | FT | Location/Qualifiers |
| XX | FT | 7..1470 |
| XX | FT | /tag= a |
| XX | FT | /product= "optimised BIAPIT" |
| XX | FT | /partial |
| XX | FT | /note= "no start codon" |
| XX | PN | EP1176205-A2. |
| XX | PD | 30-JAN-2002. |
| XX | PF | 21-JUL-2001; 2001EP-00117822. |
| XX | PR | 25-JUL-2000; 2000DE-01036491. |
| XX | PA | (HOFF) ROCHE DIAGNOSTICS GMBH. |
| XX | PA | (HOFF) HOFFMANN LA ROCHE & CO AG F. |
| XX | PI | Mueller R, Thalhofer J, Geipel F, Hoelke W, Glaeser S, Eckstein H, |
| XX | PI | Kirschbaum T, Bommarhus B; |
| XX | DR | WPI: 2002-173123/23. |
| XX | DR | P-PSDB; ADI26514. |
| XX | PT | Preparing eukaryotic alkaline phosphatase, useful as diagnostic reagent |
| XX | PT | and for dephosphorylation, by recombinant expression in yeast selected |
| XX | PT | for high gene copy number. |

PS Claim 3; SEQ ID NO 5; 23bp; German.

XX This invention describes a novel method of preparing eukaryotic alkaline
CC phosphatase in yeast cells, comprising cloning an alkaline phosphatase
CC gene sequence into different vectors, transforming, and expressing and
CC purifying. A first vector is used containing a resistance gene against a
CC selection marker and transformants that have integrated resistance gene
CC and alkaline phosphatase gene into the genome are selected by growth on
CC medium containing a low concentration of selection marker. The gene copy
CC number is increased by multiple transformation and multiple transformants
CC selected on growth medium under high selection pressure. A second vector
CC containing the alkaline phosphatase gene and a second resistance gene
CC against a second marker is introduced, its copy number increased as for
CC the first resistance gene and clones selected that have many copies of
CC the alkaline phosphatase gene and of both resistance genes, integrated
CC into the genome. The vectors used in the method are pHP10-3 and pHP10-
CC 3/9K. Preferred cells include methylotrophic yeast, particularly *Pichia*
CC *pastoris* and *Hansenula polymorpha* and specifically *P. pastoris* X-33
CC transformed with pHP10-3 and pHP10-3/9K. The amino acid sequence of
CC bovine alkaline phosphatase is known and, working back from this, an
CC optimised codon sequence was designed. This was assembled conventionally
CC from 28 synthetic oligonucleotides to give a sequence having *Eco*RI and
CC *Asp*718 recognition sites at the ends to facilitate cloning. The selection
CC markers are particularly zeomycin and G418, respectively. The alkaline
CC phosphatase is used as diagnostic reagent, as part of a conjugate and for
CC dephosphorylation of DNA. This method produces very active, glycosylated
CC alkaline phosphatase with specific activity over 3000, preferably 10000,
CC units/mg and heat stability comparable with that for commercial enzymes.
CC The expression system is resistant and stable and provides high-level
CC expression without any selection pressure. This sequence represents an
CC optimised bovine *hPAP*1 polynucleotide.
XX

SO Sequence 1476 BP; 387 A; 223 C; 346 G; 520 T; 0 U; 0 Other;

Query Match 100.0%; Score 1476; DB 6; Length 1476;
Best Local Similarity 100.0%; Pred. No. 0;

Matches 1476; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAATCTTATTCACAGCTGAGAGAAATCCAGCTTTTGGAAATGACAGAGTGTCTCA 60
DB 1 GAATCTTATTCACAGCTGAGAGAAATCCAGCTTTTGGAAATGACAGAGTGTCTCA 60
QY 61 GCTTTGGATGTTGCTAAGAGAGTTGCAACCAATTCAGTCTGCTAAGAGTGTATTG 120
DB 61 GCTTTGGATGTTGCTAAGAGAGTTGCAACCAATTCAGTCTGCTAAGAGTGTATTG 120
QY 121 TTTTGGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 180
DB 121 TTTTGGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 180
QY 181 ATGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 240
DB 181 ATGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 240
QY 241 TTTGCTAAGACTTACAAATGTTAGACAAAGTTCCAGATTCGCTGCTACTGCT 300
DB 241 TTTGCTAAGACTTACAAATGTTAGACAAAGTTCCAGATTCGCTGCTACTGCT 300
QY 301 TACTTGT 360
DB 301 TACTTGT 360
QY 361 AATCAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTA 420
DB 361 AATCAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTA 420
QY 421 GCTGTAGAGCTGT 480
DB 421 GCTGTAGAGCTGT 480
QY 481 GCTTACGCTCATACCTGTTAATGAAATTTGTAAGTGTGTGTGTGTGTGTGTGTGT 540
DB 481 GCTTACGCTCATACCTGTTAATGAAATTTGTAAGTGTGTGTGTGTGTGTGTGTGT 540

QY 541 CAAAGAAATGTTGTCAGAGATATTGCTGCTCAATTTGTTTCAATATGATGATGAT 600
DB 541 CAAAGAAATGTTGTCAGAGATATTGCTGCTCAATTTGTTTCAATATGATGATGAT 600
QY 601 ATTTTGGGTGTGTAGAAATGATGATGATGATGATGATGATGATGATGATGATGAT 660
DB 601 ATTTTGGGTGTGTAGAAATGATGATGATGATGATGATGATGATGATGATGATGAT 660
QY 661 GATGATGCTTCTGTTAATGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 720
DB 661 GATGATGCTTCTGTTAATGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 720
QY 721 GCTAAGCATCAAGAGTGTCTCAATATGTTGGAATAGAACTGTTTGTGCAAGCTG 780
DB 721 GCTAAGCATCAAGAGTGTCTCAATATGTTGGAATAGAACTGTTTGTGCAAGCTG 780
QY 781 GATTTAGTGTATCTCATTTGATGAGGTTGTTTGAACGAGTGAATGATATATGTT 840
DB 781 GATTTAGTGTATCTCATTTGATGAGGTTGTTTGAACGAGTGAATGATATATGTT 840
QY 841 CAACAAAGATCATATCTAAGATCCAACTTTGGCTGAATGATGAACTGCTTTGCAAGT 900
DB 841 CAACAAAGATCATATCTAAGATCCAACTTTGGCTGAATGATGAACTGCTTTGCAAGT 900
QY 901 TTTGCTAAGAAATCCAAAGAGTTTCTTCTGTTGTTGAAGGTGTGAATGATCATG 960
DB 901 TTTGCTAAGAAATCCAAAGAGTTTCTTCTGTTGTTGAAGGTGTGAATGATCATG 960
QY 961 CATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1020
DB 961 CATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1020
QY 1021 GCTAAGGCTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1080
DB 1021 GCTAAGGCTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1080
QY 1081 AGTCATGTTTTTCTTTTGGTGTGTACACTTTGAGAGTACTTCTAATTTTGGTTGCT 1140
DB 1081 AGTCATGTTTTTCTTTTGGTGTGTACACTTTGAGAGTACTTCTAATTTTGGTTGCT 1140
QY 1141 CCAAGTAAGGCTTTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1200
DB 1141 CCAAGTAAGGCTTTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1200
QY 1201 TATGCTTTGGGT 1260
DB 1201 TATGCTTTGGGT 1260
QY 1261 TACAGACAAGAGCTGTGTTCCATTGCTAGTGAATCTCATGCTGTGGAAGATGTTGCT 1320
DB 1261 TACAGACAAGAGCTGTGTTCCATTGCTAGTGAATCTCATGCTGTGGAAGATGTTGCT 1320
QY 1321 GTTTTGTGTAGAGTGTCAAGAGCTCATTTGTGTTCAAGAGAAATCTTTGTT 1380
DB 1321 GTTTTGTGTAGAGTGTCAAGAGCTCATTTGTGTTCAAGAGAAATCTTTGTT 1380
QY 1381 GCTCATATTATGCTTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1440
DB 1381 GCTCATATTATGCTTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1440
QY 1441 CCAAGTACTGCTACTAGATTTCCAGATTTAAGTACC 1476
DB 1441 CCAAGTACTGCTACTAGATTTCCAGATTTAAGTACC 1476

RESULT 2
ADES3386
ID ADES3386 standard; DNA; 1476 BP.
XX ADES3386;
AC
XX
DT 29-JAN-2004 (first entry)

|||||
DB 1381 GCTCATATATATGCTTTCTGCTGTGTGTGAACCATACATGATTTGTCAGCT 1440
QY 1441 CCAGCTACTGCTACTAGTATTCAGATTAGGTACC 1476
DB 1441 CCAGCTACTGCTACTAGTATTCAGATTAGGTACC 1476
RESULT 3
ADE53391
ID ADE53391 standard; DNA; 1476 BP.
XX ADE53391;
AC ADE53391;
XX 29-JAN-2004 (first entry)
DT 29-JAN-2004 (first entry)
XX Bovine alkaline phosphatase DNA encoding S92A.
XX
XX alkaline phosphatase; mutation; immunoassay; antigen;
KW interference suppressor; bovine; de; mutant.
XX Synthetic.
OS Bos taurus.
XX EP1348760-A2.
XX PD 01-OCT-2003.
XX 21-MAR-2003; 2003EP-00006426.
XX 25-MAR-2002; 2002DE-01013201.
XX (HOFF) ROCHE DIAGNOSTICS GMBH.
PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
XX
XX Muehler R, Thalhofer J, Geipel F, Hoelke W, Kirschbaum T;
PI WPI; 2003-769844/73.
XX
XX New mutants of alkaline phosphatase (AP) where enzymatic activity is
PT reduced a hundred fold, are useful as blocking reagents in AP-based
PT immunoassays.
XX
XX Claim 8; SEQ ID NO 8; 35pp; German.
XX
XX This invention describes a novel mutant of eukaryotic alkaline
CC phosphatase where the wild-type sequence is at least 77% homologous with
CC ADE53388 and where the alkaline phosphatase activity is reduced by at
CC least 100-fold, relative to the wild type. The mutations described are
CC Asp42, 316 or 357 for Asn, Val, Ala or Ser; Ser92 or 155 for Ala, Gly,
CC Val or Leu; Glu311 for Gln, Asn, Ile or Met; His320, 358 or 432 for
CC Asn, Phe, Asp or Tyr; or Gly322 for an amino acid larger than Asp.
CC Conjugates of the novel mutant with antibodies are useful in alkaline
CC phosphatase-based immunoassays for antigens as interference suppressors,
CC i.e. they prevent non-specific binding of active alkaline phosphatase-
CC based conjugates to vessel walls or first antibodies, a phenomenon that
CC may result in false positive results. The mutants have almost the same
CC tertiary and quaternary structures as wild-type alkaline phosphatase, so
CC are very specific interference suppressors. This sequence encodes a
CC variant bovine alkaline phosphatase which contains an S92A mutation and
CC an EcoRI site described in the disclosure of the invention.
XX
XX Sequence 1476 BP; 387 A; 223 C; 347 G; 519 T; 0 U; 0 Other;
SQ
Query Match 99.9%; Score 1474.4; DB 10; Length 1476;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1475; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GAATCTTGATTCACAGTGAAGAAATCCAGCTTTTGATAGACAAGCTGCTCAA 60
DB 1 GAATCTTGATTCACAGTGAAGAAATCCAGCTTTTGATAGACAAGCTGCTCAA 60
QY 61 GCTTGGATGTGCTAAGAAAGTTGCAACCAATTCAACTGCTAGTAAGATGTTATTG 120

|||||
DB 61 GCTTGGATGTGCTAAGAAAGTTGCAACCAATTCAACTGCTAGTAAGATGTTATTG 120
QY 121 TTTTGGGGGATNGATGGGTTGTTCCAACTGTTACTGCTACTAGAAATTTTGAAGGCTCAA 180
DB 121 TTTTGGGGGATNGATGGGTTGTTCCAACTGTTACTGCTACTAGAAATTTTGAAGGCTCAA 180
QY 181 ATGAATGGTAAGTGGGTTCCAGAAATCCATTTGGCTATGATGCAATTTTCCATACCTTGCT 240
DB 181 ATGAATGGTAAGTGGGTTCCAGAAATCCATTTGGCTATGATGCAATTTTCCATACCTTGCT 240
QY 241 TTGCTCTAAGACTTACCAATGTTGATGACACAGTTCCAAATTTGCTGCTGATCTGCTCTGCT 300
DB 241 TTGCTCTAAGACTTACCAATGTTGATGACACAGTTCCAAATTTGCTGCTGATCTGCTCTGCT 300
QY 301 TACTGTGTGGTGTAAAGGTTAATACGAACCTATTGGTTTCTGCTGCTGCTAGATAC 360
DB 301 TACTGTGTGGTGTAAAGGTTAATACGAACCTATTGGTTTCTGCTGCTGCTAGATAC 360
QY 361 AATCAATGTAATACTACTAGAGGTATGAAAGTTACTCTGTTATTAATAGAGCTAAGAG 420
DB 361 AATCAATGTAATACTACTAGAGGTATGAAAGTTACTCTGTTATTAATAGAGCTAAGAG 420
QY 421 GCTGGTAAGGCTGTTGGTGTGTTTACTACTACTAGAGTTCAACATGCTTCTCCAGCTGCT 480
DB 421 GCTGGTAAGGCTGTTGGTGTGTTTACTACTACTAGAGTTCAACATGCTTCTCCAGCTGCT 480
QY 481 GCTTAGGCTCACTAGCTTAATAGAAATTTGGTACTGTAAGCTGATTTGCGAGCTAGTGT 540
DB 481 GCTTAGGCTCACTAGCTTAATAGAAATTTGGTACTGTAAGCTGATTTGCGAGCTAGTGT 540
QY 541 CAAAGAAATGGTGTCAAGATATTCCTGCTCAATTTGTTTCAATATGATATTTGATGTT 600
DB 541 CAAAGAAATGGTGTCAAGATATTCCTGCTCAATTTGTTTCAATATGATATTTGATGTT 600
QY 601 ATTTGGGTGTGTGTAAGATGTAATGTTTCCAGAGGTACTCCAGATCCAGAAATACCA 660
DB 601 ATTTGGGTGTGTGTAAGATGTAATGTTTCCAGAGGTACTCCAGATCCAGAAATACCA 660
QY 661 GATGATGCTCTGCTTAATAGGTGTTAGAAAGGTAAGCAAAATTTGGTTCAAGAAATGGCAA 720
DB 661 GATGATGCTCTGCTTAATAGGTGTTAGAAAGGTAAGCAAAATTTGGTTCAAGAAATGGCAA 720
QY 721 GCTAAGCATCAAGGCTCAATATGTTTGAATAGATGCTGTTTGTCCAGGCTGCTGAT 780
DB 721 GCTAAGCATCAAGGCTCAATATGTTTGAATAGATGCTGTTTGTCCAGGCTGCTGAT 780
QY 781 GATTTAGTGTACTCAATTTGATGAGGTTTGTGTTGAACCAAGCTGATATGATATGTT 840
DB 781 GATTTAGTGTACTCAATTTGATGAGGTTTGTGTTGAACCAAGCTGATATGATATGTT 840
QY 841 CAACAAGATCACTAAGATCCAACTTGGCTGAAGGTAAGCAAGCTGCTTGAAGTT 900
DB 841 CAACAAGATCACTAAGATCCAACTTGGCTGAAGGTAAGCAAGCTGCTTGAAGTT 900
QY 901 TTGCTCTAAGAAATCCAAAGGTTTACTGTTGTTTGAAGGTGTAAGATGATCATGCT 960
DB 901 TTGCTCTAAGAAATCCAAAGGTTTACTGTTGTTTGAAGGTGTAAGATGATCATGCT 960
QY 961 CATCATGATGTAAGGCTTATATGAGCTTGTGACTGAAGCTATATATGTTGATATCTATT 1020
DB 961 CATCATGATGTAAGGCTTATATGAGCTTGTGACTGAAGCTATATATGTTGATATCTATT 1020
QY 1021 GCTAAGGCTAATGATGATGATCTTGAATTTGATGATTTTGGTATGCTGATCAT 1080
DB 1021 GCTAAGGCTAATGATGATGATCTTGAATTTGATGATTTTGGTATGCTGATCAT 1080
QY 1081 AGTCATGTTTTTTCTTTGGTGTACACTTTGAGAGGTACTTCAATTTTGGTTGGCT 1140
DB 1081 AGTCATGTTTTTTCTTTGGTGTACACTTTGAGAGGTACTTCAATTTTGGTTGGCT 1140
QY 1141 CCAGGTAAGGCTTTGGATAGTAAGTCTTACACTTCAATTTTGTATGTAATGCTCAGGT 1200

| | | | |
|----|------|--|------|
| Db | 1141 | CCAGTAAAGCCTTTGGATAGTAAAGCTTCAACTCTAATTTTGTAATGTAATGTCACAGT | 1200 |
| Qy | 1201 | TATGCTTTGGGTGGTGTCTTAGACCCAGATGTTAAATGTAAGTACTAGTGAAGAACCATCT | 1260 |
| Db | 1201 | TATGCTTTGGGTGGTGGTCTTAGACCCAGATGTTAAATGTAAGTACTAGTGAAGAACCATCT | 1260 |
| Qy | 1261 | TACAGACAAACAAGCTGCTGTTCCAATGGCTAGTGAATCAATGGTGGTGAAGATGTTGCT | 1320 |
| Db | 1261 | TACAGACAAACAAGCTGCTGTTCCAATGGCTAGTGAATCAATGGTGGTGAAGATGTTGCT | 1320 |
| Qy | 1321 | GTTTTTGTAGAGGTCCACAAGCTCAATTTGTTCAATGAGTGTTCAGAAGAAACATTTGTT | 1380 |
| Db | 1321 | GTTTTTGTAGAGGTCCACAAGCTCAATTTGTTCAATGAGTGTTCAGAAGAAACATTTGTT | 1380 |
| Qy | 1381 | GCTATATTATAGGCTTTTGTGCTGTGTGTTGAACCATCACTGATGTGTAATTTTGCACGCT | 1440 |
| Db | 1381 | GCTATATTATAGGCTTTTGTGCTGTGTGTTGAACCATCACTGATGTGTAATTTTGCACGCT | 1440 |
| Qy | 1441 | CCAGTACTGCTACTAGTATTCCAGATTAAAGTACC | 1476 |
| Db | 1441 | CCAGTACTGCTACTAGTATTCCAGATTAAAGTACC | 1476 |

RESULT 4
ADE53392
ID ADE53392 standard; DNA; 1476 BP.

AC ADE53392;

DT 29-JAN-2004 (first entry)

DE Bovine alkaline phosphatase DNA encoding G322F.

KM alkaline phosphatase; mutation; immunoassay; antigen;
 KX interference suppressor; bovine; ds; mutant.

OS Synthetic.
OS Bos taurus.

PN EP1348760-A2.

PD 01-OCT-2003.

PF 21-MAR-2003; 2003EP-00006426.

PR 25-MAR-2002; 2002DE-01013201.

PA (HOFF) ROCHE DIAGNOSTICS GMBH.

11

XXXX

XX

PT reduced a hundred fold, are useful a

XX
PS
CJ 348 6-1-68 TD NO 6-1-68 COMM 3

This invention describes a novel

phosphatase where the wild-type Bequaert 3385 and the alkaline phosphatase

CC 1EABBC 100-1010, reactive to the will
CC APPB42. 316 or 357 for APP. Val Ala

CC Asn. phe. Asp or Tyr: or Glv322 for
CC val or Leu; Glu311 for Glu, Asn, Leu

phosphatase-based immunoassays for a

based conjugates to vessel walls or

tertiary and quaternary structures a

| | |
|----------------------------|---|
| CC | are very specific interference suppressors. This sequence encodes a |
| CC | variant bovine alkaline phosphatase which contains an G32d mutation and |
| CC | an EcoRI site described in the disclosure of the invention. |
| XX | |
| SQ | Sequence 1476 BP; 387 A; 223 C; 344 G; 522 T; 0 U; 0 Other; |
| | |
| Query Match | 99.8%; Score 1472.8; DB 10; Length 1476; |
| Best Local Similarity | 99.9%; Pred. No. 0; |
| Matches 1474; Conservative | 0; Mismatches 2; Indels 0; Gaps 0 |
| OY | . 1 GAATCTGATTCGCGTGAAGAAGAAAATCAGCTTTTGGAATAGACAAGCTGTCAA 60 |
| Db | 1 GAATCTTGATTCGACTGTAAGAAAGAAAATCAAGCTTTTGGAATAGACAACTGTCAA 60 |
| OY | 61 GCTTGGATGTTGGCTAAGAGTTGGCAACCAATTCAACTGCTGTAGAAATGTTATTTTG 120 |
| Db | 61 GCTTGGATGTTGGCTAAGAGTTGGCAACCAATTCAACTGCTGTAGAAATGTTATTTTG 120 |
| OY | 121 TTTTTGGGTAGTGGTAGTGGGTGCCAACCTGTACTGCTACTAGAAATTTGAAGGTCAA 180 |
| Db | 121 TTTTTGGGTAGTGGTAGTGGGTGCCAACCTGTACTGCTACTAGAAATTTGAAGGTCAA 180 |
| OY | 181 ATGAATGGTAGTTGGGTGCAGAAACCTCATTTGGCTATAGATCAATTTCCATACGTTGCT 240 |
| Db | 181 ATGAATGGTAGTTGGGTGCAGAACTCATTTGGCTATAGATCAATTTCCATACGTTGCT 240 |
| OY | 241 TTGCTCTAAGACTTCAATAGTTAGTAGACMAATTCAGATTCTGCTGTAAGTACTGCT 300 |
| Db | 241 TTGCTCTAAGACTTCAATAGTTAGTAGACMAATTCAGATTCTGCTGTAAGTACTGCT 300 |
| OY | 301 TACTTGTGTGGTGTAAAGGTAATTACAGAACTATTTGGTCTTCTGCTGCTAGATAC 360 |
| Db | 301 TACTTGTGTGGTGTAAAGGTAATTACAGAACTATTTGGTCTTCTGCTGCTAGATAC 360 |
| OY | 361 AATCAATCTATPACTACAGAGGTAAATGAATCTCTGTTATTAATAGAGCTAAAG 420 |
| Db | 361 AATCAATCTATPACTACAGAGGTAAATGAATCTCTGTTATTAATAGAGCTAAAG 420 |
| OY | 421 GCTGGTAAAGCGTGTGTGTGTTACTACTAGTTCACATGCTTCTCACGTGGT 480 |
| Db | 421 GCTGGTAAAGCGTGTGTGTGTTACTACTAGTTCACATGCTTCTCACGTGGT 480 |
| OY | 481 GCTTACGCTCATPCTGTTAATAGAAATTGGTACTCTGATGCTGATTTGCCAGCTGATGCT 540 |
| Db | 481 GCTTACGCTCATPCTGTTAATAGAAATTGGTACTCTGATGCTGATTTGCCAGCTGATGCT 540 |
| OY | 541 CAAAAAGATGGTGTGCAGATATTGCTGCTCAATTTGGTTTACAATAATGATATTGATGTT 600 |
| Db | 541 CAAAAAGATGGTGTGCAGATATTGCTGCTCAATTTGGTTTACAATAATGATATTGATGTT 600 |
| OY | 601 ATTTTGGGTGGTGGTAGAATGATACATGTTTCCAGAAAGTACTCCGATTCAGAAATACCA 660 |
| Db | 601 ATTTTGGGTGGTGGTAGAATGATACATGTTTCCAGAAAGTACTCCGATTCAGAAATACCA 660 |
| OY | 661 GATGATGCTTCTGTTAATGTTGTTAGAAAGATAGCAAAAATTTGGTTCAGAAATGGCAA 720 |
| Db | 661 GATGATGCTTCTGTTAATGTTGTTAGAAAGATAGCAAAAATTTGGTTCAGAAATGGCAA 720 |
| OY | 721 GCTAAGCATCAAGGTGCTCAATATGTTGGAAATAGAACTGCTTTGTTCGAAGTCTGTAT 780 |
| Db | 721 GCTAAGCATCAAGGTGCTCAATATGTTGGAAATAGAACTGCTTTGTTCGAAGTCTGTAT 780 |
| OY | 781 GATTCTAGTGTACTCATTTGATGGGTTTGTGGAACAGCTGATAGAAATGATATGTT 840 |
| Db | 781 GATTCTAGTGTACTCATTTGATGGGTTTGTGGAACAGCTGATAGAAATGATATGTT 840 |
| OY | 841 CAACAGATCATACTAAGAGATCCAATTTGGCTGAATAGACTGAAGCTGCTTTGCAAGTT 900 |
| Db | 841 CAACAGATCATACTAAGAGATCCAATTTGGCTGAATAGACTGAAGCTGCTTTGCAAGTT 900 |
| OY | 901 TTGCTCTAGAAATCCAAGAGTTTCTTCTGTTTGTGAAGSTGGTAGAATTGATATGTT 960 |
| Db | 901 TTGCTCTAGAAATCCAAGAGTTTCTTCTGTTTGTGAAGSTGGTAGAATTGATATGTT 960 |

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QY 961 CATCATGATGTAAGGCTTATATGCTTGAAGTATTAATGTTGATTAATGCTATT 1020
XX |||||
CC 961 CATCATGATTTTAAGGCTTATATGCTTGAAGTATTAATGTTGATTAATGCTATT 1020
QY 1021 GCTAAGGCTTAATGATTAATGCTTGAATGATTAATGCTTGAATGCTTGAAT 1080
XX |||||
CC 1021 GCTAAGGCTTAATGATTAATGCTTGAATGATTAATGCTTGAATGCTTGAAT 1080
QY 1081 AGTCATGTTTTTTCTTTGGTGGTACCTTTGAGAGTACTCTATTTTGGTTGGCT 1140
XX |||||
CC 1081 AGTCATGTTTTTTCTTTGGTGGTACCTTTGAGAGTACTCTATTTTGGTTGGCT 1140
QY 1141 CCAGGTAAAGCTTTGGATGATTAATGCTTACCTTTATTTTGGATGATGCTCAAGT 1200
XX |||||
CC 1141 CCAGGTAAAGCTTTGGATGATTAATGCTTACCTTTATTTTGGATGATGCTCAAGT 1200
QY 1201 TATGCTTTGGTGGTGGTCTTGAACCAAGATGTTAATGTTAATGTTAATGTT 1260
XX |||||
CC 1201 TATGCTTTGGTGGTGGTCTTGAACCAAGATGTTAATGTTAATGTTAATGTT 1260
QY 1261 TACAGACAAACAGCTGCTGTTCCATTTGGCTAGTGAACCTCATGTTGTAAGT 1320
XX |||||
CC 1261 TACAGACAAACAGCTGCTGTTCCATTTGGCTAGTGAACCTCATGTTGTAAGT 1320
QY 1321 GTTTTGCTAAGAGTCCACAAGCTATTGGTTCATGTTGTTCAAGAAACCTTTGTT 1380
XX |||||
CC 1321 GTTTTGCTAAGAGTCCACAAGCTATTGGTTCATGTTGTTCAAGAAACCTTTGTT 1380
QY 1381 GCTCATATTATAGGCTTTTGTGCTGTTGTTGAACCATTAATGTTAATTTGCCAGT 1440
XX |||||
CC 1381 GCTCATATTATAGGCTTTTGTGCTGTTGTTGAACCATTAATGTTAATTTGCCAGT 1440
QY 1441 CCAGCTACTGCTACTAGTATTCAGATTAAGGTACC 1476
XX |||||
CC 1441 CCAGCTACTGCTACTAGTATTCAGATTAAGGTACC 1476
Db 1441 CCAGCTACTGCTACTAGTATTCAGATTAAGGTACC 1476

RESULT 5
ADES3393
ID ADES3393 standard; DNA; 1476 BP.
XX
AC ADES3393;
XX
DT 29-JAN-2004 (first entry)
XX
DE Bovine alkaline phosphatase DNA encoding H320N/G322F.
XX
KM alkaline phosphatase; mutation; immunoassay; antigen;
XX interference suppressor; bovine; db; mutant.
OS Synthetic.
OS Bos taurus.
XX
PN EP1348760-A2.
XX
PD 01-OCT-2003.
XX
PF 21-MAR-2003; 2003BP-00006426.
XX
PR 25-MAR-2002; 2002DE-01013201.
XX
PA (HOFF) ROCHE DIAGNOSTICS GMBH.
XX (HOFF) HOFFMANN LA ROCHE & CO AG F.
XX
PI Mueller R, Thalhofer J, Geipel F, Hoeike W, Kirschbaum T;
XX
DR WPI; 2003-769844/73.
XX
PT New mutants of alkaline phosphatase (AP) where enzymatic activity is
XX reduced a hundred fold, are useful as blocking reagents in AP-based
XX immunoassays.
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PS Claim 8; SEQ ID NO 10; 35bp; German.
XX
XX This invention describes a novel mutant of eukaryotic alkaline
CC phosphatase where the wild-type sequence is at least 77% homologous with
CC ADES3385 and where the alkaline phosphatase activity is reduced by at
CC least 100-fold, relative to the wild type. The mutations described are
CC Asp42, 316 or 357 for Asn, Val, Ala or Ser; Ser92 or 155 for Ala, Gly,
CC Val or Leu; Glu311 for Glu, Asn, Leu, Ile or Met; His320, 358 or 432 for
CC Asn, Phe, Asp or Tyr; or Gly322 for an amino acid larger than Asp.
CC Conjugates of the novel mutant with antibodies are useful in alkaline
CC phosphatase-based immunoassays for antigens as interference suppressors,
CC i.e. they prevent non-specific binding of active alkaline phosphatase-
CC based conjugates to vessel walls or first antibodies, a phenomenon that
CC may result in false positive results. The mutants have almost the same
CC tertiary and quaternary structures as wild-type alkaline phosphatase, so
CC are very specific interference suppressors. This sequence encodes a
CC variant bovine alkaline phosphatase which contains an H320N/G322F
CC mutation and an EcorI site described in the disclosure of the invention.
XX
SQ Sequence 1476 BP; 388 A; 222 C; 344 G; 522 T; 0 U; 0 Other;

Query Match 99.7%; Score 1471.2; DB 10; Length 1476;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1473; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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QY 1 GAATCTTGATTCAGCTGGAAGAAATATCCAGCTTTTGGAAATAGACAAAGCTCTCA 60
Db 1 GAATCTTGATTCAGCTGGAAGAAATATCCAGCTTTTGGAAATAGACAAAGCTCTCA 60
QY 61 GCTTGGATGTTGCTAAGAGTTGCACCAATTCMAACTGCTGCTAAGATGTTATTTTG 120
Db 61 GCTTGGATGTTGCTAAGAGTTGCACCAATTCMAACTGCTGCTAAGATGTTATTTTG 120
QY 121 TTTTGGGTGATGATGATGGGTGTTCCAACTGTTACTGCTATAGAAATTTTGAAGGTCAA 180
Db 121 TTTTGGGTGATGATGATGGGTGTTCCAACTGTTACTGCTATAGAAATTTTGAAGGTCAA 180
QY 181 ATGAATGATGATGGGTGCTCAGAAATCTCATTTGGCTATGATCAATTTCCATACGTTGCT 240
Db 181 ATGAATGATGATGGGTGCTCAGAAATCTCATTTGGCTATGATCAATTTCCATACGTTGCT 240
QY 241 TTGCTTAAGACTTACATATGTTGATGACAGATTCACGATTTCTGCTGATGCTACTGCT 300
Db 241 TTGCTTAAGACTTACATATGTTGATGACAGATTCACGATTTCTGCTGATGCTACTGCT 300
QY 301 TACTTGTGATGATTAAGGATTAATTAAGAACTATGTTGTTCTGCTGCTGCTAGATAC 360
Db 301 TACTTGTGATGATTAAGGATTAATTAAGAACTATGTTGTTCTGCTGCTGCTAGATAC 360
QY 361 AATCAATGTAATTAATTAATGATGATTAATGATTAATGATTAATGATTAATGATTA 420
Db 361 AATCAATGTAATTAATTAATGATGATTAATGATTAATGATTAATGATTAATGATTA 420
QY 421 GCTGATTAAGGCTGTTGTTGTTGTTACTACTAAGTTCAAGATTCAGATCTCTCCAGCTGCT 480
Db 421 GCTGATTAAGGCTGTTGTTGTTGTTACTACTAAGTTCAAGATTCAGATCTCTCCAGCTGCT 480
QY 481 GCTTAAGCTCATACGTTAATAGAAATTTGATCTGATGCTGATTTGCTCCAGCTGATGCT 540
Db 481 GCTTAAGCTCATACGTTAATAGAAATTTGATCTGATGCTGATTTGCTCCAGCTGATGCT 540
QY 541 CAAAAGATGTTGTTCAAGATTAATGCTGCTCAATTTGTTTCAATATGATTAATGATTT 600
Db 541 CAAAAGATGTTGTTCAAGATTAATGCTGCTCAATTTGTTTCAATATGATTAATGATTT 600
QY 601 ATTTTGGTGGTGGTGAATGATGATGTTTCCAGAGGATCTCCAGATCCAGAAATCCCA 660
Db 601 ATTTTGGTGGTGGTGAATGATGATGTTTCCAGAGGATCTCCAGATCCAGAAATCCCA 660
QY 661 GATGATGCTCTGTTAATGATGATTAAGGATTAAGGATTAAGGATTAAGGATTAAGG 720
Db 661 GATGATGCTCTGTTAATGATGATTAAGGATTAAGGATTAAGGATTAAGGATTAAGG 720
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| | | | |
|----------|--|--|------|
| QY | 721 | GCTAAGCATCAAGGCTCAATATGTTGGAAATAAACGTGTTGTGCAAGCTGCAT | 780 |
| Db | 721 | GCTAAGCATCAAGGCTCAATATGTTGGAAATAAACGTGTTGTGCAAGCTGCAT | 780 |
| QY | 781 | GATTCAGTGTACTCATTTGATGGGTTGTTTGAACCAAGCTGATATGAATATATGTT | 840 |
| Db | 781 | GATTCAGTGTACTCATTTGATGGGTTGTTTGAACCAAGCTGATATGAATATATGTT | 840 |
| QY | 841 | CACCAAGATCATATCAAGGATCCAACTTTGGCTGAATGACTGAAGCTGCTTGGACGTT | 900 |
| Db | 841 | CACCAAGATCATATCAAGGATCCAACTTTGGCTGAATGACTGAAGCTGCTTGGACGTT | 900 |
| QY | 901 | TTGCTAGAAATCCAAAGGTTTTTACTGTTTGTGTAAGGTTGGAGAAATGATCAATGCT | 960 |
| Db | 901 | TTGCTAGAAATCCAAAGGTTTTTACTGTTTGTGTAAGGTTGGAGAAATGATCAATGCT | 960 |
| QY | 961 | CATCATGATGGTAAGGCTTATATGCTTTGACTGAAGCTATATATGTTGATATGCTATT | 1020 |
| Db | 961 | CATCATGATGGTAAGGCTTATATGCTTTGACTGAAGCTATATATGTTGATATGCTATT | 1020 |
| QY | 1021 | GCTAAGGCTAATGAATTGACTTTCTGAATGGAATCTTGAATTTGGTTACTGCTGATCAT | 1080 |
| Db | 1021 | GCTAAGGCTAATGAATTGACTTTCTGAATGGAATCTTGAATTTGGTTACTGCTGATCAT | 1080 |
| QY | 1081 | AGTCATGTTTTTCTTTTGGTGGCTTACACTTTGAGAGGTAAGTACTTCAATTTTGGTTGGCT | 1140 |
| Db | 1081 | AGTCATGTTTTTCTTTTGGTGGCTTACACTTTGAGAGGTAAGTACTTCAATTTTGGTTGGCT | 1140 |
| QY | 1141 | CCAGGTAAGGCTTTGGATAGTAAGCTTACACTTCTATTTTGGTAAGTAAGTCCAGGT | 1200 |
| Db | 1141 | CCAGGTAAGGCTTTGGATAGTAAGCTTACACTTCTATTTTGGTAAGTAAGTCCAGGT | 1200 |
| QY | 1201 | TATGCTTTGGGTGGTGGCTTCTAGACCAAGATGTTATGTTAGTACTAGTGAAGAACATCT | 1260 |
| Db | 1201 | TATGCTTTGGGTGGTGGCTTCTAGACCAAGATGTTATGTTAGTACTAGTGAAGAACATCT | 1260 |
| QY | 1261 | TACAGACAAACAAGCTGCTGTTCCATTTGCTGTAAGTAACTCATGGTGGTGAAGATGTTGCT | 1320 |
| Db | 1261 | TACAGACAAACAAGCTGCTGTTCCATTTGCTGTAAGTAACTCATGGTGGTGAAGATGTTGCT | 1320 |
| QY | 1321 | GTTTTTGGCTAGAGGTCACAAGGCTCATTTGGTTCATGGTGTTCAGAAAGAAACTTTTGGT | 1380 |
| Db | 1321 | GTTTTTGGCTAGAGGTCACAAGGCTCATTTGGTTCATGGTGTTCAGAAAGAAACTTTTGGT | 1380 |
| QY | 1381 | GCTCATATTATGCTTTTGTCTGTGTGTTGAACCATATCACTGATTTGTAATTTGCCAGCT | 1440 |
| Db | 1381 | GCTCATATTATGCTTTTGTCTGTGTGTTGAACCATATCACTGATTTGTAATTTGCCAGCT | 1440 |
| QY | 1441 | CCAGCTACTGCTACTAGTATTTCCAGATTAAAGTACC 1476 | |
| Db | 1441 | CCAGCTACTGCTACTAGTATTTCCAGATTAAAGTACC 1476 | |
| RESULT 6 | | | |
| ADE53394 | | | |
| ID | ADE53394 standard; DNA; 1476 BP. | | |
| AC | ADE53394; | | |
| XX | 29-JAN-2004 (first entry) | | |
| DT | | | |
| DE | Bovine alkaline phosphatase DNA encoding S92A/H320N/S322F. | | |
| XX | | | |
| KW | alkaline phosphatase; mutation; immunoassay; antigen; | | |
| KW | interference suppressor; bovine; ds; mutant. | | |
| XX | | | |
| OS | Synthetic. | | |
| OS | Bos taurus. | | |
| XX | | | |
| PN | EP1348760-A2. | | |
| XX | | | |
| PD | 01-OCT-2003. | | |
| XX | | | |

[illegible]

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Db      |||||
481 GCTTACGCTACACTGTTATATGAAATGGTACTGAGTGCATTTGCGACGTGATGCT 540
Qy      541 CAAAAGATGGTTCACAGATATTTGCTGCTCAATGGTTTACATATGATATGATGTT 600
Db      541 CAAAAGATGGTTCACAGATATTTGCTGCTCAATGGTTTACATATGATATGATGTT 600
Qy      601 ATTTGGGGGTGGTGAATGTACATGTTCCAGAAAGTACTCCAGATCCAGATCCCA 660
Db      601 ATTTGGGGGTGGTGAATGTACATGTTCCAGAAAGTACTCCAGATCCAGATCCCA 660
Qy      661 GATGATGCTTCTGTTAATGCTGTTAGAAAGATTAAGCAAAATTTGGTTCAAGATGGCAA 720
Db      661 GATGATGCTTCTGTTAATGCTGTTAGAAAGATTAAGCAAAATTTGGTTCAAGATGGCAA 720
Qy      721 GCTAAGCATCAAGGTGCTCAATATGTTTGGAAATAGACCTGTTTGGCAAGCTGCTAT 780
Db      721 GCTAAGCATCAAGGTGCTCAATATGTTTGGAAATAGACCTGTTTGGCAAGCTGCTAT 780
Qy      781 GATTCTAGTGTACTCATTTGATGAGGTTGTTTGAACGAGTGAATGATATATGTT 840
Db      781 GATTCTAGTGTACTCATTTGATGAGGTTGTTTGAACGAGTGAATGATATATGTT 840
Qy      841 CAACAAGATCATACTAAGATCCAACTTTGGCTGAATGACTGAAGCTCTTTGCAAGTT 900
Db      841 CAACAAGATCATACTAAGATCCAACTTTGGCTGAATGACTGAAGCTCTTTGCAAGTT 900
Qy      901 TTGCTCTAGAAATCCAAAGAGTTTTCATGTTTGTGTAAGGTGCTAGATGATCATGCT 960
Db      901 TTGCTCTAGAAATCCAAAGAGTTTTCATGTTTGTGTAAGGTGCTAGATGATCATGCT 960
Qy      961 CATCATGATGATGAGGCTTATATAGGCTTTGATGCTGAAGCTATATGTTATATGCTATT 1020
Db      961 CATCATGATGATGAGGCTTATATAGGCTTTGATGCTGAAGCTATATGTTATATGCTATT 1020
Qy      1021 GCTAAGGCTAATGAATTTGACTTCTGAATTTGATCTTTGATTTTGGTTACTGCTGATCAT 1080
Db      1021 GCTAAGGCTAATGAATTTGACTTCTGAATTTGATCTTTGATTTTGGTTACTGCTGATCAT 1080
Qy      1081 AGTCATGTTTTTTCTTTTGGTGTTCACCTTTGAGAGGTACTTCTATTTTGGTTGGCT 1140
Db      1081 AGTCATGTTTTTTCTTTTGGTGTTCACCTTTGAGAGGTACTTCTATTTTGGTTGGCT 1140
Qy      1141 CGAGGTAAGGCTTTGGATGTAAGTTTACCTTCACTTATTTTGTATGATGGTCCAGGT 1200
Db      1141 CGAGGTAAGGCTTTGGATGTAAGTTTACCTTCACTTATTTTGTATGATGGTCCAGGT 1200
Qy      1201 TATGCTTTGGGTGGTGTCTTGAACCAAGATGTTTATGTAAGTACTAGTAAGAACCATCT 1260
Db      1201 TATGCTTTGGGTGGTGTCTTGAACCAAGATGTTTATGTAAGTACTAGTAAGAACCATCT 1260
Qy      1261 TACAGACAAACAGCTGCTGTTTCATTTGGCTAGTGAACCTCAGTGTGTGAAGATGTTGCT 1320
Db      1261 TACAGACAAACAGCTGCTGTTTCATTTGGCTAGTGAACCTCAGTGTGTGAAGATGTTGCT 1320
Qy      1321 GTTTTGTCTAGAGGTCCACAGAGTCAATTTGGTTCATGTTCAAGAAAGAACTTTGTT 1380
Db      1321 GTTTTGTCTAGAGGTCCACAGAGTCAATTTGGTTCATGTTCAAGAAAGAACTTTGTT 1380
Qy      1381 GCTCATATTTATGCTTTTGTGCTGTTTGTGTAACCATACGATTTGTAATTTGCCAGCT 1440
Db      1381 GCTCATATTTATGCTTTTGTGCTGTTTGTGTAACCATACGATTTGTAATTTGCCAGCT 1440
Qy      1441 CCAGCTACTGCTACTATGATTTCCAGATTAAGGTACC 1476
Db      1441 CCAGCTACTGCTACTATGATTTCCAGATTAAGGTACC 1476

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RESULT 7
AD126549
ID AD126549 standard; DNA; 1476 BP.
XX
AC AD126549;

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XX
DT 22-APR-2004 (first entry)
XX
DE Bovine biAPII DNA.
XX
KW alkaline phosphatase; resistance gene; zeomycin; G418; heat stability;
XX bovine; biAPII; yeast; gene; ds.
XX
OS Bos taurus.
XX
EN EP1176205-A2.
XX
PD 30-JAN-2002.
XX
PF 21-JUL-2001; 2001EP-00117622.
XX
PR 25-JUL-2000; 2000DE-01036491.
XX
PA (HOPE ) ROCHE DIAGNOSTICS GMBH.
XX (HOPE ) HOFFMANN LA ROCHE & CO AG F.
PI Mueller R, Thalhofer J, Geipel F, Hoelke W, Glaser S, Eckstein H;
PI Kirschbaum T, Bommaribus B;
DR WPI; 2002-173123/23.
XX
PT Preparing eukaryotic alkaline phosphatase, useful as diagnostic reagent
PT and for dephosphorylation, by recombinant expression in yeast selected
PT for high gene copy number.
XX
PS Claim 2; SEQ ID NO 1; 23bp; German.
XX
CC This invention describes a novel method of preparing eukaryotic alkaline
CC phosphatase in yeast cells, comprising cloning an alkaline phosphatase
CC gene sequence into different vectors, transforming, and expressing and
CC purifying. A first vector is used containing a resistance gene against a
CC selection marker and transformants that have integrated resistance gene
CC and alkaline phosphatase gene into the genome are selected by growth on
CC medium containing a low concentration of selection marker. The gene copy
CC number is increased by multiple transformation and multiple transformants
CC selected on growth medium under high selection pressure. A second vector
CC containing the alkaline phosphatase gene and a second resistance gene
CC against a second marker is introduced, its copy number increased as for
CC the first resistance gene and clones selected that have many copies of
CC the alkaline phosphatase gene and of both resistance genes, integrated
CC into the genome. The vectors used in the method are pHAP10-3 and pHAP10-
CC 3/9K. Preferred cells include methylotrophic yeast, particularly Pichia
CC pastoris and Hansenula polymorpha and specifically P. pastoris X-33
CC transformed with pHAP10-3 and pHAP10-3/9K. The amino acid sequence of
CC bovine alkaline phosphatase is known and, working back from this, an
CC optimized codon sequence was designed. This was assembled conventionally
CC from 28 synthetic oligonucleotides to give a sequence having EcoRI and
CC Asp18 recognition sites at the ends to facilitate cloning. The selection
CC markers are particularly zeomycin and G418, respectively. The alkaline
CC phosphatase is used as diagnostic reagent, as part of a conjugate and for
CC dephosphorylation of DNA. This method produces very active, glycosylated
CC alkaline phosphatase with specific activity over 3000, preferably 10000,
CC units/mg and heat stability comparable with that for commercial enzymes.
CC The expression system is resistant and stable and provides high-level
CC expression without any selection pressure. This sequence represents the
CC bovine biAPII gene.
XX
SQ Sequence 1476 BP; 337 A; 449 C; 441 G; 249 T; 0 U; 0 Other;
XX
Query Match 57.3%; Score 845.6; DB 5; Length 1476;
Best Local Similarity 73.3%; Pred. No. 8; 6e-193;
Matches 1082; Conservative 0; Mismatches 394; Indels 0; Gaps 0;
Qy 1 GAATCTTGATTCGACGTGAGAGAAAGAAATCCAGCTTTTGGATATGACCAAGCTGCTCA 60
Db 1 GAATCTTCATCCACGCTGAGAGAAACCCCGCTTCTGGAACCGCCAGCACCACG 60
Qy 61 GCTTGGATGTTGCTAAGAAAGTTGCACCAATTCAACTGCTGCTAAGAAATGTTATTG 120

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[illegible]

| | | | |
|----------|--|--|------|
| Db | 1141 | CCCGGCAAGGCGTTAGACAGCAAGTCTACACCTTCATCCTCTATGGCAATGGCCAGGC | 1200 |
| Qy | 1201 | TATGCTTTGGGTGGTGGTTCTTAGACCAAGATGTTATATGTAAGTACTAGTGAAGAACATCT | 1260 |
| Db | 1201 | TATGCGCTTGGCCGGGGGCTCGAGGGCCGATGTTATATGGCAGCACMACCGAGGAACCTCA | 1260 |
| Qy | 1261 | TACAGACAACAAGCTGCTGTTCCATTGGCTAGTGAACCTATGGTGGTGAAGATGTTGCT | 1320 |
| Db | 1261 | TACCGGACAGCAGGGGCGGTGCCCCCTGGCTAGCGACGCCACGGGGGCGAAGAGCTGGCG | 1320 |
| Qy | 1321 | GTTTTTGCTAGAGGTCCACAAGCTCATTTGGTTCATGTTGTTCAAGAAACTTTTGT | 1380 |
| Db | 1321 | GTCGTTCCCGCAGAGGCCCGCAGCGCACCTGTGACGCGCTGCAGAGAGAGACCTTGGTG | 1380 |
| Qy | 1381 | GCTCATATTAATGCTTTGCTGTGTTGTGTTGAACCATATACCTGATTTGTAATTGGCAGCT | 1440 |
| Db | 1381 | GCGCACATCATGCGCTTTCGGGGGTGGTGGAGCCCTACACCGACTCAATCTGCCAGCC | 1440 |
| Qy | 1441 | CCAGCTACTGCTACTACTATTTCCAGATTAAAGGTACC | 1476 |
| Db | 1441 | CCGCGCACGCGCACACAGCATCCCGACTAGGGTACC | 1476 |
| RESULT 8 | | | |
| AD553384 | AD553384 standard; DNA, 1464 BP. | | |
| XX | AD553384; | | |
| XX | 29-JAN-2004 | (first entry) | |
| DE | Bovine alkaline phosphatase DNA. | | |
| XX | | | |
| KW | alkaline phosphatase; mutation; immunoassay; antigen; | | |
| XX | interference suppressor; bovine; ds; gene. | | |
| OS | Bos taurus. | | |
| XX | | | |
| FH | Key | Location/Qualifiers | |
| FT | CDS | 1..1464 | |
| FT | | /*tag= a | |
| FT | | /product= "alkaline phosphatase" | |
| FT | | /partial | |
| FT | | /note= "no start codon given" | |
| PN | EPI348760-A2. | | |
| PD | 01-OCT-2003. | | |
| XX | | | |
| PF | 21-MAR-2003; | 2003EP-00006426. | |
| XX | | | |
| PR | 25-MAR-2002; | 2002DE-01013201. | |
| XX | | | |
| PA | (HOFF) ROCHE DIAGNOSTICS GMBH. | | |
| PA | (HOFF) HOFFMANN LA ROCHE & CO AG F. | | |
| PI | Mueller R, Thalhoffer J, Geipel F, Hoelke W, Kirschbaum T; | | |
| DR | MPI: 2003-7569844/73. | | |
| XX | P-PSDB; AD553385. | | |
| XX | | | |
| PT | New mutants of alkaline phosphatase (AP) where enzymatic activity is | | |
| PT | reduced a hundred fold, are useful as blocking reagents in AP-based | | |
| PT | immunoassays. | | |
| XX | | | |
| PS | Disclosure; SEQ ID NO 1; 35pp; German. | | |
| XX | | | |
| CC | This invention describes a novel mutant of eukaryotic alkaline | | |
| CC | phosphatase where the wild-type sequence is at least 77% homologous with | | |
| CC | AD553385 and where the alkaline phosphatase activity is reduced by at | | |
| CC | least 100-fold, relative to the wild type. The mutations described are | | |
| CC | Asp442, 316 or 357 for Asn, Val, Ala or Ser; Ser92 or 155 for Ala, Gly, | | |
| CC | Val or Leu; Glu111 for Gln, Asn, Leu, Ile or Met; His320, 358 or 432 for | | |

CC Asn, Phe, Asp or Tyr; or Gly322 for an amino acid larger than Asp.
 CC Conjugates of the novel mutant with antibodies are useful in alkaline
 CC phosphatase-based immunoassays for antigens as interference suppressors,
 CC i.e. they prevent non-specific binding of active alkaline phosphatase-
 CC based conjugates to vessel walls or first antibodies, a phenomenon that
 CC may result in false positive results. The mutants have almost the same
 CC tertiary and quaternary structures as wild-type alkaline phosphatase, so
 CC are very specific interference suppressors. This sequence encodes the
 CC wild-type bovine alkaline phosphatase described in the disclosure of the
 CC invention.

XX Sequence 1464 BP, 334 A, 446 C, 438 G, 246 T, 0 U, 0 Other;

Query Match 56.6%; Score 834.8; DB 10; Length 1464;

Best Local Similarity 73.2%; Pred. No. 3.4e-190;
 Matches 1070; Conservative 0; Mismatches 392; Indels 0; Gaps 0;

```

QY 8 TGAATTCAGCTGAAAGAAATCCAGCTTTTGAATAGACAGCTGCTCAAGCTTTGG 67
DB 2 TCATCCCACTGAGAGAAAAACCCGCTTCTGAAACGCCGACGACCCAGCCCTTG 61
QY 68 ATGTGCTAAGAGTTGCAACCAATTCAGCTGCTGAAGATGTTATTTGTTTGG 127
DB 62 ATGTAGCCAAAGAGTTGCAAGCCGATCCAGACAGCTGCAAGATGTCATCTCTTGG 121
QY 128 GTGATGATGGGTGTTCCAACTGTTACTGTAAGTATTTGAAGGTCAAATGAATG 187
DB 122 GGGATGGAGTGGGGGGTCTTACGGTGAACAGCACTGGATCTTAAAGGGGAGATGATG 181
QY 188 GTAAGTTGGGTCCAGAACTCCATGGCTATGGATCAATTTCCATTCGTTCTTGTCTA 247
DB 182 GCAAACTGGGACCTGGACACCCCTGGCATGGACAGTCCATTCGTTGCTGTGTCA 241
QY 248 AGACTTACAGTGTGATAGCAAGTTCAGATTCGCTGCTGTAAGTCTGTTACTTCTT 307
DB 242 AACACATACAGCGTGGACAGAGTGCACAGACGCGACGACCTGCTACCTCTGT 301
QY 308 GTGTGTTAAGGGTATTTACAGAACTATTTGTTTCTGCTGCTGAATCAATCAAT 367
DB 302 GTGGGGTCAAGGGCACTACAGAACCATGTGGTGAATGTCAGCCGCCCTACAACTCA 361
QY 368 GTAATATCTATAGAGTAAATGAATGTTCTTCTGTTATTAATAGAGTAAAGAGCTGTA 427
DB 362 GCACACGACGACGTGGGATGAGTCACTGTGTATCAACCGGGCCAAAGACGAGGA 421
QY 428 AGGCTGTGGTGTGTTACTACTAGAGTTCACATGCTTCTCAGCTGGTGTAG 487
DB 422 AGGCGTGGAGTGTGACACACACAGGTTGAGATGCTCTCCAGCCGAGGCTTACG 481
QY 488 CTCATATCTGTTAATAGAAATTTGTACTCTGATGCTGATTTGCCAGCTGACTCAAAAGA 547
DB 482 CGCACACGGGTGAACGAAACCTGTACTAGACGCGGACCTGCTGTATGACAGAAAGA 541
QY 548 ATGTTGTTCAAGATTTGCTGCTCAATTTGTTTCAATATGCAATTTGATTTTGG 607
DB 542 ATGGCTGCCAGACATCGCCGACAGCTGCTTCAACAACTGATATTTGACGTGATCTGG 601
QY 608 GTGGGTGTAAGATGATACATGTTTCCAGAAAGTACTCCAGATCCAGAAATCCAGATGATG 667
DB 602 GTGGAGGCCGATGTACATGTTTCTGAGGGGACCCCAACCTGTGAATACCCAGATGATG 661
QY 668 CTTCTGTTAATGTTGTTAGAAAGATTAAGCAAAATTTGGTTCCAGATGGCAAGCTAAGC 727
DB 662 CCAAGTGTAGATGAGATCGCGAAGGACAGACAACTGGTGAAGATGGCAGGCCAAGC 721
QY 728 ATCAAGGTGCTCAATATGTTTGAATAGAACTGCTTTGTTGCAAGCTGCTGATGATTTCTA 787
DB 722 ACCAGAGGCCAGATATGTGTGAACCGCACCTGCTCTTCAAGCGGCGCATGATCTCA 781
QY 788 GTGTACTCATTTGATGGTGTGTTGAACAGCTGATGATGAAGTATATGTTCAACAG 847
DB 782 GTGTACACACTCATGGGCTCTTTGAGCCGCGACAGATGAATATGTTACAGCAG 841

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QY 848 ATCATATCAAGATCCAACTTTGGCTGAATGACTGAAGCTCTTTCGAAGTTTGTCTA 907
DB 842 ACCACACCAAGAACCCGACCTTGGCGAGATGACGAGGCGGCTTCGAAGTCTGAGCA 901
QY 908 GAAATCCAAAGAGTTTAACTTTGTTGTTGTAAGGTGTAAGAAATGATCATGTGTCATCATG 967
DB 902 GGAAACCCCGGGGCTTTTAACTTTCGTGGAGGAGGCGCATTTGACCAACCGGTACACATG 961
QY 968 ATGTGAAGGCTATATGCTTTGACTGAAGCATATATGTTGATATATGCTATTGCTAAGG 1027
DB 962 ACGCAAGGCTTATATGCGACTGACTGAGGCGATCATGTTTGAACAATGCCATGCGCAAGG 1021
QY 1028 CTAAATGAATTGACTCTGAATTTGATTTGATTTGTTGTTACTGCTGATCATTAATCATG 1087
DB 1022 CTAAAGAGTCACTAGCGAATCTGACAGAGCTGATCTTGTCACTGACAGACATCCCATG 1081
QY 1088 TTTTTCCTTTTGGTGTAACTTTGAGAGTACTTCTATTTTGGTGTGCTCAAGGTA 1147
DB 1082 TCTTCTTTTGGTGTAACTGCTGAGAGCTGAGGAGCTTCAATTTTGGTGTGCGCCGCA 1141
QY 1148 AGGCTTTGATATGATGATCTTCACTTTATTTTGTATGTAATGATGTCAGGTTATGCTT 1207
DB 1142 AGGCTTTGATGACGAAGTCTTACACTTCATCTCTATGGAAGTCCAGGCTATGCGC 1201
QY 1208 TGGGTGTGTTCTTGAACAGATGTTAAATGTAAGTACTAGTAAGAACCATTTTACAGAC 1267
DB 1202 TTGGGGGGGGTCTGAGGCGCCATGTTAATGACAGACAAAGGAGAACCTTATACCGGC 1261
QY 1268 AACAGCTGCTGTTCCATTTGGCTAGTGAATCACTCATGTGTGTGAAGATGTTGCTTTTGG 1327
DB 1262 AGCAGCGCGCGTGTCCCTGTGCTAGCGAGACCAACGCGGGGGAAGACGTGGCGGTGTG 1321
QY 1328 CTAGAGGTCCACAGCTCATTTGTTGTTGATGTTTCAAGAAAGAACTTTGTTGCTCATTA 1387
DB 1322 CGCGAGGCCCGAGGCGCACTGTGTGACGGGTGACAGAGAGACTTTCGTGGGCGACA 1381
QY 1388 TTATGCTTTTGTGCTGTTGTGTTGAACCATACACTGATTTGTAATTTGCCAGCTCAGCTA 1447
DB 1382 TCATGGCTTTTGGCGGCTGCGTGGAGCCCTTACACCGACTGCAATGTGCAAGCCCCGCA 1441
QY 1448 CTGCTACTAGTATTCAGATTA 1469
DB 1442 CCGCACACGACATCCCGACTA 1463

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RESULT 9
 AB222773
 ID AB222773 standard; DNA, 1650 BP.
 XX
 AC AB222773;
 XX
 DT 02-APR-2003 (first entry)
 XX
 DE Calf intestinal alkaline phosphatase DNA sequence SEQ ID NO:26.
 XX
 KW Recombination; mutagenesis; sarcosine oxidase; phosphatase; human;
 KW human placental alkaline phosphatase; hpap; clap; gene; ds;
 XX calf intestinal alkaline phosphatase.
 XX
 OS Bos taurus.
 XX
 PN WO200302736-A2.
 XX
 PD 09-JAN-2003.
 XX
 PF 26-JUN-2002; 2002WO-EP007060.
 XX
 PR 27-JUN-2001; 2001EP-00115424.
 XX
 PA (HOFF) ROCHE DIAGNOSTICS GMBH.
 PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
 XX
 PI Shao Z, Kratzsch P, Schmuck R, Von Der Eltz H, Kenkiles J;

XX WPI; 2003-201503/19.

XX DR Forming a polynucleotide sequence for optimizing biomolecules and enzymes
XX PT by generating a nucleic acid fragment ladder, removing the chain-
XX PT terminating molecules and reassembling the polynucleotide.

XX Example 2; Fig 5; 64pp; English.

XX The present invention describes a method of forming a polynucleotide
CC sequence, comprising: (a) generating a nucleic acid fragment ladder by
CC nucleic acid synthesis; (b) removing the chain-terminating molecules or
CC changing them into non-terminating molecules; and (c) reassembling the
CC polynucleotide. Also described is a method for providing mutant
CC polypeptides or proteins. The methods of forming a polynucleotide
CC sequence and providing mutant polypeptides or proteins are useful for
CC optimizing biomolecules and enzymes. The present sequence represents a
CC calf intestinal alkaline phosphatase (ciap) DNA sequence, which is used
CC in an example from the present invention for the recombination of human
CC placental alkaline phosphatase (hnap) and ciap genes

XX SQ Sequence 1650 BP; 382 A; 495 C; 483 G; 290 T; 0 U; 0 Other;

Query Match: 56.3%; Score 831.6; DB 8; Length 1650;
Best Local Similarity 73.1%; Pred. No. 2e-189;
Matches 1068; Conservative 0; Mismatches 394; Indels 0; Gaps 0;

QY 9 GATTCAGCTGAGAAAGAAATCCAGCTTTTGGATAGACAAAGCTGCTCAAGCTTTGA 68
DB 158 GATCCAGCTGAGAGAGAAACCCCGCTTCTGGAACCGCAGGACGAGCCGCTTGA 217
QY 69 TGTGTGAAGAAATGCAACCAATTCAACTGCTGCTAAGATGTTATTTTGGG 128
DB 218 TGAAGCAAGAAATGAGCCGATCCAGACAGCTGCGAAGATGTCATCTCTTGGG 277
QY 129 TGATGATGAGGCTTCCACTGTTACTGCTAGATTTTGAAGGCTCAATGATG 188
DB 278 GAGTGGAGTGGGGTGCTACGATGACGACCTCGATCTTAAAGGAGCATGATG 337
QY 189 TAAAGTGGGCTCAAGAACTTCATGCTGATGATCAATTCATGCTGCTTTGCTAA 248
DB 338 CAAAGCTGGGACCTGAGACCCCTGGGCTAGGACCAAGTCCCATCTGCTGCTCA 397
QY 249 GACTTCAAGTGTGATGACAAATTCAGTTCTGCTGATGCTAGCTTACTGCTTATG 308
DB 398 GACATCAACGTGACAGAGGTCAGACAGCGCAGGCACTGCTTACCTGCTG 457
QY 309 TGGTGTAAAGGTAATTAACAATACTGTTGCTGCTGCTGCTAGATCAATCATG 368
DB 458 TGGGCTCAAGGCACTACAGAACATCGGTGTAAGTGCAGCCGCCGCTACATCATG 517
QY 369 TAATCTACTAGAGTATGAAATTAATCTTGTATTAATAGATGAAGAGCTGCTAA 428
DB 518 CAACACGACACGTGGAAATGAGTCAAGTGTGATCAACCGGAGCCAAAGAAACAGGAA 577
QY 429 GGGTGTGGTGTGTTACTACTACTAGATTAAGTCAATGCTTCTCCAGCTGCTTACGC 488
DB 578 GGGCTGGAGGTGTGACCAACAGGAGTGCAGCATGCTCCCGAGCCGAGGCTACAGC 637
QY 489 TCATACCTGTTAATAGAAATGTAATCTGATGCTGATGCTGATGCTCAAAAAGAA 548
DB 638 GCACACGCTGACCGAAATCTGTATCTACAGCGCCGACCTGCTGATGACAGAAAGAA 637
QY 549 TGGTGTCAAGATATGCTGCTCAATGCTTGAATGATGATGATGATGATGATGATG 608
DB 698 TGGCTCCAGGACATCGCCGACAGCTGCTTCAACATGATGATGATGATGATGATG 757
QY 609 TGGTGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 668
DB 758 TGGAGGCGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 817
QY 669 TTTCTGTTAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 728

DB 818 CAGTGTGAATGAGTCCGGAAGCAAGCAAGAACTGTGTCAGAAATGCGAGCCAAAGCA 877
QY 729 TCAAGGTGCTCAATATGTTTGAATGAACTGCTTTGTTGCAAGCTGATGATGATCTAG 788
DB 878 CAGGAGGCTCAGATATGTTGGAACCGACAGCTGCTCTTCAAGGCGGAGATCTCAG 937
QY 789 TGTACTCAATTTGATGAGTGTGTTGTAACACAGCTGATATGATATGTTCAACAGA 848
DB 938 TGTACACACCTCATGAGGCTCTTTGAGCGGAGACATGAATATGTTTACAGAGA 997
QY 849 TCATCTAAGATCAACTTTGGCTGAATGACTGAAGCTCTTTCGAAAGTTTGTCTAG 908
DB 998 CCACACCAAGAGCCCACTCGGAGATGACGAGGCGGCTCTCAAGTCTGACAG 1057
QY 909 AATTCAGAGTGTGTTTACTGTTGTTGTAAGTGTGTAATGATCATGCTCATGTA 968
DB 1058 GAACCCCGGGGCTTCTTACCTCTTGTGAGGAGGCGCCATGACAGCTACCAATGA 1117
QY 969 TGTGAAGCTTATGAGCTTTGACTGAAGCTATATGTTGATATGATGATGATGATG 1028
DB 1118 CGGCAAGCTTATATGACACTGACAGGAGATGATGATGATGATGATGATGATG 1177
QY 1029 TAAATGATGACTTGTGAATGGAATCTTGAATGTTGTTACTGCTGATCATATGATG 1088
DB 1178 TAAAGAGCTCACTAGGAACTGGAACAGCTGATCTTGTACAGACCACTCCATGT 1237
QY 1089 TTTTCTTTTGGTGTACACTTGAAGAGTACTTATTTTGGTTTGGTTCAGATTA 1148
DB 1238 CTCTCTCTTTGGGCTTACACACTGCGTGGACCTTCATTTTGGTGGCCCGGCA 1297
QY 1149 GGTGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1208
DB 1298 GGGCTTGAACAGCAAGTCTTACACTTCACTCTTATGCAATGAGCCAGCTATGCGT 1357
QY 1209 GGGTGTGTTCTTGAACAGATGTTAATGTTAATGTTAATGTTAATGTTAATG 1268
DB 1358 TGGCGGGGCTCGAGGCGCGATGTTAATGAGCAAGCAAGCAAGCAAGCAAGCA 1417
QY 1269 ACAAGTGTGTTCTTCAATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 1328
DB 1418 GCAGGGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1477
QY 1329 TAGAGTCCAAAGCTCATTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 1388
DB 1478 GCGAGGCGCGCAGGCGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1537
QY 1389 TATGCTTTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 1448
DB 1538 CATGCTTTTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1597
QY 1449 TGCTACTGATTTCCAGATTA 1470
DB 1598 CGCACACAGATCCCGACTGA 1619

RESULT 10
AAK51495
ID AAK51495 standard; cDNA; 2523 BP.
XX AAK51495;
AC
XX
DT 06-NOV-2001 (first entry)
XX
XX Human polynucleotide SEQ ID NO 40.
DE Human; cytokine; cell proliferation; cell differentiation; gene therapy;
XX vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
XX tissue growth factor; immunomodulatory; cancer; leukemia;
XX nervous system disorder; arthritis; inflammation; ss.
OS Homo sapiens.
XX
XX MO200157190-A2.

XX 09-AUG-2001.
PD
XX
PF 05-FEB-2001; 2001MO-US004098.
PR 03-FEB-2000; 2000US-00496914.
PR 27-APR-2000; 2000US-00560875.
PR 20-JUN-2000; 2000US-00598075.
PR 19-JUL-2000; 2000US-00620325.
PR 01-SEP-2000; 2000US-00654936.
PR 15-SEP-2000; 2000US-00663561.
PR 20-OCT-2000; 2000US-00693325.
PR 30-NOV-2000; 2000US-00728422.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Dmanac RT, Aundi V, Zhou P, Xu C, Cao Y,
PI Ma Y, Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;
PI Xue AJ, Yang Y, Wejhrman T, Goodrich R;
XX
DR WPI; 2001-476283/51.
DR P-PSDB; AAM78362.
XX
PT Nucleic acids encoding polypeptides with cytokine-like activities, useful
XX in diagnosis and gene therapy.
PS
XX Claim 1; Page 603-606; 6221pp; English.
XX
CC The invention relates to polynucleotides (AAK51456-AAK53435) and the
CC encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to
CC cytokine, cell proliferation or cell differentiation or which may induce
CC production of other cytokines in other cell populations. The
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC peptide therapy. The polypeptides have various cytokine-like activities,
CC e.g. stem cell growth factor activity, haemopoiesis regulating
CC activity, tissue growth factor activity, immunomodulatory activity and
CC activin/inhibin activity and may be useful in the diagnosis and/or
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111
CC (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the
CC sequence listing were missing at the time of publication
XX
SQ Sequence 2523 BP; 521 A; 856 C; 713 G; 433 T; 0 U; 0 Other;
Query Match 41.2%; Score 616; DB 4; Length 2523;
Best Local Similarity 64.2%; Pred. No. 1-4e-137;
Matches 925; Conservative 0; Mismatches 515; Indels 0; Gaps 0;
QY 6 CTTGATTCAGCTGAAGAAAGAAATTCAGCTTTTGGAAATAGACAGCTGCTCAAGCTTT 65
DB 107 CCGTATCCAGCTGAGAGAGAACCCGCTTCTGGAAACCCGAGGAGCTGAGGCCCT 166
QY 66 GGATGTTGCTAGAGAGTTGCAACCAATTCAACTGCTGCTAGAGATGTTATTTGTTT 125
DB 167 GATGCTGCAAGAGCTGACGCCATCCAGAAAGTCCCAAGACCTTATCTTCT 226
QY 126 GGGTATGATGATGAGTTCCTCACTGTTACTGCTACTAGAAATTTTGAAGGCTCAATGA 185
DB 227 GGGCATGAGGTTGGGGGTGCCACGCTGACCAACGACCAACGAGATCTTAAAGGGGCAAGAA 286
QY 186 TGGTAAAGTTGGGTCAGAAATCTCAATGCTATGATCAATTTCCATACGTTGCTTTGTC 245
DB 287 TGGCAAACTGGGGCTGAGACGCCCTTGCCATGACCGCTTCCATACCTGCTGCTGTC 346
QY 246 TAAAGCTTAACTAGTTGATAGACAGTTCCAGATTCTGCTGCTACTGCTTACTT 305
DB 347 CAAGCAATCAATGTTGACAGACAGGTTCCAGACAGCGACCAAGCCAGGCTTACTT 406
QY 306 GTGTGTTTAAAGGTTAAATTCAGAACTATTGTTGTTCTGCTGCTAGATCAATCA 365
DB 407 GTGGGGGTCAAGGCACTTCCAGACCATGCGCTTGAAGTGCAGCGCCGCTTTAAACA 466
QY 366 ATGTAATCTACTAAGAGTAAAGTTACTTCTGTTATTAATAGAGCTAAGAGGCTGG 425

DB 467 GTGCAACAGACACCGCGCAATGAGTCACTCCGTAATGAACCGGGCCAGAACGACAG 526
QY 426 TAAAGCTGTTGGTGTGTTTACTACTACTAGAGTTCAACATGCTTCTCCAGCTGTGCTTA 485
DB 527 AAAGTCAGTAGAGAGTGTGACCAACAGCGGTGACAGCGCTGCGACCGGACCTTA 586
QY 486 CGCTCATCTGTTAATAGAAATTTGGTACTGATGCTGATTTTCCAGCTGATGCTCAAA 545
DB 587 GCGACACAGTGAACCCCACTGGTACTCAGATGCTACATGCTGCTGCTGACCGCGCA 646
QY 546 GAATGTTGTCAGATATTTGCTGCTCAATTTGTTTACAAATGATATTTGATTTT 605
DB 647 GGAAGGGGTGCCAGACATTCGCCACTCACTCTCCAACTGACATTTGACGATCTCT 706
QY 606 GGGTGTGTAGATATGATCATGTTTCCAGAAAGTATCTCAAGATCCAGATCCAGATGA 665
DB 707 TGGCGGAGGCGCAAGTACATGTTTCCATGAGGAGCCCAAGACCTGAGTACCCAGCTGA 766
QY 666 TGCTTCTGTTAATGTTGTTAAGAAAGATTAACAAATTTGGTTCAAGATGCGCAAGCTTA 725
DB 767 TCCACCAAGATGGAATTCAGCTGACGGAAGAACTGTGACAGAAATGCTGGCAAA 826
QY 726 GCATCAAGTGTCTCAATATGTTGGAAATAGAACTGTTTGGCAAGCTGCTGATGATTC 785
DB 827 GCACCAAGGTGCTGTGATGTTGTGGAACCGCACTGAGCTCATGACAGGCTCCCTGACCA 886
QY 786 TAGTGTACTCATTTGATGAGGTTGTTTGAACCAAGCTGATATGAATTAATGTTCAACA 845
DB 887 GTCTGTGACCATCTCAATGAGGCTCTTTGAGCCCGGAGACAGAAATATGATGATCCAG 946
QY 846 AGATCATCTAAGATGATCCAACTTTGGCTGAATGACGAACTGCTTGGCAAGTTTGTGTC 905
DB 947 AGACCCCACTGACACCTCTCTGATGAGATATACAGAGCTGCTGCTGCTGCTGAG 1006
QY 906 TAGAAATCCAAAGAGTTTTCATCTGTTTGAAGGTTGAAATGATGATGATGATCA 965
DB 1007 CAGGAACCCCGGCTTCTACCTTTGTTGAGAGGGGGCGGATGACATGATGATCA 1066
QY 966 TGAATGTAAGCTTATATGCTTGTGATGACGAACTTATATGTTATATGATGATGCTTA 1025
DB 1067 TGAGGTTGTGCTTACAGGACCTCACTGAGGCGGTATGTTTCCAGACCGCATTTGAGAG 1126
QY 1026 GCTAATGAATTTGATCTGTAATTTGATGATCTTATTTGTTGTTGCTGATCATGATCA 1085
DB 1127 GCGCGGCACTGACAGAGAGAGACGCTACCTGTCACCGCTGACCTGCCA 1186
QY 1086 TGTCTTCTCTTGTGTTGTTACACTTTGAGAGTACTTCTATTTTGTGTTGCTCAGG 1145
DB 1187 TGTCTTCTCTTGTGTTGTTACACTTTGAGAGTACTTCTATTTTGTGTTGCTCAGG 1246
QY 1146 TAAAGCTTGAATGATGATTTTCACTTCTATTTTGTATGATGATGATGATGATGATG 1205
DB 1247 CAAGCTCAAGAGCAAGAGCTTACAGCTTCTATCTTATGAGGACCGGCTAGT 1306
QY 1206 TTTGGTGTGTTGTTCTAGACAGATGTTAATGATGATGATGATGATGATGATGATGAT 1265
DB 1307 GTTCACTCAAGGCTGTGAGACAGACGTGATGATGATGATGATGATGATGATGATGAT 1366
QY 1286 ACAACAAAGCTGCTTCTCAATTTGCTAGTAAATCACTCATGTGTGTGATGATGATG 1325
DB 1367 GCACAGAGCGGCGGTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1426
QY 1326 TGCTAGAGTGTCAACAAGCTATTTGTTGTTCAATGTTGTTCAAGAAACCTTTGTTGCTCA 1385
DB 1427 TGCAGGCGGCGCGAGGCGGACCTGTGTGATGATGATGATGATGATGATGATGATGAT 1486
QY 1386 TATTATGCTTTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 1445
DB 1487 TGTCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1546

ADN43057
ID ADN43057 standard; cDNA; 1702 BP.
XX
AC ADN43057;
XX
DT 29-JUL-2004 (first entry)
XX
DE Human secreted protein SECP-43 cDNA.
XX
XX cytostatic; anorectic; immunosuppressive; gene therapy; SECP-antagonist;
KM SECP-agonist; secreted protein; SECP; autoimmune disorder; obesity;
KM cancer; human; SECP-43; gene; ss.
XX
XX Homo sapiens.
XX
PN MO2004037987-A2.
XX
XX 06-MAY-2004.
XX
PF 22-OCT-2003; 2003MO-US033491.
XX
XX 22-OCT-2002; 2002US-0420720P.
PR 07-NOV-2002; 2002US-0425207P.
PR 15-NOV-2002; 2002US-0426679P.
PR 19-NOV-2002; 2002US-0427871P.
PR 06-JAN-2003; 2003US-0438551P.
PR 17-JAN-2003; 2003US-0441144P.
PR 27-JAN-2003; 2003US-0443135P.
XX
XX (INCY-) INCYTE CORP.
XX
PI Baughn MR, Becha SD, Bhatia US, Blake JJ, Burrill JD, Chawla NK;
PI Chien D, Elliott VS, Emerling BM, Favero KD, Hafalla AJA;
PI Harmsen BM, Ho A, Ison CH, Khare R, Lee S, Lee ST, Lu DM;
PI Marquis JP, Mirage J, Nguyen DB, Rankumar J, Richardson TW;
PI Swarnakar A, Tang TY, Tran UK, Wang JT, Yue H, Zheng W;
XX
DR WPI; 2004-365505/34.
XX
XX P-PSDB; ADN42982.
XX
XX New human secreted protein (SECP) polypeptide, useful for preparing a
PT composition for treating a disease associated with decreased expression
PT or overexpression of functional SECP e.g., autoimmune disorders, obesity
PT or cancer.
XX
XX Claim 5; SEQ ID NO 118; 289pp; English.
XX
XX The invention describes an isolated human secreted protein (SECP).
CC polypeptide. Also described are: an isolated polynucleotide encoding the
CC polypeptide; a recombinant polynucleotide comprising a promoter sequence
CC operably linked to the polynucleotide; a cell transformed with the
CC recombinant polynucleotide; a transgenic organism comprising the
CC recombinant polynucleotide; a method of producing the polypeptide; an
CC isolated antibody that specifically binds to the polypeptide; a method of
CC detecting a target polynucleotide in a sample; a method for treating a
CC disease or condition associated with decreased expression or
CC overexpression of functional SECP; a method of screening a compound for
CC effectiveness as an agonist or antagonist of the polypeptide or in
CC altering expression of the target polynucleotide; a method of screening a
CC compound that specifically binds to, or that modulates the activity of,
CC the polypeptide; a method of assessing toxicity of a test compound; a
CC diagnostic test for a condition or disease associated with the expression
CC of SECP in a biological sample; a method of diagnosing a condition or
CC disease associated with the expression of SECP in a subject; a
CC composition comprising the antibody and a carrier, or the polypeptide, or
CC agonist or antagonist compound and an excipient; a method of preparing a
CC polyclonal or monoclonal antibody; a method of detecting the polypeptide
CC in a sample; a method of purifying the polypeptide; a method of
CC generating an expression profile of a sample that contains
CC polynucleotides; and an array comprising different nucleotide molecules
CC affixed in distinct physical locations on a solid substrate, where at
CC least one of the nucleotide molecules comprises a first oligonucleotide
CC or polynucleotide sequence specifically hybridizable with at least 30

CC contiguous nucleotides of the target polynucleotide. The polypeptide is
CC useful for preparing a composition for diagnosing or treating a disease
CC or condition associated with decreased expression or overexpression of
CC functional SECP e.g., autoimmune disorders, obesity or cancer. This
CC sequence encodes a human secreted protein.

XX
SQ Sequence 1702 BP; 339 A; 562 C; 513 G; 288 T; 0 U; 0 Other;

Query Match 41.6%; Score 613.8; DB 12; Length 1702;

Best Local Similarity 64.3%; P-Id. No. 4e-137; Indels 0; Gaps 0;

Matches 921; Conservative 0; Mismatches 512; Indels 0; Gaps 0;

QY 13 CCAGCTGAAGAGAAATATCAGCTTTTGGATAGACAAAGCTCTCAAGCTTGGATGT 72
DB 150 CCAGCTGAGAGAGAGAAACCGGCTTCTGGAACCGCAGAGCTGAGCCCTGGATGT 209
QY 73 GCTAAGAGCTGCAACCAATTCMACTGCTCTAAGAAATGTTATTTTGGGTGAT 132
DB 210 GCCAAGAGCTGAGCCCACTCCAGAAAGTCCGCAAGAACCTCATCTTCTGCGCAT 269
QY 133 GGTATGGGTGTTCCACTGTACTGCTACTAGAAATTTGAAGGCTCAATGATGTAAG 192
DB 270 GGGTTGGGGGTGCGCCAGGTGACAGCCAGGATCTAAAGGGGAGAGAAATGGCAAA 359
QY 193 TTGGGTCAGAAATCTCATTTGGGTATGATCAATTTCCATACGTTGCTTGTAAAGT 252
DB 330 CTGGGGCTGAGAGCGCCCTGCGCATGACCGTTCCATCTGCTGCTGCTCAAGACA 389
QY 253 TACAAATGTTGATAGACAAAGTTCAGATTCTGCTGATCTGATCTTAACTTGTGTGT 312
DB 390 TACAATGTGAGACAGACAGGTGCGACAGCGGACGACAGCCGCTTACGCTGCGGG 449
QY 313 GTTAAAGGATATTAACAAGATATGTTGTTTCTGCTGCTGCTGATATCAATGTAAT 372
DB 450 GTCMAAGCCAACTTCCAGACCAATCGGCTTGAGTGCAGCGCCGCTTTAAACGTCAC 509
QY 373 ACTACTAGAGATTAAGTAAAGTACTTCTGTTATTAATAGAGCTAAGAGGCTGTAAGGT 432
DB 510 ACGACACGGGCAATAGATGATCTCTCGTATGATACCTGGGCCAAGCAGAGAAATGTA 589
QY 433 GTTGTGTTGTTACTACTACTAGATGTTCAACATGCTTCTCAGCTGCTGTTACGTCAT 492
DB 570 GTAGAGTGTGTGACCAACAGCGGTGACAGACGCTCCGACCGGACCTACGACAC 629
QY 493 ACTGTTAATGAATTTGTAATCTGATGCTGATTTGCCAGCTGATGCTCAAAAGATGCT 552
DB 630 ACAGTGAACCGCAACTGTGTAATCTGATGCTGATGCTGCTGCTGCTGCTGCTGCTG 689
QY 553 TGTCAAGATATTGCTGCTCAATTTGTTTCAATATGATATGATGTTATTTGGGTGT 612
DB 690 TGCAGAGACATGCGCACTGCTCATCTCCACATGACATGACATGACATGATCTTGGCGA 749
QY 613 GGTAGATGTACATGTTTCCAGAGGTAATCTCCAGATCCAGAAATCCAGATGCTTCT 672
DB 750 GCGCGCAAGTACATGTTTCCATGAGGACCCAGACCTGAGTACCAAGTATGTCAGC 809
QY 673 GTTATGTGTTTGAAGAGATGAACAAATTTGTTCAAGATGCGAAGTAAAGTCA 732
DB 810 CAGAAATGATCAGGCTGAGACGGGAGAACTGTGTCAGAAATGCTGCGCAAGCACAG 869
QY 733 GGTGCTCAATATGTTTGAATGAATGAATGCTTTGTTGCAAGCTGCTGATGTTAGTGT 792
DB 870 GGTGCTGTTATGTGTAACCGCAGTGAAGCTCATGAGCGTCTCTGAGCAGTCTGTG 929
QY 793 ACTCATTTGATGGGTTTGTGTTGAACAGCTGATATGATATGATATGTTCAACAAGATCAT 852
DB 930 ACCCATCTATAGGCTCTTTTGAAGCCGAGACAGAAATATGATATTCACGAGACCC 989
QY 853 ACTAAGATCAACTTTGCTGCTGAATGACTGAAGCTGCTTGTGCAAGTGTGCTAGAAAT 912
DB 990 ACACCTGACCCCTCCCTGATGATGAATGACAGAGGCTCCCTGCGCTGCTGACAGAAC 1049
QY 913 CCAAGAGGTTTACTTGTGTTGTAAGGTGTAAGATGATGATGATGATGATGATGAT 972

DB 1050 CCCCCGGCTTACCTCTTTGGAGGGCGCCCGCATGACCATGTCATATGAGGT 1109
QY 973 AAGCTTATATGAGCTTGAAGCTATATGTTGATATGCTATTTGCTAAGCTAT 1032
DB 1110 GGGCTTACAGGACTCATAGGGGCTCATGTTGACGAGCCATTAGAGGGGGGCG 1169
QY 1033 GAATGACTTCTGAATTTGATCTTTGATTTGGTTACTGCTGATCATGTCTTTT 1092
DB 1170 CAGCTCACGAGGAGGACACGCTGACCTGTCACCGCTGACCATCCCATGTCTTC 1229
QY 1093 TCTTTGGGTGTTACCTTTGAGAGTACTTATATTTTGGTTGGCTCAGGTAGGCT 1152
DB 1230 TCTTTGGGTGTTACCTTTGAGAGTACTTATATTTTGGTTGGCTCAGGTAGGCT 1289
QY 1153 TTGATAGTAACTTCACTTCTATTTTGTATGTATGTATGATGCTTTGGT 1212
DB 1290 CAGGACAGCAAGCTTACAGTCCATCTGTACGGCAATGGCCGGGCTACGTTCAC 1349
QY 1213 GGTGTTCTAGACCAAGATTTAATGTTACTAGTAAAGAACATCTTACAGACAA 1272
DB 1350 TCAGCGGTGACCAAGATGATGAGAGGAGGAGGAGCCCGATTACAGCAGCAG 1409
QY 1273 GGTGCTGTTCCATTTGCTAGTAACTCATGTTGTTGATGTTGCTTTTGTCTAG 1332
DB 1410 GGGCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1469
QY 1333 GGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1392
DB 1470 GGGCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1529
QY 1393 GCTTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1445
DB 1530 GCTTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1582

RESULT 12
AA078135
ID AA078135 standard; cDNA to mRNA, 1587 BP.
XX
AC AA078135;
XX
DT 24-JUL-1995 (first entry)
XX
DE Human enteric alkaline phosphatase cDNA.
XX
KW Human enteric alkaline phosphatase; homogeneous quality production;
XX clinical diagnosis; db.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..1587
FT CDS /*tag= a
XX
PN JP06284885-A.
XX
PD 11-OCT-1994.
XX
PF 02-APR-1993; 93JP-00076883.
XX
PR 02-APR-1993; 93JP-00076883.
XX
PA (TOYU) TOSOH CORP.
XX
XX MPI; 1994-36252/45.
XX DR P-PSDB; AAR63438.
XX
PT Recombinant human enteric alkaline phosphatase - for cheap and large
XX scale prodn. of homogeneous HIP.
XX
PS Disclosure; Page 3-5; 9pp; Japanese.
XX

CC AA078135 encodes AAR63438 human enteric alkaline phosphatase (HIP), using
CC the mutagenic primers described in AA078137-Q78140 the 1422, 1464 and
CC 1491 bp mutants described in AA090638-Q90640 were produced. Using
CC recombinant DNA techniques homogeneous quality HIP mutants could be
CC produced, avoiding the problems associated with poor quality labelled
CC enzymes in clinical diagnosis
XX
SQ Sequence 1587 BP; 317 A; 514 C; 491 G; 265 T; 0 U; 0 Other;
Query Match 41.4%; Score 611.2; DB 2; Length 1587;
Best Local Similarity 64.0%; Pred. No. 1.6e-136;
Matches 922; Conservative 0; Mismatches 518; Indels 0; Gaps 0;
QY 6 CTGATTTCCAGCTAAGAGAAATCCAGCTTTTGGAAATGACAGCTGCTCAAGCTT 65
DB 57 GGTATTTCCAGCTAAGAGAAATCCAGCTTTTGGAAATGACAGCTGCTCAAGCTT 116
QY 66 GATGTTGCTAAGAGAAATCCAGCTTTTGGAAATGACAGCTGCTCAAGCTT 125
DB 117 GATGTTGCTAAGAGAAATCCAGCTTTTGGAAATGACAGCTGCTCAAGCTT 176
QY 126 GGTGATGATATGGGTGTTCCACTGTTTACTGTTTAAATTTTGAAGGCTCAATGAA 185
DB 177 GGGCGATGGGTGGGGGGTGGCCAGGTGACAGCCAGATCTTAAAGGGGAGAAAGAA 236
QY 186 TGGTAAATGGGTGCTCAGAACTCCATTTGGCTATGATGATCAATTTTCAATGCTTGTG 245
DB 227 TGGCAACTGGGGCTTGAAGCGCCCTTGGCATGAGCGCTTCCATCTGCTGCTGCTG 296
QY 246 TAAAGTCTAAGATTTGTAAGCAAGTTCCAGATTTCTGCTGCTGCTGCTGCTGCT 305
DB 297 CAAGCATACATATGATGACAGCAGGTGCTCAGACAGCCAGCAGCAGCGCTTACCT 356
QY 306 GTGTGCTGTTAAGGTAATTTACAGAACTATTTGCTTCTGCTGCTGCTGCTGCTGCT 365
DB 357 GTGCGGGTCAAGGCGCACTTCCAGACCATGCTGCTGCTGCTGCTGCTGCTGCTGCT 416
QY 366 ATGTAATCTACTAGGTAATGAAATTAATTTCTGTTTAAATGAGCTAAGAAAGCTG 425
DB 417 GTGCAACAGACAGCGCGCATGAGTATCTCCGTATGAAACGGGCGCAAGCAAGAG 476
QY 426 TAAAGCTGTTGCTGTTTACTACTACTAGATTTCAATGCTTCTGCTGCTGCTGCT 485
DB 477 AAAGTCAAGAGAGTGTGACCAACAGCGGTGACAGGCTTCCAGCGCGGACCTTA 536
QY 486 CGCTATATCTGTTAATGAAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 545
DB 537 CGCACACAGTGAACCGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 596
QY 546 GAATGTTGCTAAGATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 605
DB 597 GAGAGGGTCCAGAGCATGCGCATCTAGCTATCTCCAAATGAGCATTTGAGTATCT 656
QY 606 GGTGTTGCTAAGATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 665
DB 657 TGGCGAAGGCGCAAGTATGTTTCCATGAGGAGCCCGAGACCTTGATGCCAGCTGA 716
QY 666 TGGCTTCTGTTAATGATTTGAAAGGATTAAGAAATTTGTTGAAAGTGAAGTGA 725
DB 717 TGGCGAAGGCGCAAGTATGTTTCCAGAGGATTTGTTGAAAGTGAAGTGAAGTGA 776
QY 726 GCATCAAGGCTCAATATGTTTGAATGAACTGTTTGGTCAAGCTGCTGATGATTC 785
DB 777 GCAACAGGTGCTGCTGATGTTGTAACCGCATCTAGCTCATGCAAGGCTGCTGGA 836
QY 786 TAGTGTACTATTTGATGAGGTTGTTGTAACCACTGATATGAAATGTTTGAACA 845
DB 837 GTCTGTAACCATCTCATGAGGCTCTTTGAGGCCCGAGACAGAAATATGATCTCG 896
QY 846 AGATCATATTAAGATTTCAACTTTGGTGAATGACTGAGAGCTGTTGCAAGTTTGT 905
DB 897 AGACCCCACTGAGACCTCTCCCTGATGATGACAGAGGCTGCCCTGCGCTGCTGAG 956

| | | | |
|----|------|---|------|
| QY | 906 | TAGAATCCAAAGAGGTTTTTAACTTGTGTGGTGAAGGCTGTGAATGTATCAATGGCATCA | 965 |
| DB | 957 | CAGAAACCCCGGGGCTTCACCTCTTTGTGAGGGCGGCGGATCGACATAGTGTATCA | 1016 |
| QY | 966 | TGATGCTAAGGCTTATATATGCTTTGACTGAAAGCTATTAATGTTTGAATATGCTATTGCTAA | 1025 |
| DB | 1017 | TGAGGGTGTGGCTTACAGAGGCAGTCACTGAGGCGGCTATGTTCCAGACGGCATTTGAGAG | 1076 |
| QY | 1026 | GAGCTATGAAATGAATTGCTGAATGGATCTTGAATTTGGTATCTGCTGATCATATGCA | 1085 |
| DB | 1077 | GCGGGGCGAGCTCACACGAGAGAGAACGCTGACCTCGTCAACCGCTGACACTCCCA | 1136 |
| QY | 1086 | TGTTTTTTCTTTGGTGGTTACCTTTGAGAGGTACTTCTAATTTTGGTTTTGGCTCCAG | 1145 |
| DB | 1137 | TGCTCTTCCTTTGGTGGCTACACCTTCGAGGGAGCTCACTTCCTGGGTTGGCCCCAG | 1196 |
| QY | 1146 | TAAAGCTTTGATATATAGTCTTAACTTCAATTTTGTATAGTAAATGCTCCAGGTTATGC | 1205 |
| DB | 1197 | CAGAGCTCAGACACACAAAGCTTACAGCTCCATCTGTACGGCAATGGCCGGGGTACGT | 1256 |
| QY | 1206 | TTTGGGTGTGTTCTTAGACCAAGATGTTAATGTATAGTACTAATGAAACCATCTTACAG | 1265 |
| DB | 1257 | GTTCAACTCAGGGCGTGGCAGCAGAGGTGAATGAGAGCAGAGCGGAGACCCCGATTACCA | 1316 |
| QY | 1266 | ACAACAACACTGTGTTCCATTGGCTATAGTAAATCATATGTGTGTAAGATGTTGCTGTTTT | 1325 |
| DB | 1317 | GCAAGAGCGGGGGGCGCCCTGTCTGTCCGAACCCACGGAAGCGAAGACGTGGGGGTGTT | 1376 |
| QY | 1326 | TGCTAAGAGGTCCACAAAGCTCAATTTGGTTCATGTGTTCATGATCMAAGAAATTTTGTGTCTCA | 1385 |
| DB | 1377 | TGCGGGCGGCGCGAGCGCACAATGTGTCAATGTGTGTGACAGAGCAGACCTTCGTATGGGCA | 1436 |
| QY | 1386 | TATATATGCTTTTGTGGTGTGTGTAACATACACTGATGTGTAATTTTCCAGCTCCAGC | 1445 |
| DB | 1437 | TGTATAGGCTTCGTGCTGCTGTGAGAACCCCTTACACGGGCTGTGAGCACTGTGGGCTTCCCGC | 1496 |

| | |
|----|--|
| XX | RESULT 13 |
| XX | AAT27384 |
| ID | AAT27384 standard; DNA; 1587 BP. |
| XX | |
| AC | AAT27384; |
| XX | |
| DT | 20-SEP-1996 (first entry) |
| XX | |
| DE | Human alkaline phosphatase coding sequence. |
| XX | |
| KW | alkaline phosphatase; label; antibody; IgG; fusion protein; chimera; |
| RN | immunoassay; ds. |
| XX | |
| OS | Homo sapiens. |
| XX | |
| FH | Key |
| FT | CDS |
| FT | Location/Qualifiers 1..1587 /*tag= a /product= "Alkaline_phosphatase" |
| FT | |
| XX | |
| PN | JP08070875-A. |
| XX | |
| PD | 19-MAR-1996. |
| XX | |
| PF | 05-SEP-1994; 94JP-00211035. |
| XX | |
| PR | 05-SEP-1994; 94JP-00211035. |
| XX | |
| PA | (TOYJ) TOSOH CORP. |
| XX | |
| DR | WPI; 1996-203155/21. |
| DR | P-PsDB; AAR91805. |
| XX | |
| PT | Recombinant alkaline phosphatase (AP)-antibody fusion protein - comprises |
| PT | AP fused downstream of antibody heavy or light chain, useful as |
| PT | immunoassay reagent. |

| | |
|----|---|
| PS | Example 1; Page 10-12; 44pp; Japanese. |
| XX | |
| CC | The gene coding for human alkaline phosphatase is fused downstream of a |
| CC | gene coding for either the variable and CH1 regions of an antibody heavy |
| CC | chain or an antibody light chain. Coexpression of the H- and L-chain |
| CC | sequences, one of which is fused to the AP gene, results in production of |
| CC | AP-labellled antibodies suitable for use in immunoassays. The present |
| CC | sequence codes for human AP |
| XX | |
| SQ | Sequence 1587 BP; 317 A; 515 C; 490 G; 265 T; 0 U; 0 Other; |
| | |
| | Query Match 41.4%; Score 611.2; DB 2; Length 1587; |
| | Best Local Similarity 64.0%; Pred. No. 1.6e-136; |
| | Matches 922; Conservative 0; Mismatches 518; Indels 0; Gaps 0 |
| Oy | CTTGATTCACAGCTGAGAAGAAATCCAGCTTTTGGAAATAGACAAGCTGTCAAGCTTT 65 |
| Db | 6 CGTATGCCACTAGAGAGAACCGGCCTTCGGAAACCGCAGCGAGCTGAAGCCCT 116 |
| Oy | 66 GGATGTTGCTAAGAAATTGCAACCATAATCTGCTCTAAGAAATGTAATTTTGT 125 |
| Db | 117 GGATGCTGCCAAGAAAGCTGACGCCCATCAAGAGGTCCCAAGAACTCATCTCTCC 176 |
| Oy | 126 GGGGTATGSGTATGGGTGTTCCAAGTCTTACTGCTACTAGAAATTTTGAAGGGTCAATGA 185 |
| Db | 177 GGGCGATGGTGTGGGGGTGCCCGGTACAGCCACAGATCTTAAAGGGCAGAAAGNA 236 |
| Oy | 186 TGGTAAAGTGGAGTCCAGAAATCCATTTGGCTATGGATCAATTTCCATAGCTTTGTC 245 |
| Db | 237 TGGCAAATGGGGCTGAGAGGCCCTTGCCATGGAACCGCTTCCATATCTGGCTGTG 296 |
| Oy | 246 TAAAGCTTACATGTTGATAGACAAGTTCCAGATTTCTGCTGACTCTACTGCTTACTT 305 |
| Db | 297 CAAGCATACATGTGACAGACAGAGTCCAGACAGCACAGCACAGCACAGGCTTACCT 356 |
| Oy | 306 GTGTGSGTAAAGGGAATTAACAGACTATTTGGTGTCTTCTGCTGTACTAATACATCA 365 |
| Db | 357 GTGGGGGTCAAGGCCCAATTCACAGACCATGGCTTAGTGCACGCGCCGCTTTAACCA 416 |
| Oy | 366 ATGTAAATCTACTAGAGGTATGAAAGTACTTCTGTTATTAATAGAGCTAAGAAAGCTGG 425 |
| Db | 417 GTGCACACGACAGCGGCATGAGGTATCTCCGTATGAACCGGCCAAGCAACGACG 476 |
| Oy | 426 TAAAGCTGTGGTGTGTTTACTACTAGAGTTCAACATCTTCTCCAGCTGTGCTTA 485 |
| Db | 477 AAATGCTAGTAGAGTGTGACCAACAACGGGTGAGACGCGCTGCCAGCGGACGCA 536 |
| Oy | 486 CGCTCATACTGTTAATAGAAATGGTACTGTATGCTGATTTGCCAGCTGATCTCAAAA 545 |
| Db | 537 CGCACACACAGTGAACCGCAACTGGTACTCAGATGCTGACATGCTCGCTCAGCCCCCA 596 |
| Oy | 546 GAATGTTGTCAATATTTGCTGCTCAATTTGGTTTCAATATNGATATGTAATGTAATTT 605 |
| Db | 597 GGAGGGGTGCGAGGACATCGCACTCAGCTATCTTCAACATGACATTTAGAGTATCTCT 656 |
| Oy | 606 GGGTGTGSGTAAAGTATGATAGTTTCCAGAAGTACTCAATCCAGATACCCAGATGA 665 |
| Db | 657 TGGCGAGAGCCGCAAGTACATGTTTTCCATGGGACCCCAACCTGTAGTACCCAGCTGA 716 |
| Oy | 666 TGCTTCTGTATATGSGTGTAGAAAGATAGCAAAATTTGGTTCAAGATGGCAAGCTAA 725 |
| Db | 717 TGCCAGCCAGAAATGAATCAGGCTGTGACGGGAAGAACCTGGTGCAGGAATGGCTGGCAA 776 |
| Oy | 726 GCATCAAGSGCTCAATATGTTTGGAAATGAAACGTGCTTTGTGCAAGCTGTGAAGATTC 785 |
| Db | 777 GCACCAAGGGTCCGTGATATGTGTGAACCGGACTGAGCTCATGACGGGTCCCTGGACCA 836 |
| Oy | 786 TAGTGTTACTATTTGAATGGGTTTGTGTTGAACCAAGCTGATATGAAGTATTAATGTTCA 845 |
| Db | 837 GTCTGTACCATCTCATGGGCTCTTTGAGCCCGGAGACAGAAATATGAGATCTCTCG 896 |
| Oy | 846 AGATCATACTAAGATCCAACTTTGGCTGAATGATCAAGAGCTGCTTTGCAAGTTTGTG 905 |

DB 897 AGACCCCACTGAGCCCTCCCTGATGAGATGACAGAGCGCTGCCCTGGCTGAG 956
QY 906 TAGAATCCAAAGGCTTTTACTGTTGTTGTAAGGTGGTAAGTAATGATCATGTATCA 965
DB 957 CAGGAACCCCCGGGCTTCTACCTCTTGTGGAGGGCGCGCATGACCATGTGTATCA 1016
QY 966 TGAATGTAAGGCTTATATGAGCTTTGACTGAACTATTTATGTTATGATATGCTATTGCTAA 1025
DB 1017 TGAAGGTGGCTTACCAGGCACTCACTAGGGGCTCATGTTGACAGAGCCATTAGAG 1076
QY 1026 GCGTAATGATGACTTCTGAAATGGAATCTTTGATTTGTTACTGCTGATCATAGTCA 1085
DB 1077 GCGGGGCCAGCTCACCGAGGAGACAGCTGACCCCTGCTACCGCTGACACTCCCA 1136
QY 1086 TGTCTTTCTTTGTTGGTGTACCTTTGAGAGTACTTCTATTTTGGTTGGCTCAG 1145
DB 1137 TGTCTCTCTTTGGTGGCTACCTTGGAGGAGCTCATCTTGGGTTGGCCCCAG 1196
QY 1146 TAAGCTTTGATGATGATGATCTTACACTTCTATTTGTAATGTAATGTCAGGTTATGC 1205
DB 1197 CAAAGCTCAGACAGAAAGCCATACGTCATCTGTACGCAATGGCCCCGGCTACGT 1256
QY 1206 TTTGGGTGTGTTCTTACACAGAGTGAATGTAATGTAATGTAATGTAATGTAATGTAATG 1265
DB 1257 GTTCAACTCAGGCGGTGCGACAGACGTAATGAGACGAGAGCGGAGCCCCGATTACCA 1316
QY 1266 ACAACAAGCTGCTGTTCCATTTGGCTGTAAGTAATGTAATGTAATGTAATGTAATGTAATG 1325
DB 1317 GCAGCAGGCGGCGGTGCTCCCTGCTGTCAGACCCAGAGGAGGAAGTGGCGGTGTT 1376
QY 1326 TGTAGAGGTGCAACAAGCTCATTTGGTGTGTTCAAGAAAGAACTTTTGTGCTCA 1385
DB 1377 TCGGCGGCGCGCGAGCGCACTGCTGATGCTGTGTCAGAGAGAGCTTGTAGCGCA 1436
QY 1386 TATTATGCTTTTGTGCTGTTGTGTGAACCAATCACTGATTTGTAATTTGCCAGCTCAGC 1445
DB 1437 TGTCTATGCGCTTGTGCTGCTGCTGTGAGCCCTACACAGGCGCTGCACTGGCCTCCCCGC 1496

RESULT 14

ADP45468
ID ADP45468 standard; DNA; 2516 BP.

AC ADP45468;

DT 12-FEB-2004 (first entry)

DE Human vasodilator-responsive gene #65.

KW Vasodilating substance; vasodilation response gene; vasodepressor;

KW antihypertensive drug; vasodilator-responsive gene; hypotensive;

KW vasodilator; human; gene; de.

OS Homo sapiens.

PN JP2003310272-A.

PD 05-NOV-2003.

PF 26-APR-2002; 2002JP-00126514.

PR 26-APR-2002; 2002JP-00126514.

PA (TANAKA T.

PA (ASAH) ASAH KASEI KK.

PA (SUMO) SUMITOMO SEIYAKU KK.

DR WPI; 2004-015357/02.

Obtaining vasodilating substance by contacting test substance with
PT vascular smooth muscle cell, comparing change in gene expression and
PT selecting vasodilator which increases expression of vasodilation response

PT genes.
XX Claim 6; SEQ ID NO 65; 98bp; Japanese.
PS The present invention relates to a method for obtaining a vasodilating
CC substance which increases expression of vasodilation response gene, and
CC obtaining a vasodepressor which increases or decreases the expression
CC level of vasodilation response genes. The method is useful for obtaining
CC vasodilating substance which increases/decreases expression of
CC vasodilation response genes. The vasodepressor substance obtained by the
CC method of the invention is useful as an antihypertensive drug. The method
CC is also useful for identifying the specific vasodilator response gene.
XX The present sequence represents a human vasodilator-responsive gene.
SQ Sequence 2516 BP; 517 A; 853 C; 712 G; 434 T; 0 U; 0 Other;
Query Match 41.4%; Score 611.2; DB 12; Length 2516;
Best Local Similarity 64.0%; Pred. No. 1.9e-136;
Matches 922; Conservative 0; Mismatches 518; Indels 0; Gaps 0;
QY 6 CTGATTCACAGTGAAGAAATCCAGCTTTTGGAAATGACAGCTGCTCAAGCTTT 65
DB 102 CTTATCCCTCAGCTGAGAGAAACCGGCTTCTGGAACCGCAGGAGCTGAGGCCCT 161
QY 66 GATGTTGCTAAGAAAGTTGCAACCAATTCAAACTGCTCTAAGAAATGTTATTTGTTT 125
DB 162 GATGCTCCCAAGAAAGCTGCAAGCCATTCAGAAAGTGGCCAAAGAACTCATCTTCTCT 221
QY 126 GGTGATGTAATGGGTGTTCCAACTGTTACTGTAATGAAATTTGAAGGGTCAATGAA 185
DB 222 GGGCGATGGTGGGGGGTGGCCAGGTGACAGCCAGAGATCTTAAAGGGGAGAAAGAA 281
QY 186 TGTGTAAGTTGGGTCCAGAAATCTCATTTGCTATGATGATCAATTCATTCCTGTTGTC 245
DB 282 TGGCAACTGGAGGCTTGAGCGCCCTGGCCATGACCGCTTCCATACCTGGCTCTGTC 341
QY 246 TAAAGCTTCAATGTTGATGACAAAGTTCCAGATTTGCTGATGCTGCTACTTACTT 305
DB 342 CAAGCATACATGTTGACACACAGTGTCCAGACAGGCGCAACAGCCAGCGCTTACT 401
QY 306 GTGTGTTTAAAGGTAAATTAACAATTAATTTGCTGCTGCTGCTGATACATCA 365
DB 402 GTGGGGGTCAAGGCCCAATTCAGACCATGCGCTTGAAGTCAACCGCCGCTTTAAACA 461
QY 366 ATGTAATCTACTAGAGGTAAATGAAATTAATCTTCTGTTATTAATGAGTAAAGGCTGG 425
DB 462 GTGCAACAGACGCGCAATGAGTATCTCGTGAAGAACCGGCGCAAGCAGAG 521
QY 426 TAAAGCTGTTGTTGTTTACTACTAGAGTTCAACATGCTTCTCAGCTGGTGTGA 485
DB 522 AAAGTCAGTAGAGTGGTGAACCAACAGGGGTGACAGCGCTCGCAGCGGACACTA 581
QY 486 CGCTCATGCTTAAATGAAATTTGTAATCTGATGCTGATTTGCCAGCTGATGCTCAAAA 545
DB 582 CGCACACAGTGAACCGCACTGTACTCAGATGCTGACATGCTGCTCAGCGCCCA 641
QY 546 GAATGTTGCAATATTTGCTGCTCAATTTGTTTAAATTAATGATTAATGATTTT 605
DB 642 GAGGGGTGCGAGACATTCGCACTCAGCTATCTTCAACATGAGACATTCGAGTCT 701
QY 606 GGTGTGTGTAATGTAATGATTTTCCAGAAAGTACTCCAGATCCAGAAATCCAGATGA 665
DB 702 TGGCGAAGGCGGCAAGTATGTTTCCCATGAGGAGCCAGACCTGATGATCCAGCTGA 761
QY 666 TGTCTTCTGTTATGTTGTTGAAGAAAGTAAAGCAAAATTTGTTCAAGATGCAAGCTAA 725
DB 762 TGCAGCCAGATGAAATCAGGCTGAGCGGGAAGAACTGGTGAAGAAATGGCTGAGAAA 821
QY 726 GCATCAAGGTGCTAATATGTTTGAATAGAACTGTTTGTGCAAGCTGATGATTC 785
DB 822 GCACAGAGGTGCTGATGTTGTAACCGCATGAGCTCATGAGAGCGCTCGGAGCA 881
QY 786 TAGTGTACTCATTTGATGGGTTTGTGAAACGAGCTGATATGAAATGTTATCAACA 845

Db 702 TGGCGAGGAGCCGCAAGTACATGTTTCCATGGGGACCCCGAGACCTGAGTACCCAGCTGA 761
QY 666 TGGCTCTGTTAATGCTGTAGAAAGATTAAGCAAAATTTGGTTCAGAAATGGCAAGCTAA 725
Db 762 TGGCAGCCAGAAATGGAATCAGGCTGAGCGGAAAGAACTGTGTCAGAAATGGCTGGCAAA 821
QY 726 GCATCAAGGTGCTCATATGTTTGAATGAATGCTTTGTGCAAGCTGCTGATGATTC 785
Db 822 GCAACGGGTGCTGTGATGTGTGAACCGCACTGAGCTCATGCAAGCGTCCCTGAGCCA 881
QY 786 TAGGTACTCATTTGATGAGGTTTGTGTAACCGCTGATATGATATATGTTCAACA 845
Db 882 GTCTGTGACCACTCATATGAGGCTCTTTGAGCCCGAGACAGAAATATGATCTCCG 941
QY 846 AGATCACTACTAAGATCCAACTTTGGCTGAATGACTGAAGCTGCTTTGCAAGTTTGTG 905
Db 942 AGACCCCACTGAGACCTCCCTGATGAGATGACAGAGGCTGCCCTGCGCTGAG 1001
QY 906 TAGAAATCCAAAGGTTTACTTGTGTTGTAAGGTGTAAGTATGATCATGTGATCA 965
Db 1002 CAGGAAACCCCGGCTTCTACTCTTTGTGAGGCGCGCCGATGACCATGTCATCA 1061
QY 966 TGAATGTAAGGCTTATATGACTTTGAAGCTATATGTTGATATGCTAATGCTAA 1025
Db 1062 TGAAGGTGTGGCTTACAGGAGATCACTGAGCGGTCAITGTCAGACGCCATGAGAG 1121
QY 1026 GGCATAATGAATGACTTCTGAATGGAATGACTTTGTTTGTACTGCTGATCATAGTCA 1085
Db 1122 GGGGGGCCAGCTCACAGGAGAGAGACGCTGACCTGTGACCGCTGACCACTCCCA 1181
QY 1086 TGTCTTTCTTTTGTGTTGTTTACACTTTGAGAGGTACTTCTATTTTGTGTTGCTCCAG 1145
Db 1182 TGTCTTCTCTTTGTGTTGCTTACACTTTGAGAGGAGCTCATTTGGGTTGGCCCCAG 1241
QY 1146 TAAAGCTTTGATATGATAGTCTTACACTTCTATTTTGTATGTAATGTCAGGTTATGC 1205
Db 1242 CAAAGCTCAGAGACAGCAAGCTTACAGTCCATCTGTACGGCAATGCCCGGGTACGT 1301
QY 1206 TTTGGGTGTTGTTCTAGACCAAGATGTTAATGTAATGTAATGTAATGTAATGTAATG 1265
Db 1302 GTTCAACTCAGGGGTGCGACCAAGCTGAATGAGCGAGCGGAGCCCGATTACCA 1361
QY 1266 ACAACAAGCTGCTGTTCCATTTGCTAGTGAATCTCATGAGTGAAGATGTTGCTGTTT 1325
Db 1362 GCAAGCAGGCGGCGGTGCTGCTGTCAGAACCCAGAGGCGAAGACGTGGCGGTGTT 1421
QY 1326 TGGTAGAGTCCAAAGCTCATTTGTTCAATGTTCAATGTTCAATGTTCAATGTTCAATG 1385
Db 1422 TGGCGCGGCGCGCAGCGCAGCTGATGATGTTGTCAGAGCAGAGCTTGTAGCGCA 1481
QY 1386 TATTAATGCTTTTGTGCTGTTGTGTGTAACCATACATGATTTGATTTTGGCAGCTCCAG 1445
Db 1482 TGTCAATGCTTGTGCTGCTGCTGTGAGGCCCTTACAGGCTGCGACCTGCGCTCCCGC 1541

Search completed: October 20, 2004, 06:32:36
Job time : 774 secs

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OM nucleic - nucleic search, using sw model

Run on: October 19, 2004, 10:21:12 : Search time 138.5 Seconds

(without alignments)
7574.905 Million cell updates/sec

Title: US-09-911-132a-5

Perfect score: 1476
Sequence: 1 gattcttcgattccagctga.....gtatccagatgaagtgacc 1476

Scoring table: IDENTITY_NUC

Gapop 10.0, Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

Issued Patents NA:
1: /cgn2_6/prodata/1/ina/5A COMB. seq: *
2: /cgn2_6/prodata/1/ina/5B COMB. seq: *
3: /cgn2_6/prodata/1/ina/6A COMB. seq: *
4: /cgn2_6/prodata/1/ina/6B COMB. seq: *
5: /cgn2_6/prodata/1/ina/PC/TUS COMB. seq: *
6: /cgn2_6/prodata/1/ina/backfile1.seq: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|---------------------|--------------------|
| 1 | 833.8 | 56.5 | 1798 | 4 US-09-305-681-1 | Sequence 1, Appl1 |
| 2 | 777 | 52.6 | 2460 | 4 US-09-305-681-3 | Sequence 3, Appl1 |
| 3 | 772.2 | 52.3 | 2542 | 4 US-09-305-681-5 | Sequence 5, Appl1 |
| 4 | 572.8 | 38.8 | 1956 | 3 US-08-867-352-20 | Sequence 20, Appl1 |
| 5 | 572.8 | 38.8 | 13910 | 3 US-09-263-933-1 | Sequence 1, Appl1 |
| 6 | 572.8 | 38.8 | 13910 | 3 US-09-263-933-8 | Sequence 8, Appl1 |
| 7 | 572.8 | 38.8 | 13910 | 3 US-09-263-933-15 | Sequence 15, Appl1 |
| 8 | 572.8 | 38.8 | 13910 | 4 US-09-919-901-1 | Sequence 1, Appl1 |
| 9 | 572.8 | 38.8 | 13910 | 4 US-09-919-901-8 | Sequence 8, Appl1 |
| 10 | 572.8 | 38.8 | 13910 | 4 US-09-919-901-15 | Sequence 15, Appl1 |
| 11 | 572.8 | 38.8 | 13910 | 4 US-10-191-966-1 | Sequence 1, Appl1 |
| 12 | 572.8 | 38.8 | 13910 | 4 US-10-191-966-8 | Sequence 8, Appl1 |
| 13 | 572.8 | 38.8 | 13910 | 4 US-10-191-966-15 | Sequence 15, Appl1 |
| 14 | 571.2 | 38.7 | 4989 | 4 US-09-693-011-12 | Sequence 12, Appl1 |
| 15 | 571.2 | 38.7 | 5083 | 4 US-09-693-011-11 | Sequence 11, Appl1 |
| 16 | 571.2 | 38.7 | 5928 | 4 US-09-932-581-25 | Sequence 25, Appl1 |
| 17 | 571.2 | 38.7 | 6314 | 4 US-09-693-011-10 | Sequence 10, Appl1 |
| 18 | 571.2 | 38.7 | 6408 | 4 US-09-693-011-9 | Sequence 9, Appl1 |
| 19 | 571.2 | 38.7 | 7076 | 4 US-09-837-863-20 | Sequence 20, Appl1 |
| 20 | 571.2 | 38.7 | 7076 | 4 US-09-837-863-21 | Sequence 21, Appl1 |
| 21 | 571.2 | 38.7 | 7092 | 4 US-09-837-863-19 | Sequence 19, Appl1 |
| 22 | 571.2 | 38.7 | 7092 | 4 US-09-837-863-22 | Sequence 22, Appl1 |
| 23 | 571.2 | 38.7 | 7573 | 4 US-09-837-863-27 | Sequence 27, Appl1 |
| 24 | 570.8 | 38.7 | 4951 | 2 US-08-752-307B-1 | Sequence 1, Appl1 |
| 25 | 570.8 | 38.7 | 4951 | 2 US-09-707-802-1 | Sequence 1, Appl1 |
| 26 | 570.8 | 38.7 | 4951 | 3 US-09-991-326-1 | Sequence 1, Appl1 |
| 27 | 566.4 | 38.4 | 1467 | 3 US-09-330-317B-17 | Sequence 17, Appl1 |

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| 28 | 566.4 | 38.4 | 1467 | 4 US-09-808-589A-17 | Sequence 17, Appl1 |
| 29 | 560 | 37.9 | 8299 | 1 US-08-462-014-2 | Sequence 2, Appl1 |
| 30 | 560 | 37.9 | 8299 | 3 US-08-923-137-3 | Sequence 3, Appl1 |
| 31 | 560 | 37.9 | 8299 | 3 US-08-973-334-5 | Sequence 5, Appl1 |
| 32 | 560 | 37.9 | 8299 | 3 US-09-563-869A-5 | Sequence 9, Appl1 |
| 33 | 118.8 | 8.0 | 5399 | 1 US-08-368-071-9 | Sequence 9, Appl1 |
| 34 | 118.8 | 8.0 | 5399 | 1 US-08-458-181-9 | Sequence 9, Appl1 |
| 35 | 118.8 | 8.0 | 5399 | 5 PCT-US93-02172-9 | Sequence 9, Appl1 |
| 36 | 95.8 | 6.5 | 5293 | 4 US-09-900-708-1 | Sequence 1, Appl1 |
| 37 | 86.8 | 5.9 | 3489 | 2 US-08-728-323A-1 | Sequence 1, Appl1 |
| 38 | 86.8 | 5.9 | 3489 | 3 US-09-298-568-1 | Sequence 1, Appl1 |
| 39 | 86.8 | 5.9 | 3489 | 4 US-09-410-399-1 | Sequence 1, Appl1 |
| 40 | 86.8 | 5.9 | 3489 | 4 US-09-894-273-1 | Sequence 1, Appl1 |
| 41 | 86.8 | 5.9 | 32207 | 2 US-08-770-379-20 | Sequence 20, Appl1 |
| 42 | 86.8 | 5.9 | 32207 | 3 US-08-757-669A-20 | Sequence 20, Appl1 |
| 43 | 86.8 | 5.9 | 32207 | 3 US-09-230-371A-20 | Sequence 20, Appl1 |
| 44 | 77.2 | 5.2 | 884 | 4 US-09-570-767-11859 | Sequence 11859, A |
| 45 | 70.8 | 4.8 | 220 | 3 US-09-263-933-22 | Sequence 22, Appl1 |

ALIGNMENTS

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RESULT 1
US-09-305-681-1
; Sequence 1, Application US/09305681
; Patent No. 6406899
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Highly active alkaline phosphatase
; NUMBER OF SEQUENCES: 54
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/305,681
; FILING DATE:
; CLASSIFICATION:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1798 base pairs
; TYPE: nucleotide
; STRANDEDNESS: single strand
; TOPOLOGY: linear
; MOLECULAR TYPE: genomic DNA
US-09-305-681-1

Query Match      56.5%; Score 833.8; DB 4; Length 1798;
Best Local Similarity 73.2%; Pred. No. 2,9e+211;
Matches 1069; Conservative 0; Mismatches 392; Indels 0; Gaps 0;

6 CTGATTCCAGCTGAGAGAAATCCAGCTTTTGGATAGACAGTCTCAAGCTTT 65
107 CCGATCCAGCTGAGAGAGAAATCCAGCTTTTGGATAGACAGTCTCAAGCTTT 166
66 GGATGTTGTAAGAGTCAACCAATTCGCTGCTAAGATGTTATTTGTTTT 125
167 TGATGAGCAAGAGATTCAGCGGATCCAGACAGCTGCCAAGATGTCATCTTCTT 226
126 GGGTATGTTGAGTGGGTTCCCAACTTCTGCTATAGAAATTTGAAGGTCGAATGAA 185
227 GGGGATGAGTGGGTTCCCAACTTCTGCTATAGAAATTTGAAGGTCGAATGAA 286
186 TGGTATGTTGAGTGGGTTCCCAACTTCTGCTATAGAAATTTGAAGGTCGAATGAA 245
287 TGGCAACTGGGATCCGACACCCCTGCGCATGACAGTTCCCATAGCTGCTGTC 346
246 TAAGACTTCAATGTTGATAGCAAGATTCGCTGCTAGCTAGCTAGCTTACTT 305
347 CAAGACATCAACGTGAGCAGACAGGTCGACAGCGCAGGCACTGCACACTGCTACT 406
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| | | | |
|----|------|--|------|
| QY | 306 | GTGTGAGTGTAAAGGTTATTAACAGAACTATTGGTGTCTTCTGCTGCTGATATCAATCA | 365 |
| Db | 407 | GTGTGGGGTCAAGGGCAACTACAGAACCATGGGTGAAGTCAACCCGGCTCAATCA | 466 |
| QY | 366 | ATGTAAATCTCTAGAGGTTAATGAAGTACTCTTGTTATTAATAGAGCTAAGAGCGTGG | 425 |
| Db | 467 | GTGCACACGACAGTGGGAATGAGGTACGCTCTGTATCAACCGGGCCAAAGAAACAGG | 526 |
| QY | 426 | TAAAGCTTGGTGTGTGTACTACTACTAGAGTTCAACATGCTTCTCCAGCTGGTCTTA | 485 |
| Db | 527 | GAAGGCCGTGGGAAGTGTGACCAACCAACAGGGTGAGATGCTCTCCAGCCGGGGCTTA | 586 |
| QY | 486 | CGCTCATCTGTTAATAGAATTTGGTACTTGAATGCTGATTTGGCAGTGATGCTCAAA | 545 |
| Db | 587 | CGCGCACACGGTGAACCCMAACTGGTACTAGACGGCCCACTGCTGTGATGACAGAA | 646 |
| QY | 546 | GAATGGTTGTCMAAGTATTTGCGCTCAATTGGTTTACAAATPAGATATGATGTTATTTT | 605 |
| Db | 647 | GAATGGCTGCAGGACATCGCCGACAGCTGGTCTACAACTGGATATTGACGTGATCTT | 706 |
| QY | 606 | GGGTGGTGTGAATGTACATGTTTCCAGAAAGTACTCCAGATCCAGATACCCAGATGA | 665 |
| Db | 707 | GGGTGGAAGCCGAATGTACATGTTTCTGAAGGGAGCCCAAGACCTGTAAATCCAGATGA | 766 |
| QY | 666 | TGCTTCTGTTAATGCTGTTAGAAGAGATTAAGCAAAATTTGGTCTCAAGATGGCAAGTAA | 725 |
| Db | 767 | TGCCAGTGTGAATGGAGTCCGMAAGAACACAGAACCTGGTGCAGAGATGGCGGCCAA | 826 |
| QY | 726 | GCATCAAGGTGCTCAATATGTTTGGAAATAGAATCGCTTGTTCAGAGCTGTGATGATTC | 785 |
| Db | 827 | GCAACAGGAAGCCAGTATGTGTGGAACCGCACTGCGTCTTCAAGCGCGCGATGACTC | 886 |
| QY | 786 | TAGTGTACTCATTTGATGGTGTGTGTGAACCAAGCTGATATGAAGTAAATGTTCAACA | 845 |
| Db | 887 | CAGTGTACACACCTCATGGGCGCTTTGAGCGCGGACAGATGAAGTATATGTTCAAGA | 946 |
| QY | 846 | AGATATATCTAAGATCCAACTTTTGGCTGAATATGACTGAACTGCTTTGCAAGTTTGTCT | 905 |
| Db | 947 | AGACCACACCAAGGACCCGACCCTGGCGGAATGACGAGGCGGCGCTGCAAGTGCAGAG | 1006 |
| QY | 906 | TAGAATCCAGAGGTTTTTACTTGTTGTGAAGGTGGTGAATATGATCAATGGTCAATCA | 965 |
| Db | 1007 | CAGGAACCCCGGGGCTTCTACTCTTGTGTGAGGAAGCGGCATTGACCAAGGTACCA | 1066 |
| QY | 966 | TGATGTAAAGGCTTATATGCTTTGACTGGAAGCTATTAATGTTGATATGCTATTTGCTAA | 1025 |
| Db | 1067 | TGACGGCAAGGTTATATGAGCAGTACGAGGCGATCATGTTTGACATATGCAATGCGCAA | 1126 |
| QY | 1026 | GGCTAATGAATGACTTCTGAATTTGGATCTTTGATTTTGGTACTGCTATCATPATGCA | 1085 |
| Db | 1127 | GGCTAACAGCTCACTAACGAACTGGAACGCTGATCTCTGTCACTGACAGACACTCCCA | 1186 |
| QY | 1086 | TGTTTTCTTTTGGTGGTACACTTGAAGAGTACTTAATTTTGGTGTGGTCCAGG | 1145 |
| Db | 1187 | TGCTTCTCTTTTGGTGGTACACTGCGTGGAGCTTCAATTTTCGGTCTGGACCCCGG | 1246 |
| QY | 1146 | TAAAGCTTGGATAGTAACTTTCACTTCTAATTTTGTATGATATGCTCCAGGTTATGC | 1205 |
| Db | 1247 | CAAGGCTTGAACACAGAACTCTTAACCTCATCTCTATATGGCAATGGCCAGAGTATGC | 1306 |
| QY | 1206 | TTTGGGTGGTGTCTTAAGCACAGATGTTAATGTATAGTACTAATGTAAGAACATCTTACAG | 1265 |
| Db | 1307 | GCTTGGCGGGGCTCGAAGGCCGATGTTAATGGCAGCAACAAGCGGAGAACCTCATACCG | 1366 |
| QY | 1266 | ACAAACAAGTGTCTTCCATTTGGCTAGTGAACCTAATGATGTGTAAGATGTTGCTGTTTT | 1325 |
| Db | 1367 | GCAGCAGCGCGCGTGGCTCTGCTAGCGAAGCCACGAGGCGCAAGCGTGGCGGTGTT | 1426 |
| QY | 1326 | TGCTAAGAGTCCACAGAGCTCATTTGGTTCATGATGTTTCAAGAAAGAACTTTTGTGTCTCA | 1385 |
| Db | 1427 | CGCGGAGAGCCCGCAGCGCACCTGTGTGACGCGCTGACAGAGAGAGACCTTCTGTGGCGCA | 1486 |
| QY | 1386 | TATTAATGCTTTTGTCTGTGTGTGAACATACATGATGTAAATTTGCCAGCTCCAGC | 1445 |

| DB | 1487 | CATCATGCGCTTTTGGCGGCTCGTGGAGCCTTACACCGACTGCAATCTGCCAGCCCCGC | 15446 |
|---|------|--|-------|
| QY | 1446 | TACTGCTACTAGTATTCAGA | 1466 |
| DB | 1547 | CACCGCCACCGACTCCCGA | 1567 |
| RESULT 2 | | | |
| US-09-305-681-3 | | | |
| ; Sequence 3, Application US/09305681 | | | |
| ; Patent No. 6406899 | | | |
| ; GENERAL INFORMATION: | | | |
| ; APPLICANT: | | | |
| ; TITLE OF INVENTION: Highly active alkaline phosphatase | | | |
| ; NUMBER OF SEQUENCES: 54 | | | |
| ; COMPUTER READABLE FORM: | | | |
| ; MEDIUM TYPE: Floppy disk | | | |
| ; COMPUTER: IBM PC compatible | | | |
| ; OPERATING SYSTEM: PC-DOS/MS-DOS | | | |
| ; SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO) | | | |
| ; CURRENT APPLICATION DATA: | | | |
| ; APPLICATION NUMBER: US/09/305,681 | | | |
| ; FILING DATE: | | | |
| ; CLASSIFICATION: | | | |
| ; INFORMATION FOR SEQ ID NO. 3: | | | |
| ; SEQUENCE CHARACTERISTICS: | | | |
| ; LENGTH: 2460 base pairs | | | |
| ; TYPE: nucleotide | | | |
| ; STRANDEDNESS: single strand | | | |
| ; TOPOLOGY: linear | | | |
| ; MOLECULE TYPE: genomic DNA | | | |
| ; US-09-305-681-3 | | | |
| Query Match 52.6%; Score 777; DB 4; Length 2460; | | | |
| Best Local Similarity 71.2%; Pred. No. 3.8e-196; | | | |
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| QY | 66 | GGATGTTCTAAGAAAGTTGCAACCAATTCAAACCTGCTCTAAGAAATGTTATTTGTTTT | 125 |
| DB | 182 | TGATGTGCTAAGAAAGCTGACGCCCTTCAGAAAGCCGCAAGATGTCATCTCTTTCT | 241 |
| QY | 126 | GGGTGATGTTAGGGTGTTCACAAGCTGTTACTGTTCTACTGAAATTTTGAAGGTTCAATGAA | 185 |
| DB | 242 | GGGAGATGGATGGGGGTGCTTACGTTGACAGCCACTGCGATCTGGAAGGGGAGATGAA | 301 |
| QY | 186 | TGTTAAGTTGGGTCAGAAACTCCATTGGCTATGGATCAATTTCCATACGTTGCTTGTTC | 245 |
| DB | 302 | TGACAAAGCTGGGAACTGAGACACCCCTGGCATGGACAGTTCCATACGTGGCTGTGC | 361 |
| QY | 246 | TAAAGCTTACATGTTGATATACAAAGTTCCAGATTTCTGCTGTACTGTACTGCTTACTT | 305 |
| DB | 362 | CAAAGCATACAAACGGGACAGACAGGTGCCAGACAGCGACAGCACTGCTGCTTACTT | 421 |
| QY | 306 | GTTGAGTATTAAAGGTTAATTAACAGAACTAATTGGTGTCTCTGCTGTAGATCAATCA | 365 |
| DB | 422 | GTTGTGGGTCAAGGGCACTACAGAACCATGGGTGTAAAGTGCAGCCGCCCTACATCA | 481 |
| QY | 366 | ATGTAACTACTAGAGAGTAATGAAGTTACTTCTGTTTAAATAGAGTTAAGAAAGCTGG | 425 |
| DB | 482 | GTGCAACACGACAGTGGGAATGAGGTACCGTCTGTATGTAACCGGGCCAAAGAAAGAGG | 541 |
| QY | 426 | TAAAGCTTGGTGTGTTTACTACTACTAGAGTTCAACATGCTTTTCCAGCTGGTGTCTTA | 485 |
| DB | 542 | GAAAGCAATGGGAAGTGTGACACACACAGGGGTGAGACGCCCTCCAGCGGGTCTTA | 601 |
| QY | 486 | CGTCATCTCTTAAATGAATTTGGTACTCTGATGCTGATTTGCCAGCTGATGCTCAAA | 545 |
| DB | 602 | TGCACACCGGTGAACCTGACTGGTACTTACAGACCGCGCACTGCTGCCAGTACAGAC | 661 |

841 GCACCGAGGAGCCAGATATGTGTGAACCGACGAGCTCTTTCAGGACCAATGACCC 900
QY 786 TAGTGTACTCATTTGATGGGTTTGTGTAACCGAGTGAATGAAATTAATTTAAACA 845
DB 901 CAGTGTAAACACCTCATGGGCTCTTTTGAACCGGAGACATGAATTAATGTTAGACA 960
QY 846 AGATCATTAAGGATCAACTTTGAGTGAATGAACTGAAGGCTTGGCAAGTTTGTGC 905
DB 961 AGACCCCAACCAAGAGCCCACTTGAGAGATGACGAGGCGGCTTGCAGTGTGAG 1020
QY 906 TAGAAATCCAGAGTTTCTTGAATGTTTGTGTAAGGTGTGAGATTTGATCATGTCATCA 965
DB 1021 CAGGAACCCCAAGGCTTCTACTCTTCGAGGAGGAGCCGATTTGACACGAGTCAACA 1080
QY 966 TGATGTAAAGGCTTATATGAGCTTTGACTGAAGTATTAATGTTGATTAATGCTTAA 1025
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QY 1026 GAGTATGAATGACTTCTGAATTTGATTTGATTTGTTTACTGCTGATCATAGTCA 1085
DB 1141 GAGTAAAGGCTCATCTAGGAACTGACACGCTGATCTTGCACATGACACATCTCCA 1200
QY 1086 TGTTTTTTTCTTTGTTGTTTACACTTTGAGAGGTAATTTTGTGTTGCTTCCAG 1145
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QY 1146 TAAAGCTTTGATAGTACTCTTCACTTTTATTTGTAATGTAATGTCAGTTATGC 1205
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QY 1206 TTTGGGTGTTGTTTGAACGAGATTTATGTTAGTAACTGAAGAACATCTTACAG 1265
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DB 1381 GCAGCAGGCGGCGCTGCTCTGATGATCCACGAGGAGGAGAGACGTCGCTGTT 1440
QY 1326 TGTCTAGAGTCCACAGCTCATTTGTTGATGTTTCAAGAAAGAACTTTTGTCTCA 1385
DB 1441 CGCGCAGGCGCGCAGGCGCACTGTGACGCGGTGAGAGAGAACCTTCGTGCGCA 1500
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QY 1446 T 1446
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RESULT 4
US-08-867-352-20
Sequence 20, Application US/08867352
Patent No. 6060273
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Multicistronic expression unites and their use
NUMBER OF SEQUENCES: 25
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPA)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/867,352
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/387,847
FILING DATE:
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:

LENGTH: 1956 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
CLONE: pSO2-SEAP (Berger et al., 1988)
FEATURE:
NAME/KEY: CDS
LOCATION: 43..1560
OTHER INFORMATION: /note= "human SEAP gene, flanked
OTHER INFORMATION: by 5'-BcoRI and 3'-HindIII restriction cleavage
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 94..1560
OTHER INFORMATION: /product= "mature protein"
PUBLICATION INFORMATION:
AUTHORS: Berger, J.
AUTHORS: Hauber, J.
AUTHORS: Hauber, R.
AUTHORS: Geiger, R.
AUTHORS: Cullen, B. R.
JOURNAL: Gene
VOLUME: 66
PAGES: 1-10
DATE: 1988
PUBLICATION INFORMATION:
AUTHORS: Millan, J. L.
JOURNAL: J. Biol. Chem.
VOLUME: 261
PAGES: 3112-3115
DATE: 1986
US-08-867-352-20

Query Match 38.8%; Score 572.8; DB 3; Length 1956;
Best Local Similarity 62.4%; Pred No. 4.7e-142;
Matches 898; Conservative 0; Mismatches 542; Indels 0; Gaps 0;

QY 6 CTTGATTCAGCTGAGAGAAATTCAGCTTTTGAATGACAGCTGCTCAAGCTT 65
DB 93 CATCATCCAGATTGAGAGAGAACCCGACTTCTGAAACCGCAGGACCGAGGCCCT 152
QY 66 GAGTGTGTTGAAGAGTTGCAACCAATTCAACTCTGCTAGAGATGTTATTTGTTT 125
DB 153 GGTGCGCGCAAGAAAGCTGCAAGCTGCAAGACAGCCGCAAGAACTTCATCTTCT 212
QY 126 GGTGATGTTAGGTTGTTCCAACTGTTACTGCTACTGAAATTTGAAGGTCATATGTA 185
DB 213 GGGCAATGGAGTGGGGTGTCTACGTTGACAGCTCCAGATCTTAAAGGCAAGAA 272
QY 186 TGTGAATGGTTCAGAAACTCCATTTGCTATGATGATCAATTTCCATAGTTGTTGTC 245
DB 273 GGAACAACCTGGGGCTGAGATACCCCTGGCATGAGCCGCTTCCATATGTTGCTGTC 332
QY 246 TAAAGCTTAATGTTGATGACAGAGTTCCAGATTTCTGCTGATCTGCTACTGCTTACT 305
DB 333 CAAGACATACATATGAGCAAAACATGTGCAAGAGTGAAGCAAGCCAGCCCTACTCT 392
QY 306 GTGTGTTTAAAGGTTAATTAAGAACTTTGTTCTGCTGCTGCTAGATCAATCA 365
DB 393 GTGCGGGTCAAGGCAACTTCAAGCCATTTGCTTGAAGTGAAGCCGCGCTTTAAACA 452
QY 366 ATGTAATACTAGAGTAAATGAAGTTACTTCTGTTTAAATAGAGTAAAGAGCTGG 425
DB 453 GTGCAACAGACAGCGGGAAGAGTCAATCTCGTATGAATCGGCAAGAAAGCAGG 512
QY 426 TAAAGCTGTGTTGTTTACTACTACTAGATTAAGATTTTCCAGCTGCTGCTTAA 485
DB 513 GAAGTCAGTGGAGTGTAAACACACACAGAGTGAAGACGCTGCGCAGCCGACCTTA 572

QY 486 CGCTACTACTGTTAATGAATGGTACTGTAAGTGAATGGCCAGCTGATCTCAAAA 545
 Db 573 CGCCACACCGGTGAACCGCAACTGTGTAAGTGAAGCGGAGCGTGCCTCGGCGCCCA 632
 QY 546 GAATGGTGTCAAGATATTTCTGCTCAATGGTTTACAAATATGATATTTGATATTT 605
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 QY 846 AGATCATACTAGAGATCCAACTTGGCTGAATGACTGAAGCTGCTTGGCAAGTTTGTCTC 905
 Db 933 AGACTCCACACTGAGACCCCTCCCTGATGAGATGACAGAGGCTGCCCTGGCTGCTGAG 992
 QY 906 TAGAAATCCAAAGAGTTTCTTCTGTTTGTGAAGGTGTGAATTTGATCATGCTCTCA 965
 Db 993 CAGGAACCCCGCGGCTTCTCTCTCTGAGAGGGGTGCGCATGACCATGATGATCA 1052
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 Db 1053 TGAAGAGAGGCTTACCGGCACTGATGAGATCATGTGACACACCCATGAGAG 1112
 QY 1026 GGTAAATGAATGATCTTGAATTTGATTTGATTTGTTGTTGCTGATCATATGTC 1085
 Db 1113 GGGGGGCGAGCTCACGAGGAGGAGACAGCTGAGCTGCTGATGCGACCACTCCCA 1172
 QY 1086 TGTCTTTCTTTTGTGTGTACACTTTGAGAGGTACTTCTAATTTTGTGTGCTCCAGG 1145
 Db 1173 CGTCTTCTCTCTGAGAGGTAACCCCTGCGAGGAGCTCATCTGCGGCTGAGCCCTGG 1232
 QY 1146 TAAGCTTTGATGATGATGATCTTCACTTATTTTGTATGATGATGATGATGATG 1205
 Db 1233 CAAGGCGCGGAGAGAGGCTTACAGGCTCTCTATAGGAAACGCTCAGGCTATGT 1292
 QY 1206 TTTGGGTGTGTCTTACACAGATGTTAATGTTAGTATGATGATGATGATGATG 1265
 Db 1293 GCTCAAGAGAGGCGCGCGCGGAGTGTACCGAGAGCGAGAGCGGAGCCCGAGATGCG 1352
 QY 1266 ACAACAGCTGCTGTTCATTTGCTAGTGAAGTCAATGTTGTTGAAAGTGTGCTGTTT 1325
 Db 1353 GCAGCAGTACAGTGCCTTGAACGAGAGACCCAGGAGGAGGAGGAGCTGCGGAGTGT 1412
 QY 1326 TGTCTAAGTGTCCCAAGCTATTTGTTTCAATGTTTCAAGAGAAATTTGTTGCTCA 1385
 Db 1413 CCGGCGCGGCGCGAGGCGGACCTGTGTCAAGGCTGACAGAGACAGCTTCTATAGGCA 1472
 QY 1386 TATTATGCTTTTGTGTGTGTGTAACATACATGATGTTAATTTGCAAGCTCAGC 1445
 Db 1473 CGTCAATGCTTTCGCGCGCTGCTGAGGCTTACACGCGCTGCGAGCTGCGCGCCCGC 1532

RESULT 5
 US-09-263-933-1
 ; Sequence 1, Application US/09263933
 ; Patent No. 6289940
 ; GENERAL INFORMATION:
 ; APPLICANT: Polts, Karen E.
 ; APPLICANT: Jackson, Roberta L.
 ; APPLICANT: Patrick, Amy K.

; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
 ; FILE REFERENCE: 0125-0005A
 ; CURRENT APPLICATION NUMBER: US/09/263,933
 ; EARLIER FILING DATE: 1999-03-08
 ; EARLIER FILING DATE: 1998-08-05
 ; NUMBER OF SEQ ID NOS: 33
 ; SOFTWARE: Patent In Ver. 2.0
 ; SEQ ID NO 1
 ; LENGTH: 13910
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: plasmid phcap 1
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (497)..(772)
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (1425)..(6500)
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (8579)..(9034)
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (10191)..(10445)
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (11877)..(12734)
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: (1)..(774)
 ; OTHER INFORMATION: Vaccinia Virus thymidine kinase gene recombination
 ; FEATURE:
 ; NAME/KEY: promoter
 ; LOCATION: (794)..(816)
 ; OTHER INFORMATION: T7 promoter
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: (846)..(1424)
 ; OTHER INFORMATION: EMC/Internal Ribosome Entry Site (IRES)
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: (1426)..(1437)
 ; OTHER INFORMATION: MCS (Multiple Cloning Site)
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: (1445)..(2318)
 ; OTHER INFORMATION: HCV E2/ NS2 domain
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: (2319)..(4231)
 ; OTHER INFORMATION: HCV NS3 domain containing the serine protease and
 ; OTHER INFORMATION: helicase enzymes
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: (4203)..(4260)
 ; OTHER INFORMATION: HCV NS3-NS4A cleavage site
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: (4375)..(4424)
 ; OTHER INFORMATION: HCV NS4A-4B cleavage site
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: (4233)..(4394)
 ; OTHER INFORMATION: HCV NS4A domain
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: (4395)..(4919)
 ; OTHER INFORMATION: HCV NS4B Domain
 ; FEATURE:

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/ NAME/KEY: misc feature
/ LOCATION: (4920)..(4991)
/ OTHER INFORMATION: HCV NS5A-NS5B cleavage site
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: (4992)..(6501)
/ OTHER INFORMATION: SEAP Protein
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: (7915)..(7945)
/ OTHER INFORMATION: MCS (Multiple Cloning Site)
/ FEATURE:
/ NAME/KEY: terminator
/ LOCATION: (7938)..(8078)
/ OTHER INFORMATION: term T7
/ FEATURE:
/ NAME/KEY: promoter
/ LOCATION: (8080)..(8365)
/ OTHER INFORMATION: Vaccinia virus promoter; early/late promoter
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: (8560)..(11317)
/ OTHER INFORMATION: E. coli gpt; for selection of recombinants
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: (11318)..(13909)
/ OTHER INFORMATION: remaining DNA from 3' end of Tropic PCMV/SEAP
/ OTHER INFORMATION: plasmid
US-09-263-933-1
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Query Match      38.8%; Score 572.8; DB 3; Length 13910;
Best Local Similarity 62.4%; Pred. No. 1.2e-141;
Matches 898; Conservative 0; Mismatches 542; Indels 0; Gaps 0;
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QY 6 CTTGATTCAGCTGAGAGAAATCCAGCTTTTGAATAGACAGCTGCTCAAGCTTT 65
DB 5033 CATCATCCAGATTGAGAGAGAGAACCCGACCTTCTGAAACCGGAGGACGCGAGCCCT 5092
QY 66 GAGATGCTGAAGAGTTGCAACCAATTCAACTGCTGCTAGAGATGTTATTTTGT 125
DB 5093 GGGTCCGCGCAAGAGAGCTGAGCTGAGACAGAGCGCGCAAGACCTCATCTTCT 5152
QY 126 GGGTATGATGAGGCTTCAACTGCTGCTAGAGATTTTGAAGGCTCAATGAA 185
DB 5153 GGGGCAATGAGATGAGGAGTCTTACGCTGAGCTGAGATCTTAAAGGAGAGAA 5212
QY 186 TGGTAAGTTGGGTCAGAACTCCATTTGCTATGATCAATTTCCATAGCTTGTGTC 245
DB 5213 GAGCAAACTGGGGCTGAGATACCCCTGGCATGAGCCGCTTCCATATGTGCTGTG 5272
QY 246 TAAAGCTTCAATGTTGATAGACAAAGTTCCAGATTCTGCTGATGCTACTGCTTACT 305
DB 5273 CAAGCATATCAATGATAGACAAATGTGCAAGCACTGAGACCAAGCCGCTTACCT 5332
QY 306 GTGTGATGTTAAGGATTTACAGAACTATGATGTTTCTGCTGCTGCTAGATACATCA 365
DB 5333 GTGCGGGGTCAAGGGGAACTTCCAGACCAATTTGCTTGAATGACCGCCGCTTTAACCA 5392
QY 366 ATGTAATACTACTAGAGATGATGAAATTTCTTGTATTAATAGAGCTAAGAGGCTGG 425
DB 5393 GTGCAACACGACCGGGGCAACGAGGTCACTCCGATGATGATTCGGGCAAGAAAGCAAG 5452
QY 426 TAAAGCTGTTGCTGTTTACTTACTTACTAGAGTTCAATGCTTCTCCAGCTGCTGCTTA 485
DB 5453 GAAGTCAGAGGAGTGTGTAACCAACAGAGTGCAGACGCTCCGACCGGACCTTA 5512
QY 486 CGCTCATCTGTTAATAGAAATGTAAGTCTGATGCTGATGTTCCAGCTGATGCTCAAA 545
DB 5513 CGGCCACAGGTTGAAACCGCACTGTAATCTGAGCGCCGACGTCCTCGGCGCCCA 5572
QY 546 GAATGTTGTCAAGATATGCTGCTCAATTTGTTTAAATATGATATGATGTTTATTTT 605
DB 5573 GAGGGGTCACGAGATCGCTTACGCACTTCTCAACATGAGCATTTGAGCTGATCTT 5632
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QY 606 GGGTGTGTAGATGATGATGTTTCCAGAAAGTACTCCAGATCCAGATACCGAGATGA 665
DB 5633 AGGTGAGGCGCAAGATGATGTTTCCATGAGGAAACCCAGACCTTGATGATCCAGATGA 5692
QY 666 TGCCTTCTGTTAATGAGTTAGAAAGATAGCAAAATTTGTTTCAAGATGCAAGCTTA 725
DB 5693 CTACAGCCAGGTGGAGCCAGGCTGACGGGAGAGATCTGATGCAAGATGCTGGCGAA 5752
QY 726 GCATTAAGGTGCTCAATATGTTTGAATGAACTGCTTTGTTGCAAGCTGCTGATGATTC 785
DB 5753 GCGCAGGAGTGGCCGATATGTTGGAACCGCACTAGCTGATGACGAGCTTCCCTGACCC 5812
QY 786 TAGTGTCTCACTTTGATGAGGTTTGTGAAACCACTATATGAGTAAATGTTCAACA 845
DB 5813 GTCTGTGACCATCTCATAGAGTCTCTTTGAGCTGTGAGACATGAATATCGAATCCACCG 5872
QY 846 AGATCATACTAAGATCCAACTTTGCTGAAATGACTGAAGCTGCTTTCGAAGTTTGTGTC 905
DB 5873 AGACTCCACACAGACCCCTCCCTGATGAGATGACAGAGCTGCTGCGCTGCTGAG 5932
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DB 5933 CAGGAACCCCGCGGCTTCTTCTCTGAGAGGAGTGTGCGATGACATGATGATCA 5992
QY 966 TGAATGAGGCTTATGAGCTTTGAGCTGAGCTATTTATGTTGATTAATGCTATTGCTTA 1025
DB 5993 TGAAGACAGGCTTACCGGACCTGACATGAGATCATGTTGACAGACCATTTAGAG 6052
QY 1026 GGTATATGAAATTTGATCTGATGATGATGATGATGATGATGATGATGATGATGATGATCA 1085
DB 6053 GCGGAGGACAGCTCACACAGAGAGAGACAGCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCA 6112
QY 1086 TGTTTTCTTCTTGTGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1145
DB 6113 GCTTCTTCTTCTGAGGCTACCCCTGAGAGGAGCTGATCTTCTGAGGCTGAGGCTGAG 6172
QY 1146 TAAAGCTTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1205
DB 6173 CAAGGCGGAGCAGAGAGGCTTACAGCTGCTCTCTTATACGAAAGGCTGAGCTGATGAT 6232
QY 1206 TTTGGTGTGTTTGAACAGCAGATGTTAATGATGATGATGATGATGATGATGATGATGAT 1265
DB 6233 GCTCAAGAGACGCGCGCGCGGAGTATGACGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 6292
QY 1266 ACAAGAGCTGCTGTTCAATTTGCTAGTGAATCTATGATGATGATGATGATGATGATGAT 1325
DB 6293 GCAGCAGTCAAGAGGCTTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 6352
QY 1326 TGTAGAGGCTCAGAGAGCTATTTGTTCAATGATGATGATGATGATGATGATGATGATGAT 1385
DB 6353 CGCGGCGGCGCGGAGGAGCTGTTTCAAGCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAG 6412
QY 1386 TATTATGCTTGTGCTGTTGTTGTTGAACATATGATGATGATGATGATGATGATGATGATGAT 1445
DB 6413 CGTATGAGCTTGGCGGCTGCTGAGAGCTTCAACCGCGCTGAGAGCTGAGAGAGAGAGAG 6472
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RESULT 6
US-09-263-933-8
Sequence 8, Application us/09263933
Patent No. 6280940
GENERAL INFORMATION:
APPLICANT: Potts, Karen E.
APPLICANT: Jackson, Roberta L.
APPLICANT: Patrick, Amy K.
TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
FILE REFERENCE: 0125-0005A
CURRENT APPLICATION NUMBER: US/09/263,933
CURRENT FILING DATE: 1999-03-08
EARLIER APPLICATION NUMBER: 09/129,611
EARLIER FILING DATE: 1998-08-05

NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 8
LENGTH: 13910
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: plasmid phcap 3
FEATURE:
NAME/KEY: CDS
LOCATION: (497)..(772)
FEATURE:
NAME/KEY: CDS
LOCATION: (1425)..(6500)
FEATURE:
NAME/KEY: CDS
LOCATION: (8579)..(9034)
FEATURE:
NAME/KEY: CDS
LOCATION: (10191)..(10445)
FEATURE:
NAME/KEY: CDS
LOCATION: (11877)..(12734)
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)..(774)
OTHER INFORMATION: Vaccinia Virus thymidine kinase gene recombination
OTHER INFORMATION: site
FEATURE:
NAME/KEY: promoter
LOCATION: (794)..(816)
OTHER INFORMATION: T7 promoter
FEATURE:
NAME/KEY: misc feature
LOCATION: (846)..(1424)
OTHER INFORMATION: EMC/Internal Ribosome Entry Site (IRES)
FEATURE:
NAME/KEY: misc feature
LOCATION: (1425)..(1437)
OTHER INFORMATION: MCS (Multiple Cloning Site)
FEATURE:
NAME/KEY: misc feature
LOCATION: (1446)..(2318)
OTHER INFORMATION: HCV E2/ NS2 domain
FEATURE:
NAME/KEY: misc feature
LOCATION: (2319)..(4231)
OTHER INFORMATION: HCV NS3 Domain containing the serine protease and
OTHER INFORMATION: helicase enzymes
FEATURE:
NAME/KEY: misc feature
LOCATION: (4203)..(4260)
OTHER INFORMATION: HCV NS3-NS4A cleavage site
FEATURE:
NAME/KEY: misc feature
LOCATION: (4233)..(4394)
OTHER INFORMATION: HCV NS4A domain
FEATURE:
NAME/KEY: misc feature
LOCATION: (4375)..(4424)
OTHER INFORMATION: HCV NS4A-4B cleavage site
FEATURE:
NAME/KEY: misc feature
LOCATION: (4233)..(4394)
OTHER INFORMATION: HCV NS4B Domain
FEATURE:
NAME/KEY: misc feature
LOCATION: (4920)..(4991)
OTHER INFORMATION: HCV NS5A-NS5B cleavage site
FEATURE:
NAME/KEY: misc feature
LOCATION: (4992)..(6501)
OTHER INFORMATION: SEAP Protein

FEATURE:
NAME/KEY: misc feature
LOCATION: (7915)..(7945)
OTHER INFORMATION: MCS (Multiple Cloning Site)
FEATURE:
NAME/KEY: terminator
LOCATION: (7938)..(8078)
OTHER INFORMATION: term T7
FEATURE:
NAME/KEY: promoter
LOCATION: (8080)..(8365)
OTHER INFORMATION: Vaccinia virus promoter; early/late promoter
FEATURE:
NAME/KEY: misc feature
LOCATION: (8560)..(11317)
OTHER INFORMATION: E. coli gpt; for selection of recombinants
FEATURE:
NAME/KEY: misc feature
LOCATION: (11318)..(13909)
OTHER INFORMATION: remaining DNA from 3' end of Tropicix pcMV/SEAP
OTHER INFORMATION: plasmid
US-09-263-933-8

Query Match 38.8%; Score 572.8; DB 3; Length 13910;
Best Local Similarity 62.4%; Pred. No. 1.2e-141;
Matches 898; Conservative 0; Mismatches 542; Indels 0; Gaps 0;

QY 6 CTTGATTCACGCTGAAGAAAGAAATCCAGCTTTTGGAAATGACAGAGCTCAAGCTT 65
DB 5033 CATCATCCAGGTGAGAGAGAGAACCCGACCTTCGAAACCCGAGCAGCCAGCCCT 5092
QY 66 GGATGTTGCTAAGAGTGTCAACCAATTCAACTGCTGTAGAGTATTTGTTTT 125
DB 5093 GGGTCCGCGCAAGAGCTCAGCTGACAGACAGCCGCAAGAACTCATCTTCTCT 5152
QY 126 GGGTGTGATGATGGGTGTTCCAACTGTTACTGTTACTAGAAATTTGAGGGTCAATGAA 185
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QY 486 CGCTCATCTGTTAATAGAAATTTGGTACTCTGATGCTGATTTGCCAGCTGATCTCAAA 545
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DB 5573 GGAGGGGTCCAGCATGCTACGACGCTCATCTCAACATGACATTTGAGTGATCTCT 5632
QY 606 GGGTGTGTGAATGTATATTTTCCAGAGTACTCCAGATTCAGAAATATCCCAATGA 665
DB 5633 AGGTGAGGCCAAGAAATATGTTTCCATGGAACCCCAAGACCTGATATCCAGATGA 5692
QY 666 TGCTTCTGTTATGTTGTTAGAAAGATTAAGCAAAATTTGTTCAAGATGCAAGCTAA 725

| | | | |
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| Qy | 726 | GCATCAAGGTGCTCAATATGTTTGGAAATAGAATCTGTTGTTGCAAGCTGCTGATGATTC | 785 |
| Db | 5753 | GGCGCAAGGTGCGCGGTATGTGTGGAAACCGCATCTAGCTGATGACAGGCTTCCTCCGGACC | 5812 |
| Qy | 786 | TAGTGTTAATCTATTTGATGGGTTTGTGGAACCAAGCTGATATGAAGTATTAATGTTCAACA | 845 |
| Db | 5813 | GTCGTGTGACCATCTCATGTGGGCTCTTTTGAAGCTGTGAACAATGAAATACGATGATCAACG | 5872 |
| Qy | 846 | AGATCATCTAAAGATCCAACTTTGGCTGAATGACTGAAGCTGCTTTGCAAGTTTGTTC | 905 |
| Db | 5873 | AGACTTCCACACTGGACCCCTCCTATGAGATGACAAAGGCTGCTCCGCTGCTGAG | 5932 |
| Qy | 906 | TAGAAATCCAAAGAGGTTTTTAATCTTTGTTTGAAGGTGATGAATTCATATGTCATCA | 965 |
| Db | 5933 | CAGGAACCCCGCGGCTTCCTCCTTTCGTGGAAGGTTGTCGATCGACATGGTCATCA | 5932 |
| Qy | 966 | TGATGCTAAGGCTTATATATGCTTTGACTGGAAGCTATTAATGTTTGAAATGCTATTGCTAA | 1025 |
| Db | 5993 | TGAAAGCAGGCGCTTACCGGGCACTGACTGAGACGATCATGTTTGCAGACGCCATTTGAAG | 6052 |
| Qy | 1026 | GGCTAATATTAATGTAATTCGAAATTTGGATTAATTTGATTTGTGTACTGATCATATGCA | 1085 |
| Db | 6053 | GGCGGGCAGCTCACACAGCGAAGAGAACACGCTGAGCCTTCGTCATGCGACCAATCCCA | 6112 |
| Qy | 1086 | TGTTTTTCTTTTGGTGTACTCTTATGAGAGTACTTCTATTTTGGTTTGGCTCCAG | 1145 |
| Db | 6113 | CGTCTTCCTTCGGAAGCTACCCCTCGAGGAGATGCAATCTTCGGGGCTGGCCCCCTGG | 6172 |
| Qy | 1146 | TAAAGCTTGGATAGTAAATGCTTACCTTATTTTGTATGTAATGTCACAGTTATGC | 1205 |
| Db | 6173 | CAAGGCCCGGAGACAGGAAGGCTACACGCTCCTCTATACGGAACCGTCCACAGGCTATGT | 6232 |
| Qy | 1206 | TTTGGGTGTGTTCTTAGACCAAGATGTTAAATGTATAGTACTATGTGAAGAACCATCTTACAG | 1265 |
| Db | 6233 | GCTCAAGAGCGCGCGCGCGGAGTGTACCGAAGCGAGACCGGAGACCCCGAGTACG | 6292 |
| Qy | 1266 | ACAACAAAGCTGCTGTTTCATTTAGGCTAGTGAAGCATGATGATGTAAGATGTTGCTGTTTT | 1325 |
| Db | 6293 | GCAGAGTCAGCAATGCCCCCTGAGCAAGAAAGACCCAGCAGGCGAGACGTGGCGGTGT | 6352 |
| Qy | 1326 | TGCTAAGAGTCCACAAGCTCATTTGGTTCATGTTTCAAGATGTAAGAACTTTTGTGTC | 1385 |
| Db | 6353 | CGCGGCGGCGCGGAGCGGCAACTGTGTTCACGGCGTGCAGAGAGCACTTCATAGCGCA | 6412 |
| Qy | 1386 | TATTAATGCTTTTGTGTGTGTGTGAACCATCACTGATTTGTAATTTTCCAGCTCCAGC | 1445 |
| Db | 6413 | CGTATATGCTTTCGCGGCTGCTGAGAACCCCTTACACCGCTGCGACCTGGGGCGCCCCCGC | 6472 |

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1 OTHER INFORMATION: Description of Artificial Sequence: plasmid phcap 4
2 FEATURE:
3 NAME/KEY: CDS
4 LOCATION: (497)..(772)
5 FEATURE:
6 NAME/KEY: CDS
7 LOCATION: (1425)..(6500)
8 FEATURE:
9 NAME/KEY: CDS
10 LOCATION: (8579)..(9034)
11 FEATURE:
12 NAME/KEY: CDS
13 LOCATION: (10191)..(10445)
14 FEATURE:
15 NAME/KEY: CDS
16 LOCATION: (11877)..(12734)
17 FEATURE:
18 NAME/KEY: misc_feature
19 LOCATION: (11..774)
20 OTHER INFORMATION: Vaccinia Virus thymidine Kinase gene recombination
21 FEATURE:
22 NAME/KEY: promoter
23 LOCATION: (794)..(816)
24 OTHER INFORMATION: T7 promoter
25 FEATURE:
26 NAME/KEY: misc_feature
27 LOCATION: (846)..(1424)
28 OTHER INFORMATION: EMC/Internal Ribosome Entry Site (IRES)
29 FEATURE:
30 NAME/KEY: misc_feature
31 LOCATION: (1426)..(1437)
32 OTHER INFORMATION: MCS (Multiple Cloning Site)
33 FEATURE:
34 NAME/KEY: misc_feature
35 LOCATION: (1146)..(2318)
36 OTHER INFORMATION: HCV E2/ NS2 domain
37 FEATURE:
38 NAME/KEY: misc_feature
39 LOCATION: (2319)..(4231)
40 OTHER INFORMATION: HCV NS3 Domain containing the serine protease and
41 OTHER INFORMATION: helicase enzymes
42 FEATURE:
43 NAME/KEY: misc_feature
44 LOCATION: (4203)..(4260)
45 OTHER INFORMATION: HCV NS3-NS4A cleavage site
46 FEATURE:
47 NAME/KEY: misc_feature
48 LOCATION: (4375)..(4424)
49 OTHER INFORMATION: HCV NS4A-4B cleavage site
50 FEATURE:
51 NAME/KEY: misc_feature
52 LOCATION: (4233)..(4394)
53 OTHER INFORMATION: HCV NS4A domain
54 FEATURE:
55 NAME/KEY: misc_feature
56 LOCATION: (4395)..(4919)
57 OTHER INFORMATION: HCV NS4B Domain
58 FEATURE:
59 NAME/KEY: misc_feature
60 LOCATION: (4920)..(4991)
61 OTHER INFORMATION: HCV NS5A-NS5B cleavage site
62 FEATURE:
63 NAME/KEY: misc_feature
64 LOCATION: (4992)..(6501)
65 OTHER INFORMATION: SEAP Protein
66 FEATURE:
67 NAME/KEY: misc_feature
68 LOCATION: (7915)..(7945)
69 OTHER INFORMATION: MCS (Multiple Cloning Site)
70 FEATURE:
71 NAME/KEY: terminator
72 LOCATION: (7938)..(8078)

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OTHER INFORMATION: term T7
FEATURE:
NAME/KEY: Promoter
LOCATION: (8080)..(8365)
OTHER INFORMATION: Vaccinia virus promoter; early/late promoter
FEATURE:
NAME/KEY: misc feature
LOCATION: (8560)..(11317)
OTHER INFORMATION: E. coli gpt; for selection of recombinants
FEATURE:
NAME/KEY: misc feature
LOCATION: (11318)..(11390)
OTHER INFORMATION: remaining DNA from 3' end of Tropicx pcMV/SEAP
US-09-263-933-15

Query Match      38.8%; Score 572.8; DB 3; Length 13910;
Best Local Similarity 62.4%; Pred. No. 1.2e-141;
Matches 898; Conservative 0; Mismatches 542; Indels 0; Gaps 0;

QY 6 CTTGATTCCAGCTGAAGAAATCCAGCTTTTGGAAATGACAGCTCTCAAGCTT 65
DB 5033 CATCATCCCGAGTTGAGAGAGAAACCGGACTTCTGGAACCGGAGGCAAGCCGAGGCCCT 5092
QY 66 GAGATGTGCTAAGAAAGTTCACCAATTCAGCTGCTAAGAAATGTTATTTGTTT 125
DB 5093 GGGTCCGCGCAAGAGCTGACGCTGACACAGACGCGCCAAAGAACTTCATCTTCT 5152
QY 126 GGGGTATGATGAGGTTGTCACACTGTTACTGCTACTAGAAATTTGAAGGTCAAATGAA 185
DB 5153 GGGCGATGGGATGGGGGTGTCTAGGTTGACAGCTGCGAGATCCTAAAGGGGAGAAAGAA 5212
QY 186 TGGTAAGTGGGTCGCAAACTCGATTGGCTATGATCAATTTCCATAGCTTGTCTTGT 245
DB 5213 GGAACAACCTGGGCTGAGATACCCCTGGCCATGACCGCTTCCCATATGTGGCTGTGTC 5272
QY 246 TAAGACTTACATGTTGATGACAAAGTTCCAGATTCGCTGATCTACTGCTTACTT 305
DB 5273 CAAGACATACATGTTAGAACAACTGTGCCAGACAGTGGAGCCACAGCCACGGCTTACT 5332
QY 306 GTGTGTGTTAAGGATTAATTAAGAACTATTTGTTTCTGCTGCTGCTAGATCAATCA 365
DB 5333 GTCCGGGGGTCAAGGGCAATCTCCAGACCATTTGGCTTGAAGTGAAGCCGCGCTTTAACCA 5392
QY 366 ATGTATATCTAATAGAGATTAAGATTAATCTTCTGTTATTAATAGACTTAAGAGCTGG 425
DB 5393 GTGCAACACGACACGCGGCAACGAGTCTATCTCGTATGAATCGGGCCAAAGAAAGAGG 5452
QY 426 TAAGGCTGTTGTTGTTTACTACTACTAGATTCACATGCTTCTGACGCTGGTCTTA 485
DB 5453 GAAGTCACTGGAGTGTAAACACACACAGAGTGCACAGCCTTCGCGACGCGCACCTTA 5512
QY 486 CGCTCACTACTGTTAATGAATTTGTTACTGATGATGATTTGCTCAGCTGATGCTCAAAA 545
DB 5513 CGGCCACACGCTGAACCGCACTGTTACTGGAAGCCGAGTGTCTGCTGCGCCGCCCA 5572
QY 546 GAATGTTGTCAGATATTCCTGCTCAATGTTTACATATGATGATATGATGTTATTTT 605
DB 5573 GAGAGGGGTGCACAGATCTGCTACGAGCTCATCTCCAAATGATGATGATGATGATGAT 5632
QY 606 GGGTGGTGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 665
DB 5633 AGGTGGAGGCGCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5692
QY 666 TGCTTCTGTTAATGTTTGAAGAAAGATTAAGCAAAATTTGTTCAAGATGAGCAAGTAA 725
DB 5693 CTAGAGCAGAGTGGAGCAAGGCTGAGCGGAGAAATCTGCTGAGAAATGCTGCGGAGAA 5752
QY 726 GCATCAAGGTGCTCAATATGTTGAAATGAACTGCTTGTGCAAGCTGCTGATGATTC 785
DB 5753 GCGCCAGGGGTGCCCGGATGTGTGAAACCGCAGCTGAGCTGATGAGGCTTCCCTGAGCC 5812
QY 786 TAGTGTTACTCATTTGATGAGGTTTGTGTTGAACAGCTGATGATGAATGATGATGATGATG 845
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DB 5813 GTCGTGACCACTCATGAGGTCTCTTTGAGCTCGAGACATGAATACAGATATCCACCG 5872
QY 846 AGATCATCTAAGATTCACACTTTGCTGAAATGACTGAAGCTGCTTTGCAAGTTTGTTC 905
DB 5873 AGACTCCACACTGAGACCTCCCTGATGAGATGAGACAGAGGCTGCTGCTGCTGAG 5932
QY 906 TAGAAATCCAAAGAGTTTACTTGTGTTGTAAGGAGTGAATGATGATGATGATGATGATG 965
DB 5933 CAGAAACCCCGGCGCTTCTTCTTCTGAGAGGTGCTGATGATGATGATGATGATGATGATG 5992
QY 966 TGATGTAAGGCTTATATGCTTTGACTGTAAGTATGATGATGATGATGATGATGATGATG 1025
DB 5993 TGAACACAGGCTTACCGGCACTGAGACATGATGATGATGATGATGATGATGATGATGAG 6052
QY 1026 GGTAAATGAATGACTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1085
DB 6053 GCGGGCCAGCTCACAGGAGAGAGACAGCTGAGACCTGCTGCTGCTGCTGCTGCTGCTGCT 6112
QY 1086 TGTGTTTCTTGTGTTGTTTACACTTGAAGGATCTTATTTGTTGTTGTTGTTGTTGTTG 1145
DB 6113 GCTTCTTCTTCTGAGGCTTACCTTCTGAGGAGCTGATTTGAGGCTGCTGCTGCTGCTG 6172
QY 1146 TAAGCTTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1205
DB 6173 CAGGCGCGGAGACAGAGGCTTACAGGCTTCTATAGGAAACGCTCAGGCTATGT 6232
QY 1206 TTTGGTGTGTTTCTAAGCAGATGTTATGTTAGTACTGATGATGATGATGATGATGATG 1265
DB 6233 GCTCAAGACGCGCGCGCGGCTGATGTTACGAGACGAGAGCGGAGCCCGAGATGTC 6292
QY 1266 ACAACAAGCTGCTGTTCCATGTCCTAGTGAATCTGATGATGATGATGATGATGATGATG 1325
DB 6293 GCAGCAGTACAGGCTCCCTGAGCAAGAGACCCAGAGGAGAGCTGCGGGGT 6352
QY 1326 TGCTAAGGCTCCAGACTCATTTGCTGATGTTGTTCAAGAAAGAACTTTGCTCA 1385
DB 6353 CGCGCGCGCGCGCGAGCGCACTGTTTCAAGGCTGAGAGACACCTTCAATAGGCA 6412
QY 1386 TATTATGCTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 1445
DB 6413 CGTATGAGCTTGTGCGCGCTGCTGAGGCTTACACGCGCTGAGCCTGCGCGCGCG 6472

RESULT 8
US-09-919-901-1
Sequence 1, Application US/09919901
GENERAL INFORMATION:
APPLICANT: Potts, Karen E.
APPLICANT: Jackson, Amy K.
APPLICANT: Jackson, Roderica L.
TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
FILE REFERENCE: 0125-0005A
CURRENT APPLICATION NUMBER: US/09/919,901
CURRENT FILING DATE: 2001-08-02
PRIOR APPLICATION NUMBER: 09/263,933
PRIOR FILING DATE: 1999-02-08
PRIOR APPLICATION NUMBER: 09/129,611
PRIOR FILING DATE: 1998-08-05
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 13910
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: plasmid phcap 1
NAME/KEY: CDS
LOCATION: (497)...(772)
FEATURE:
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NAME/KEY: CDS
LOCATION: (1425)..(6500)
FEATURE:
NAME/KEY: CDS
LOCATION: (8579)..(9034)
FEATURE:
NAME/KEY: CDS
LOCATION: (10191)..(10445)
FEATURE:
NAME/KEY: CDS
LOCATION: (11877)..(12734)
FEATURE:
NAME/KEY: misc.feature
LOCATION: (1)..(774)
OTHER INFORMATION: Vaccinia Virus thymidine kinase gene recombination
OTHER INFORMATION: site
FEATURE:
NAME/KEY: promoter
LOCATION: (794)..(816)
OTHER INFORMATION: T7 promoter
FEATURE:
NAME/KEY: misc.feature
LOCATION: (846)..(1424)
OTHER INFORMATION: EMC/Internal Ribosome Entry Site (IRES)
FEATURE:
NAME/KEY: misc.feature
LOCATION: (1426)..(1437)
OTHER INFORMATION: MCS (Multiple Cloning Site)
FEATURE:
NAME/KEY: misc.feature
LOCATION: (1446)..(2318)
OTHER INFORMATION: HCV E2/ NS2 domain
FEATURE:
NAME/KEY: misc.feature
LOCATION: (2319)..(4231)
OTHER INFORMATION: HCV NS3 Domain containing the serine protease and
OTHER INFORMATION: helicase enzymes
FEATURE:
NAME/KEY: misc.feature
LOCATION: (4203)..(4260)
OTHER INFORMATION: HCV NS3-NS4A cleavage site
FEATURE:
NAME/KEY: misc.feature
LOCATION: (4375)..(4424)
OTHER INFORMATION: HCV NS4A-4B cleavage site
FEATURE:
NAME/KEY: misc.feature
LOCATION: (4233)..(4394)
OTHER INFORMATION: HCV NS4A domain
FEATURE:
NAME/KEY: misc.feature
LOCATION: (4395)..(4919)
OTHER INFORMATION: HCV NS4B Domain
FEATURE:
NAME/KEY: misc.feature
LOCATION: (4920)..(4991)
OTHER INFORMATION: HCV NS5A-NS5B cleavage site
FEATURE:
NAME/KEY: misc.feature
LOCATION: (4992)..(6501)
OTHER INFORMATION: SEAP Protein
FEATURE:
NAME/KEY: misc.feature
LOCATION: (7915)..(7945)
OTHER INFORMATION: MCS (Multiple Cloning Site)
FEATURE:
NAME/KEY: terminator
LOCATION: (7938)..(8078)
OTHER INFORMATION: term T7
FEATURE:
NAME/KEY: promoter
LOCATION: (8080)..(8365)
OTHER INFORMATION: Vaccinia virus promoter; early/late promoter

FEATURE:
NAME/KEY: misc.feature
LOCATION: (8560)..(11317)
OTHER INFORMATION: E. coli gpt; for selection of recombinants
FEATURE:
NAME/KEY: misc.feature
LOCATION: (11318)..(13909)
OTHER INFORMATION: remaining DNA from 3' end of Tropix pCMV/SEAP
OTHER INFORMATION: plasmid
US-09-919-901-1
Query Match 38.8%; Score 572.8; DB 4; Length 13910;
Best Local Similarity 62.4%; Pred. No. 1.2e-141;
Matches 898; Conservative 0; Mismatches 542; Indels 0; Gaps 0;
QY 6 CTTGATTCAGCTGAAGAAATTCAGCTTTTGGAAATGACAGAGCTGCTCAAGCTT 65
DB 5033 CATCATCCCAAGTTGGAGAGAAACCGAGCTTCTGAAACCGGAGGAGCGGCGCT 5092
QY 66 GGATGTGCTAAGAGTTGCAACCAATTCAACTGCTGTAAGAAATGTAATTTGTTT 125
DB 5093 GGGTCCCGCAAGAGCTGCAAGCTGCAAGAGAGCGGCAAGAACTCATCTTCT 5152
QY 126 GGGTATGATGATGGGTGTTCCAACTGTAAGTCTAAGAAATTTGAAAGGTCAATGAA 185
DB 5153 GGGCATGGAAATGGGGGTGTCTACGGTGACAGCTGCCAGATCTTAAAGGAGAGAA 5212
QY 186 TGGTAAGTTGGTCCAGAACTCCATTGGCTATGATCAATTTCCATACGTTGCTTGC 245
DB 5213 GACAAACTGGGGCTGAGATACCCCTGCCATGACCGCTTCCATATGGCTCTGTC 5272
QY 246 TAAAGCTTACATATGTTAGTACAAAGTTCAGATTCCTGTAAGTCTGTAAGTCTTACTT 305
DB 5273 CAAGACATCAATGTAGCAAAACATGTCCAGACAGTGAACCAAGCCAGGCTTACT 5332
QY 306 GTGTGTGTTAAGGTAATACAGAACTATTGGTGTCTGCTGCTGTAAGTACATCA 365
DB 5333 GTGGGGGTCAAGGCACTTCCAGACCATTTGGTGTGAGTCAAGCGCGCGCTTAAACA 5392
QY 366 ATGTAATCTACTAGAGTAATGAAGTACTTCTGTTTAAATAGAGTAAGAGGCTGCG 425
DB 5393 GTGCAACAGACACCGGCAACGAGTCACTCCGTATGATCGGGCAAGAAAGCAGG 5452
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DB 5573 GGAGGGGTGCCAGGACATCGCTACGACCTCATCTCCAAATGACCATTTGACGATCT 5632
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DB 5693 CTACAGCCAGGTGGACCAAGCTGACGAGGAAGAACTGCTGACGAATGGCTGGCAA 5752
QY 726 GCATCAAGGTGTCAATATGTTTGAATAGAACTGTTTGTGCAAGCTGCTGATGATTC 785
DB 5753 GGGCAGGGGTGCCGATATGTGTGAACCGCATGAGCTGATGACGCTTCCCTGAGCC 5812
QY 786 TAGTGTACTGATTTGATGGGTTGTTTGAACCAAGCTGATAGTAAGTAAATGTTCAACA 845
DB 5813 GTCTGTGACCATCTCATGGGTCTCTTTGAGCTTGGAGACATGAATACGAGATCCACG 5872
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| Db | 5873 | AGACTCCACACTGAGACCCCTCCCTATGATGAATGACAGAGGCTGCGCTGGCCCTGCTGAG | 5992 |
| Qy | 906 | TAGAAATTCAMAGAGCTTTTACTGTTGTTGTTGAAGGTGTGTAATGATCATGTGCATCA | 965 |
| Db | 5933 | CAGGAACCCCGCGGCTTCTTCTTGTGTGAGGGTGTGTGCATCGACATGTGTCA | 5992 |
| Qy | 966 | TGATGTTAAGGCTTATATGAGCTTTGACTGTAAGCTTATATGTTGTAATGCTATTTGCTAA | 1025 |
| Db | 5993 | TGAAAGCAGGGCTTACCGGGCACTGACTGAGACGATCATGTTTCGACGCGCATTTGAGAG | 6052 |
| Qy | 1026 | GGCTAATGAATGACTTCTGTAATGGATATCTTGAATTTTGGTTACTGCTGATCATATCA | 1085 |
| Db | 6053 | GGCGGGCAGGCTACACAGCAGGAGGAGCAGCGTAGCCTGCTACCTCGACACACTCCCA | 6112 |
| Qy | 1086 | TGTTTTTCTTTTGTGTTGTTACACTTTGAGAGTACTTCAATTTTGTGTTGCTCCAGG | 1145 |
| Db | 6113 | CGTCTTCTCTCGGAGGCTACCCCTTGCAGGGAGCTGCATCTTCGGGGCTGGCCCTGG | 6172 |
| Qy | 1146 | TAAAGCTTGAATGTAAGTACTTACCTTCAATTTTGTATGTAATGTTCCAGGTTATGC | 1205 |
| Db | 6173 | CAGGCGCCGGACAGAAAGGCTTACACGGTCTCTCTATACGAAACGTTCCAGGCTATGT | 6232 |
| Qy | 1206 | TTTGGGTGTGTTCTTAGACAGATGTTAATGTAGTACTGATGTAAGAACATCTTACAG | 1265 |
| Db | 6233 | GCTCAGAGACGGCGCCCGCGCGGATGTTACCGAGCGAGCGGAGCCCGAGTATCG | 6292 |
| Qy | 1266 | ACAAACAACCTGCTGTTCATTGGCTAGTGAACCTCATGTTGTTGAAGTGTGCTGTTT | 1325 |
| Db | 6293 | GCAGACGTACAGACGTGCCCTCGAAGAGACCCACGACGAGCGAGCGTGGCGGT | 6352 |
| Qy | 1326 | TGCTAGAGCTCCACAAGCTCATTTGTTGTTGATGCGTTTAAAGAAACTTTTGTGCTCA | 1385 |
| Db | 6353 | CGCGGCGGCGCGGAGGCGACCTGTGTTCAAGCGGTGACAGAGACACTTCATATAGCGCA | 6412 |
| Qy | 1386 | TATTATGCTTTTGTGTTGTTGTTGAACATACACTGATTTGTAATTTGCCAGCTCCAGC | 1445 |
| Db | 6413 | CGTATGCGCTTCGCGCGCTGCTGAGGCTTACACGCGCTGCGACCTGGCGCCCGCGC | 6472 |
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| US-09-919-901-8 | | | |
| Sequence 8, Application US/09919901 | | | |
| Patent No. 6599738 | | | |
| GENERAL INFORMATION: | | | |
| APPLICANT: Potts, Karen E. | | | |
| APPLICANT: Jackson, Roberta L. | | | |
| APPLICANT: Patrick, Amy K. | | | |
| TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT | | | |
| TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE | | | |
| FILE REFERENCE: 0125-0005A | | | |
| CURRENT APPLICATION NUMBER: US/09/919,901 | | | |
| CURRENT FILING DATE: 2001-08-02 | | | |
| PRIOR APPLICATION NUMBER: 09/263,933 | | | |
| PRIOR FILING DATE: 1999-02-08 | | | |
| PRIOR APPLICATION NUMBER: 09/129,611 | | | |
| PRIOR FILING DATE: 1998-08-05 | | | |
| NUMBER OF SEQ ID NOS: 33 | | | |
| SOFTWARE: PatentIn Ver. 2.0 | | | |
| SEQ ID NO 8 | | | |
| LENGTH: 13910 | | | |
| TYPE: DNA | | | |
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| LOCATION: (8579)..(9034) | | | |

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LOCATION: (10191)..(10445)
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NAME/KEY: CDS
LOCATION: (11877)..(12734)
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)..(774)
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OTHER INFORMATION: site
FEATURE:
NAME/KEY: promoter
LOCATION: (794)..(816)
OTHER INFORMATION: T7 promoter
FEATURE:
NAME/KEY: misc_feature
LOCATION: (846)..(1424)
OTHER INFORMATION: EMC/Internal Ribosome Entry Site (IRES)
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1426)..(1437)
OTHER INFORMATION: MCS (Multiple Cloning Site)
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1446)..(2318)
OTHER INFORMATION: HCV E2/ NS2 domain
FEATURE:
NAME/KEY: misc_feature
LOCATION: (2319)..(4231)
OTHER INFORMATION: HCV NS3 Domain containing the serine protease and
OTHER INFORMATION: helicase enzymes
FEATURE:
NAME/KEY: misc_feature
LOCATION: (4203)..(4260)
OTHER INFORMATION: HCV NS3-NS4A cleavage site
FEATURE:
NAME/KEY: misc_feature
LOCATION: (4375)..(4424)
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FEATURE:
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NAME/KEY: misc_feature
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OTHER INFORMATION: SEAP Protein
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OTHER INFORMATION: MCS (Multiple Cloning Site)
FEATURE:
NAME/KEY: terminator
LOCATION: (7938)..(8078)
OTHER INFORMATION: term T7
FEATURE:
NAME/KEY: promoter
LOCATION: (8080)..(8365)
OTHER INFORMATION: Vaccinia virus promoter; early/late promoter
FEATURE:
NAME/KEY: misc_feature
LOCATION: (8560)..(11317)
OTHER INFORMATION: E. coli gpt; for selection of recombinants
FEATURE:

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LOCATION: (11877)..(12734)
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 NAME/KEY: misc feature
 LOCATION: (11..)(774)
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 OTHER INFORMATION: site
 FEATURE:
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 LOCATION: (794)..(816)
 OTHER INFORMATION: T7 promoter
 FEATURE:
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 LOCATION: (846)..(1424)
 OTHER INFORMATION: EMC/Internal Ribosome Entry Site (IRES)
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 OTHER INFORMATION: helicase enzymes
 FEATURE:
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 OTHER INFORMATION: HCV NS4A-4B cleavage site
 FEATURE:
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 LOCATION: (4395)..(4919)
 OTHER INFORMATION: HCV NS4B Domain
 FEATURE:
 NAME/KEY: misc feature
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 LOCATION: (7938)..(8078)
 OTHER INFORMATION: term T7
 FEATURE:
 NAME/KEY: promoter
 LOCATION: (8080)..(8365)
 OTHER INFORMATION: Vaccinia virus promoter; early/late promoter
 FEATURE:
 NAME/KEY: misc feature
 LOCATION: (8560)..(11317)
 OTHER INFORMATION: E. coli gpc; for selection of recombinants
 FEATURE:
 NAME/KEY: misc feature
 LOCATION: (11318)..(13909)
 OTHER INFORMATION: remaining DNA from 3' end of Tropic pCMV/SEAP
 OTHER INFORMATION: plasmid
 US-09-919-901-15

Query Match 38.8%; Score 572.8; DB 4; Length 13910;
 Best Local Similarity 62.4%; Pred. No. 1.2e-141;
 Matches 1898; Conservative 0; Mismatches 542; Indels 0; Gaps 0;

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| QY | 6 | CTTGATTCCAGCTGGAAGAAATCCAGCTTTTGGAAATAGACAAAGCTGCTAAGCTTT | 65 |
| DB | 5033 | CATCATCCCAAGTTGAGAGAGAGAAACCGGACCTTCGAAACCGGAGCAGCCAGGCCCT | 5092 |
| QY | 66 | GGATGTTGCTAAGAAATTCGCAACCAATTCMAACTGCTGTAGAAATGTTATTTT | 125 |
| DB | 5093 | GGGTGCGCCAGAGAGCTGAGCTTGACAGACAGCCGCGCAAGACTTATCTTCT | 5152 |
| QY | 126 | GGGTGATGATGAGGTGTTTCAACTGTTACTGTTACTAGAAATTTGAAGGTCMAATGA | 185 |
| DB | 5153 | GGGCGATGGGATGGGGGTCTTACGTTAGAGCTGACGAGATCTTAAAGGCGAAGAA | 5212 |
| QY | 186 | TGCTAAGTTGGTCCAGAACTCCATTGGCTATGATCAATTTCCATAGCTTCTTGT | 245 |
| DB | 5213 | GGACAAACTGGGGCTGAGATACCCCTGGCCATGACCCCTTCCATATGTGCTGT | 5272 |
| QY | 246 | TAAAGCTTACATGTTGATAGACAAATTCAGATTCGTGTGATCTAAGCTTACTT | 305 |
| DB | 5273 | CAGACATACAAATGAGACAAACATGTGCAAGTGAAGCCACAGCCGCTTACCT | 5332 |
| QY | 306 | GTGTGTTTAAAGGTTAATTAAGAACTATTGGTGTCTGTGCTGATAGATACATCA | 365 |
| DB | 5333 | GTGCGGGGTCAAGGCACTTCAGACCATTTGCTGATGACGCGCCGCTTTAACCA | 5392 |
| QY | 366 | ATGTAATACTACTAGAGATAGAAATGTAATCTTGTATTAATAGATTAAGAGCTGG | 425 |
| DB | 5393 | GTGCAACACGACGCGGCAAGAGGTCACTCCGTGATGAATCGGGCAAGAACAGG | 5452 |
| QY | 426 | TAAAGCTGTTGGTGTGTTACTACTAGATTCAAATGCTTCTCCAGCTGCTGCTTA | 485 |
| DB | 5453 | GAAGTAGTGGAGGTGTGAACCAACAGAGTGCACAGCTCCGCGCCGCACTTA | 5512 |
| QY | 486 | CGCTCATCTGTTAATAGAAATGTAATCTGTGATGCTGATTTGCGAGCTGATCTCAAA | 545 |
| DB | 5513 | CGCCCAAGGTGACCGCACTGTAATCTGAGCGCGAGTCTGCTCGGCGCCCA | 5572 |
| QY | 546 | GATGTTGTCAAGATATGCTGCTCAATTTGTTTCAATATGATATGATGTTATTT | 605 |
| DB | 5573 | GAGGGGTGCGAGGACATGCTACGCACTCAATCTCAATGATGATGACGTATCT | 5632 |
| QY | 606 | GGGTGTTGTAATATGATGATGATGATGATGATGATGATGATGATGATGATGATG | 665 |
| DB | 5633 | AGGTGAGGCGGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATG | 5692 |
| QY | 666 | TGCTTCTGTTAATGTTAAGAAATGTAAGAAATTTGTTCAAGAAATGCAAGCTTA | 725 |
| DB | 5693 | CTACAGCCAAAGGTGGACAGGCTGAGCGGAAATGTTGTCAGAAATGTCGCGAA | 5752 |
| QY | 726 | GCATCAAGTGTCTCAATATGTTTGAATAGAACTGTTTGGCAAGCTGCTGATATTC | 785 |
| DB | 5753 | GGCCAGGAGTGGGTTATGTGTGAACCGCACTGAGCTGATGCAAGCTTCCCTGACCC | 5812 |
| QY | 786 | TAGTGTACTCATTTGATGAGGTTTGTGAACAGCTGATATGATGATGATGATGATG | 845 |
| DB | 5813 | GTCTGTGACCCATCTCATGAGGCTCTTTGAGCTGAGAGCATGAATATACAGATCCACC | 5872 |
| QY | 846 | AGATCATCTAAGATCCAACTTGGCTGAATATGATGAAGCTGCTTGCAGTTTGTTC | 905 |
| DB | 5873 | AGACTCCACACTGAGACCTCCCTGATGAGATGAGAGAGGCTGCGCTGCTGAG | 5932 |
| QY | 906 | TAGAATCCAAAGGTTTATCTTGTGTTGATGAGGTGATGATGATGATGATGATGATG | 965 |
| DB | 5933 | CAGGAACCCCGGGGCTTCTTCTCTTCTGAGAGGTTGATGATGATGATGATGATGATG | 5992 |
| QY | 966 | TGATGTAAAGCTTATATGCTTTGACTGAAGCTATATGATGATGATGATGATGATG | 1025 |
| DB | 5993 | TGAACCAAGGCTTACCGGGCACTGACGATGATGATGATGATGATGATGATGATGAG | 6052 |

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| QY | 1026 | GGCTAATGAATTGACTCTTGAAATTGGATACCTTTGATTTTGGTACTGCTGATCATATGCA | 1085 |
| Db | 6053 | GGCGGGCCAGCTCACACGACGAGAGAACGCTGAGCCTGCTCATCTGCCACACTCCCA | 6112 |
| QY | 1086 | TGTTTTCTTTTGGTGGTTACACTTGTAGAGGTACTCTAATTTTGGTTTGGCTCCAGG | 1145 |
| Db | 6113 | CGTCTTCTCTTGGAGGCTACCCCTCGAGGAGCTGCACTCTTCGGGCTGGCCCCCTGG | 6172 |
| QY | 1146 | TAAAGCTTTGGATAGTAAGTCTTACACTTCTAATTTTGTATGTAATGGTCCAGGTTATGC | 1205 |
| Db | 6173 | CAAGGCCCGGGAACAGAAAGGCTTACACAGTCCCTCTATACGAAACGGTCCAGGCTATGT | 6232 |
| QY | 1206 | TTTGGGTGTGGTTTAAACCAAGATGTTAAATGTATGTACTATGTGAAGAACCATCTTACAG | 1265 |
| Db | 6233 | GCTCAGAGACGGCGCCGCCGCGGAGTATACGAGACGACGAGCCGGAGCCCCGAGTATCG | 6292 |
| QY | 1286 | ACAACAACTGCTGTTTCATATGGCTAGTGAAGAACTCATGATGGTGAAGATGTTGCTGTTT | 1353 |
| Db | 6293 | GCAGCACTCAGCAGTGTCCCTTGACGAAGAGACCCACGACGGCCGAGACGTGGCGGTCTT | 6352 |
| QY | 1326 | TGCTAGAGGTCCACAGCTCAATTTGGTTCATAGTGTTCMAAGAAACATTTTGTGTCTCA | 1385 |
| Db | 6353 | CGCGGGGGCCGACGAGGCAACTGTCTTCAAGCGGTGACGAGACGACCTTCATAGCGCA | 6412 |
| QY | 1386 | TATTTATGGCTTTTGTGTGTGTGTGAACCATACCTGATGTGTAATTTGCCAGCTCCAGC | 1445 |
| Db | 6413 | CGTACATGCTCTTCGCGCGCTGCTGTGAGCCCTTACACCGCTCTGCACCTGGGCGCCCCCGC | 6472 |

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1 RESULT 11
2 US-10-191-966-1
3 ; Sequence 1, Application US/10191966
4 ; Patent No. 6790612
5 ; GENERAL INFORMATION:
6 ; APPLICANT: Potts, Karen E.
7 ; APPLICANT: Jackson, Roberta L.
8 ; APPLICANT: Patck, Amy K.
9 ; TITLE OF INVENTION: REORDERER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
10 ; TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
11 ; FILE REFERENCE: 0125-0005A
12 ; CURRENT APPLICATION NUMBER: US/10/191,966
13 ; CURRENT FILING DATE: 2002-07-10
14 ; PRIOR APPLICATION NUMBER: US/09/263,933
15 ; PRIOR FILING DATE: 1999-03-08
16 ; PRIOR APPLICATION NUMBER: 09/129,611
17 ; PRIOR FILING DATE: 1998-08-05
18 ; NUMBER OF SEQ ID NOS: 33
19 ; SOFTWARE: PatentIn Ver. 2.0
20 ; SEQ ID NO 1
21 ; LENGTH: 13910
22 ; TYPE: DNA
23 ; ORGANISM: Artificial Sequence
24 ; FEATURE:
25 ; OTHER INFORMATION: Description of Artificial Sequence: plasmid phcap 1
26 ; NAME/KEY: CDS
27 ; LOCATION: (497)..(772)
28 ; NAME/KEY: CDS
29 ; LOCATION: (1425)..(6500)
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31 ; LOCATION: (18579)..(9034)
32 ; NAME/KEY: CDS
33 ; LOCATION: (10191)..(10445)
34 ; NAME/KEY: CDS
35 ; LOCATION: (11877)..(12734)
36 ; NAME/KEY: misc_feature
37 ; LOCATION: (1)..(774)
38 ; OTHER INFORMATION: Vaccinia Virus thymidine kinase gene recombination
39 ; NAME/KEY: promoter
40 ; LOCATION: (794)..(816)
41 ; OTHER INFORMATION: T7 promoter
42 ; NAME/KEY: misc_feature
43 ; LOCATION: (846)..(1424)

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1 OTHER INFORMATION: EMC/Internal Ribosome Entry Site (IRES)
2 NAME/KEY: misc feature
3 LOCATION: (1426)..(1437)
4 OTHER INFORMATION: MCS (Multiple Cloning Site)
5 NAME/KEY: misc feature
6 LOCATION: (1445)..(2318)
7 OTHER INFORMATION: HCV E2/ NS2 domain
8 NAME/KEY: misc feature
9 LOCATION: (2319)..(4231)
10 OTHER INFORMATION: HCV NS3 Domain containing the serine protease and
11 OTHER INFORMATION: helicase enzymes
12 NAME/KEY: misc feature
13 LOCATION: (4203)..(4260)
14 OTHER INFORMATION: HCV NS3-NS4A cleavage site
15 NAME/KEY: misc feature
16 LOCATION: (4375)..(4424)
17 OTHER INFORMATION: HCV NS4A-4B cleavage site
18 NAME/KEY: misc feature
19 LOCATION: (4233)..(4394)
20 OTHER INFORMATION: HCV NS4A domain
21 NAME/KEY: misc feature
22 LOCATION: (4395)..(4919)
23 OTHER INFORMATION: HCV NS4B Domain
24 NAME/KEY: misc feature
25 LOCATION: (4920)..(4991)
26 OTHER INFORMATION: HCV NS5A-NS5B cleavage site
27 NAME/KEY: misc feature
28 LOCATION: (4992)..(6501)
29 OTHER INFORMATION: SEAP Protein
30 NAME/KEY: misc feature
31 LOCATION: (7915)..(7945)
32 OTHER INFORMATION: MCS (Multiple Cloning Site)
33 NAME/KEY: terminator
34 LOCATION: (7938)..(8078)
35 OTHER INFORMATION: term T7
36 NAME/KEY: promoter
37 LOCATION: (8080)..(8365)
38 OTHER INFORMATION: Vaccinia virus promoter; early/late promoter
39 NAME/KEY: misc feature
40 LOCATION: (8560)..(11317)
41 OTHER INFORMATION: E. coli gpt; for selection of recombinants
42 NAME/KEY: misc feature
43 LOCATION: (11318)..(113909)
44 OTHER INFORMATION: remaining DNA from 3' end of Tropic pCMV/SEAP
45 OTHER INFORMATION: plasmid
46 US-10-191-966-1

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| Query Match | 38.8% | Score 572.8; | DB 4; | Length 13910; |
| Best Local Similarity | 62.4% | Pred. No. 1.2e-141; | | |
| Matches 898; Conservative | 0; | Mismatches 542; | Indels 0; | Gaps 0 |

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| Oy | 6 | TTTGATTCCACTGAAGAAATAATCCAGCTTTTGGAAATGACAAAGTGCTCAAGCTTT | 65 |
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| Oy | 66 | GGATGTGCTAAGAAATTGCCAACCAATTCAACTGCTCTAAGATGTATTATTTGGTTTT | 125 |
| Db | 5093 | GGGTGCCGCCAAGAAAGCTGACGCTTCGACACAGACGCGCCAAAGACCTCATCATCTTCC | 515 |
| Oy | 126 | GGGTGATGGTATGGGTGTTCCAACTGTACTGCTACTAGAAATTTTGAAGGGTCAATGAA | 185 |
| Db | 5153 | GGGGGATGGGATGGGGGGTGTCTACGGTGACAGCTGCCAGGATCTCCAAAAGGGCAGAAAGA | 521 |
| Oy | 186 | TGTGTAAGTTGGGATCCAGAAATCCATTGGCATGGATCAATTTCCATACGTTGCTTGGC | 245 |
| Db | 5213 | GGACAACTGGGGCCCTGAGATACCCCTGGCCATGGACCGCTTCCCAATATGGGCTCTGTC | 527 |
| Oy | 246 | TAAGACTTACATGTTGATTAGACAAGTTCAGATTCTGCTGTACTGCTTACTT | 305 |
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| Oy | 306 | GTGTGTGTTTAAGGGTAAATTACAGAACTATTGGTGTCTTCTGCTGCTAGATACATCA | 365 |


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LOCATION: (4992)..(6501)
OTHER INFORMATION: SEAP Protein
NAME/KEY: misc_feature
LOCATION: (7915)..(7945)
OTHER INFORMATION: MCS (Multiple Cloning Site)
NAME/KEY: terminator
LOCATION: (7938)..(8078)
OTHER INFORMATION: term T7
NAME/KEY: promoter
LOCATION: (8080)..(8365)
OTHER INFORMATION: Vaccinia virus promoter; early/late promoter
NAME/KEY: misc_feature
LOCATION: (8560)..(11317)
OTHER INFORMATION: E. coli gpt; for selection of recombinants
NAME/KEY: misc_feature
LOCATION: (11318)..(113909)
OTHER INFORMATION: remaining DNA from 3' end of Tropic pCMV/SEAP
IS-10-191-966-8

```

| | | | | |
|-----------------------|-----------------|---------------------|-----------|---------------|
| Query Match | 38.8% | Score 572.8; | DB 4; | Length 13910; |
| Best Local Similarity | 62.4%; | Pred. No. 1.2e-141; | | |
| Matches 898; | Conservative 0; | Mismatches 542; | Indels 0; | Gaps 0; |

| | | | |
|----|------|--|------|
| QY | 6 | CTTAATTCACACTGAAAGAAAGAAATCCAGCTTTTGGATATGACAAGCTGCTCAAGCTTT | 65 |
| Db | 5033 | CATCATCCCACTGTAGAGAGAGAACCCGGACTTCTGGAACCGCAGGACGCCAGGCCCC | 5092 |
| QY | 66 | GGATGTTGCTAAGAAAGTTGCAACCAATTCAGCTGCTCTAAGATGTATTTGTTTT | 125 |
| Db | 5093 | GGGTGCGCCCAAGAAAGCTGACGCTCGACAAGACGCCGCAAGAACCTCATCTTCC | 5155 |
| QY | 126 | GGGTGATGTGATGCGTGTTCCACTGTTACTGCTACTTGAAATTTGAAAGGTCMAATGA | 185 |
| Db | 5153 | GGGGGATGGGATGGGGGGTGTCTACCGTACACGCTCCAGCATCTCTAAAGGGCAGAA | 5212 |
| QY | 186 | TGTGAATGTTGGGATCCAGAAACCTCCATTGGCATATGGATCAATTCATAGTTGCTTTC | 245 |
| Db | 5213 | GGACAACTGGGGGCTTGATATCCCTGACATGGACCGCTTCCATATGTGGCTGTGC | 5272 |
| QY | 246 | TAAACTTACATGTTGATAGACAAGTTCAGATTCTGCTGTACTGCTACTGCTTACTT | 305 |
| Db | 5273 | CAAGACATACATGTATGACAAACAATGTGCCAGACAGTGGAGCCACAGCCAGCCCTACT | 5333 |
| QY | 306 | GTTGTGTGTTAAGGTTAATTACAGAACTAATGTGTGTTTCTGCTGCTAGATACATCA | 365 |
| Db | 5333 | GTCGGGGGTCAAGGGCACTTCCAGACATTGGCTTGAATGGAGCGCCCGCTTTAACCA | 5392 |
| QY | 366 | ATGTATATCTATAGAGGTATGAAGTTACTTCTGTATTTAATAGACTAAGAAAGCTGG | 425 |
| Db | 5393 | GTGCAAACCGACACCGCGCAACGAGGTATCTCCGTGATGAATCGGGCCAAAGAAAGCAG | 5452 |
| QY | 426 | TAAAGCTGTTGATGTGTTTACTACTACTAGAGTTCAACATGCTTCTCCAGCTGGTCTTA | 485 |
| Db | 5453 | GAACTCACTGGGAATGTGTATCCACCAACACAGATGACACGCTTCCAGCGCGACCTA | 5512 |
| QY | 486 | CGCTCATATCTGTATATAGAAATTTGTACTCTGATGCTGATTTGCCAGCTGATGCTCAAA | 545 |
| Db | 5513 | CGCCCAACGGTGAACCGCAATCGTATCTCGGAGCGCAACGCTGCTCGGCGCCGCA | 5572 |
| QY | 546 | GAATGTGTCTAAGATATTTGCTGCTCAATTTGGTTTACATATGATATTTGATTTATTT | 605 |
| Db | 5573 | GGAGGGGTCCAGGACATCGCTACGACACTCATCTCAACATGGAACATTTGACGTATCTT | 5632 |
| QY | 606 | GGGTGGGTGTGAATGTACATGTTTCCAGAAAGTATCTCAATCCAGAAATCCAGATGA | 665 |
| Db | 5633 | AGGTGGAGGCCGAAAGTACATGTTTCCATGGGAAACCCAGACCTGTGATACCCAGATGA | 5692 |
| QY | 666 | TGCTTCTGTTATGATGTGTTAAGAAAGATTAACAAATTTGGTTCAAGATGGCAAGTAA | 725 |
| Db | 5693 | CTACAGCCAAAGTGGGACCAAGCTGACCGGAAAGATCTGGTGCAGGAATGGCTGGCAGA | 5755 |
| QY | 726 | GCATCAAGTGCTCAATATGTTTGGAAATGAACTGCTTGTGTGCAAGCTGCTGATATTC | 785 |

| | | | | | | | | | | |
|---|------|------|-----------|--------------|----------|----------|------------|------------|-------------------------|------|
| Db | 5753 | GC | CGCAGAGG | ATCCCGGATATG | TGGAACCG | CAGCTG | AGACTATG | CAGGCTTCC | TGGAACC | 5812 |
| Qy | 786 | TAG | TGTTACTAT | TGATGGG | TTGTTTGA | ACGAGCTG | ATATGA | ATGAATATG | TTCAACA | 845 |
| Db | 5813 | GTC | TGTAGCCAT | CTCATGGG | TCTCTTTG | AGCC | TGAGACAT | GAATGAATAC | GAGATCCACG | 5872 |
| Qy | 846 | AGAT | CATAC | TAAAGGAT | CCAACTT | TGGCTGA | ATATG | ATC | TGAAGCTGCTTTGCAAGTTTGTG | 905 |
| Db | 5873 | AGAC | TCACAC | CTGAGCCCT | CCCTCGAT | GATGAG | ATACAG | AGGCTG | CCCTGCGCCGCTGAG | 5932 |
| Qy | 906 | TAGA | ATCCAA | GAGGTTT | TACTGTTT | GTGTAAG | GAGGTG | AGATATATC | ATGCTGATCA | 965 |
| Db | 5933 | CAG | AGACCCCG | CGGCTTCTT | CTCTTC | TGAGAGG | TGTG | CGATCA | CCATGCTATCA | 5992 |
| Qy | 966 | TGAT | GTAAGG | CTTATATG | CGTTTG | ACTGTA | GAGCTATATG | TTGTAATG | CTATTTGCTAA | 1025 |
| Db | 5993 | TGA | AGCAGG | GGCTTAC | CGGGGCA | CTGATGA | GACATATG | TGACAG | CGCATTTGAGAG | 6052 |
| Qy | 1026 | GGCT | ATATGA | ATTGACTT | CTGTAATT | GATCTG | TAATTTG | GGTTACTG | CTGATCA | 1085 |
| Db | 6053 | GGC | GAGCCAG | CTCAC | CGAGAG | GAGACAG | CTGAGC | CTGCTG | CACTGCGACCTCCA | 6112 |
| Qy | 1086 | TGTT | TTTTCT | TTTGGT | GTGACA | CTTTGAG | AGGACTCT | TATTTTGG | TTTGGCTCAG | 1145 |
| Db | 6113 | CGT | TTCTCT | CTCGAG | GGCTTAC | CCCCCTG | CGAGGGAG | CTGCATCTT | CGGGCTGGCCCTGG | 6172 |
| Qy | 1146 | TAA | GGCTTTGG | ATATG | ATGCTT | TACACTT | TATTTTGT | ATGTAATG | GTCCAGGTTATGC | 1205 |
| Db | 6173 | CAG | AGCCCCGG | GACAGAA | GGCCCTAC | ACGCTC | CTCTTAC | GGAACCG | CTTCAAGCTATGT | 6232 |
| Qy | 1206 | TTTG | GGTGTG | TGTTCT | TAGACCA | ATGTTAA | TGTTAG | TACTAG | TATGAGAACCACTTATCAG | 1265 |
| Db | 6233 | GCT | ACAGGA | CGGCGCC | CGCGCGG | ATGTTAC | CGAGAG | CGAGAG | CGGCGGACCCCGAGTATCG | 6292 |
| Qy | 1266 | ACA | ACAGCTG | CTGTTCCAT | TGGTAT | GTAATCA | CTGATG | TGTG | GAAGATATGTCGTGTTT | 1325 |
| Db | 6293 | GCA | CACTAC | AGCAATG | CCCCCTG | ACGAAG | AGACCCAG | CGAGGAG | GAAGCTGTGGGAGTTT | 6352 |
| Qy | 1326 | TGCT | AGAGGT | CCACAAG | CTATTTG | GTTCATG | TGTTCA | AGAAAGAA | CTTTTGTGTCTCA | 1385 |
| Db | 6353 | CGC | CGGGGCG | CCCGAG | CGGAC | CTCGTT | CAAGGCG | TGACAG | ACAGACTTCAATAGCGCA | 6412 |
| Qy | 1386 | TATT | ATGAGCTTT | TGCTGTT | GTGTGA | CCATAC | CTGATTT | GTAAATTT | TGCCAGCTCCAG | 1445 |
| Db | 6413 | CGT | ATGAGCTT | TGCGCG | CTGCGCT | GAGCC | CTACAC | CGCTG | GAGACTGCGCCCGCG | 6472 |
| RESULT 13 | | | | | | | | | | |
| US-10-191-966-15 | | | | | | | | | | |
| Sequence 15, Application US/10191966 | | | | | | | | | | |
| Patent No. 6790612 | | | | | | | | | | |
| GENERAL INFORMATION: | | | | | | | | | | |
| APPLICANT: Potts, Karen E. | | | | | | | | | | |
| APPLICANT: Jackson, Roberta L. | | | | | | | | | | |
| APPLICANT: Patrick, Amy K. | | | | | | | | | | |
| TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT | | | | | | | | | | |
| FILE REFERENCE: 0125-0005A | | | | | | | | | | |
| CURRENT APPLICATION NUMBER: US/10/191,966 | | | | | | | | | | |
| CURRENT FILING DATE: 2002-07-10 | | | | | | | | | | |
| PRIOR APPLICATION NUMBER: US/09/263,933 | | | | | | | | | | |
| PRIOR FILING DATE: 1999-03-08 | | | | | | | | | | |
| PRIOR APPLICATION NUMBER: 09/129,611 | | | | | | | | | | |
| PRIOR FILING DATE: 1998-08-05 | | | | | | | | | | |

NAME/KEY: CDS
LOCATION: (497)..(772)
NAME/KEY: CDS
LOCATION: (1425)..(6500)
NAME/KEY: CDS
LOCATION: (8579)..(9034)
NAME/KEY: CDS
LOCATION: (10191)..(10445)
NAME/KEY: CDS
LOCATION: (11877)..(12734)
NAME/KEY: misc feature
LOCATION: (1)..(774)
OTHER INFORMATION: Vaccinia Virus thymidine Kinase gene recombination
NAME/KEY: promoter
LOCATION: (794)..(816)
OTHER INFORMATION: T7 promoter
NAME/KEY: misc feature
LOCATION: (846)..(1424)
OTHER INFORMATION: EMC/Internal Ribosome Entry Site (IRES)
NAME/KEY: misc feature
LOCATION: (1426)..(1437)
OTHER INFORMATION: MCS (Multiple Cloning Site)
NAME/KEY: misc feature
LOCATION: (1446)..(2318)
OTHER INFORMATION: HCV NS3 Domain
NAME/KEY: misc feature
LOCATION: (2319)..(4231)
OTHER INFORMATION: HCV NS3 Domain containing the serine protease and
OTHER INFORMATION: helicase enzymes
NAME/KEY: misc feature
LOCATION: (4203)..(4260)
OTHER INFORMATION: HCV NS3-NS4A cleavage site
NAME/KEY: misc feature
LOCATION: (4375)..(4424)
OTHER INFORMATION: HCV NS4A-4B cleavage site
NAME/KEY: misc feature
LOCATION: (4233)..(4394)
OTHER INFORMATION: HCV NS4A domain
NAME/KEY: misc feature
LOCATION: (4395)..(4919)
OTHER INFORMATION: HCV NS4B Domain
NAME/KEY: misc feature
LOCATION: (4920)..(4991)
OTHER INFORMATION: HCV NS5A-NS5B cleavage site
NAME/KEY: misc feature
LOCATION: (4992)..(6501)
OTHER INFORMATION: SEAP Protein
NAME/KEY: misc feature
LOCATION: (7915)..(7945)
OTHER INFORMATION: MCS (Multiple Cloning Site)
NAME/KEY: terminator
LOCATION: (7938)..(8078)
OTHER INFORMATION: term T7
NAME/KEY: promoter
LOCATION: (8080)..(8365)
OTHER INFORMATION: Vaccinia virus promoter; early/late promoter
NAME/KEY: misc feature
LOCATION: (8560)..(11317)
OTHER INFORMATION: E. coli gpt; for selection of recombinants
NAME/KEY: misc feature
LOCATION: (11318)..(11309)
OTHER INFORMATION: remaining DNA from 3' end of Tropic PCMV/SEAP
OTHER INFORMATION: plasmid
US-10-191-966-15

Query Match 38.8%; Score 572.8; DB 4; Length 13910;
Best Local Similarity 62.4%; Pred. No. 1.2e-141;
Matches 898; Conservative 0; Mismatches 542; Indels 0; Gaps 0;
QY 6 CTGATTCAGCTGAAGAAATCCAGCTTTTGGATAGACAAGCTGCTCAAGCTTT 65
DB 5033 CATCATCCAGCTTGAAGAGAAACCGGACTTCTGGAACCGGAGCAGCCAGGCGCT 5092

QY 66 GGATGTTGCTAAGAGTTCACAATTCAACTGCTGCTAAGAAATGTTATTTGTTTT 125
DB 5093 GGGTCCCGCCAGAGAGCTGACCTGACAGACAGCCGCGCAAGACTATATCTTCC 5152
QY 126 GGGTATGATGATGGGTGTTCCAACTGTTACTGCTACTAGAAATTTGAAGGCTCAATGAA 185
DB 5153 GGGCGATGGGATGGGGGTGTCTACGGTGAACGTGCAAGATCTCTAAAGGGCAGAAAGA 5212
QY 186 TGGTAAGTTGGGTCAGAAATCCATTTGCTATGATCAATTTCCATAGCTTGTTC 245
DB 5213 GGACAACTGGGGCCCTGAGATACCCCTGGCCATGACCCGCTTCCATATGTGCTGTGTC 5272
QY 246 TAAGCTTCAATGTTATGACAAAGTTCCAGATTCCTGCTGATCTGCTACTTACTT 305
DB 5273 CAGACATCAATGTGACAAACATGTGCAACAGTGAACCAAGCCACGACCTTACCT 5332
QY 306 GTGTGTGTTAAGGTAATTAAGAACTATTTGTTCTGCTGCTGATATCAATCA 365
DB 5333 GTGCGGGGTCAAGGGCACTTCAGACATTTGGCTTGAATGACGCGCGCTTTAACA 5392
QY 366 ATGTAATCTACTAGAGTAATGAAGTACTTCTGTTATTAATAGCTTAAGAGCTG 425
DB 5393 GTGCAACAGACACCGGCGCAAGGTCTATCTCCGATGAATCGGGCCAAAGAACAG 5452
QY 426 TAAGCTGTTGGTGTGTTACTACTACTAGATTCACATGCTTCCAGCTGCTTCA 485
DB 5453 GAAGTATGAGGATGTTAACCAACACAGATGACAGCCGCTCCAGCCGACCTTA 5512
QY 486 CGCTCACTGTTAATGAATTTGTTACTCTGATGCTGATTTGCCAGTGAATGCTA 545
DB 5513 CGCCACAGAGTGAACCGCACTGATCTGAGCCGCGAGCGCTGCGCTCGGCCGCA 5572
QY 546 GAATGTTGTCAAGATATGCTGCTCAATTTGTTTCAATATGATATGATTTT 605
DB 5573 GAGGGGTGTCAGGACATGCTACGACGCTCATCTTCAACATGAGCATGATGATTC 5632
QY 606 GGGTGTGTTAGATGATGATGTTTCAGAAATCTCAGATTCAGAAATCCAGATG 665
DB 5633 AGGTGAGCCCGAAGTATCATGTTTCCATGGAAACCCAGACCTGATGCCAATGA 5692
QY 666 TGCTTCTGTTAATGTTGTTGAAGATGAAGAAATTTGTTCAAGATGCGAAGCTTA 725
DB 5693 CTACAGCCAAAGTGGGACAGGCTGGAAGGAAATCTGTTGAGGAATGCTGCGAA 5752
QY 726 GCATCAAGGTGCTCAATATGTTTGAATGAATGCTTTGTTGCAAGCTGCTGATATTC 785
DB 5753 GCGCCAGGGTGCCTGGTATGTGGAACCGCACTGAGTGAAGCAAGGCTTCCCTGAGCC 5812
QY 786 TAGTGTACTCAATTTGATGAGGTTTGTGTAACCAAGCTGATATGATATGTTCA 845
DB 5813 GTCTGTGACCCATCTCATGATGCTCTTTGAGCTGAGACATGAATATGAGATCCACG 5872
QY 846 AGATCATACTAAGATTCACACTTGGCTGAATGAAGTGAAGCTGCTTTCAGATTTGTC 905
DB 5873 AGACTCCACATGGAACCTCTCCCTGATGAGATGAAGAGCTGCTGCTGCTGAG 5932
QY 906 TAGAAATCCAAAGGTTTACTTGTGTTGAAGTGTGAATGATGATGCTGATCA 965
DB 5933 CAGGAACCCCGCGGCTTCTCTCTGCTGAGGAGGTGCTGATGACATGATGATCA 5992
QY 966 TGAATGTAAGCTTATATGAGCTTGAACAGCTATATGATGATATGCTATGCTAA 1025
DB 5993 TGAAGCAGAGGCTTACCGGCACTGATGAAGATCATGTTGAGAGAGCCATAGAG 6052
QY 1026 GGCTAATGAATGACTTCTGAATTTGATGATCTTGTGTTACTGCTGATCATAGTCA 1085
DB 6053 GGGGGGACGCTCACAGGAGAGAGACAGCTGAGCCCTGTCACCTGCGACCATCCCA 6112
QY 1086 TGTTTTCTTTTGTGTTTACCTTGAAGATCTTATTTTGTGTTGCTTCAAG 1145
DB 6113 CGTCTTCTCTTCGAGGCTACCCCTCGAGAGGAGCTCATCTTCGAGGCTGCGCCCTG 6172

| | | | |
|----|------|--|------|
| OY | 1146 | TAAGCTTTGGATAGTAAAGTCTTACCTTCAATTTTGGATAGTAAAGTCCAGGTATAGC | 1205 |
| Db | 6173 | CAAGGCCCGGAGCAGGAAGGCTCTACCGGCTCTCTATACGAAACGGTCCAGGCTATGT | 6232 |
| OY | 1206 | TTTGGGTGGTGTCTTAGACCAAGATGTTAATGTAGTACTAGTGAAGAACCATCTTACAG | 1265 |
| Db | 6233 | GCTCAAGGACGGCGCGCGCGCGGATGTTACCGAAGGCGAGGCGGGAACCCCGAGTATCG | 6292 |
| OY | 1266 | ACAAACAAGCTGCTGTTTCATTGGCTGATGAAACATCATGATGATGAAGATGTTGCTGTTTT | 1325 |
| Db | 6293 | GCACAGTCACACATGCGCCCTTGGAACGAAGAAGCCACGCAAGCGAGGACGCGGGATTT | 6352 |
| OY | 1326 | TGCTAGAAGTCCACAAGCTCATTTGGTTCATGTTGTTTCAAGAGAACTTTTGTGTCTCA | 1385 |
| Db | 6353 | CGCGGGCGGCGCGAGCGGACACTGGTTCAAGGGGTGACGAGGACGACCTTCATATGCGCA | 6412 |
| OY | 1386 | TATTATGGCTTTTGTGCTGTTGTGTGAAACATACATCATATTGTATTTTGGACAGCTCCAGC | 1445 |
| Db | 6413 | CGTATAGGCTTTCGCGCGCTCGCTCGAGACCCCTACACCGCTCGGACCTCGGGCGCCCCCGC | 6472 |

RESULT 14
US-09-693-011-12
; Sequence 12, Application US/09693011

```

? Patent No. 6532978
? GENERAL INFORMATION:
? APPLICANT: Kaellin, Edgar
? APPLICANT: Luyten, Edgar
? APPLICANT: Zewes, Hans-Gunter
? TITLE OF INVENTION: Transgenic Animals For Studying
? TITLE OF INVENTION: Regulation Of Genes
? FILE REFERENCE: 4-31176A
? CURRENT APPLICATION NUMBER: US/09/693,011
? CURRENT FILING DATE: 2000-10-20
? NUMBER OF SEQ ID NOS: 12
? SOFTWARE: FastSeq for Windows Version 4.0
? SEQ ID NO 12
? LENGTH: 4989
? TYPE: DNA
? ORGANISM: Artificial Sequence
? FEATURE:
? OTHER INFORMATION: DNA CONSTRUCT
US-09-693-011-12

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|---------------------------|-------|-------|------------|------------|-----|--------|------|
| Query Match | 38.7% | Score | 571.2 | DB | 4 | Length | 4989 |
| Best Local Similarity | 62.3% | Pred. | No. 2e-141 | | | | |
| Matches 897; Conservative | | | | Mismatches | 543 | Indels | 0 |
| | | | | | | Gaps | 0 |

| | | | |
|----|------|--|------|
| Qy | 6 | CTTGATTCAGCTGAAGAAAGAAAATCCAGCTTTTGGATATGACAAGCTGCTCAAGCTTT | 65 |
| Db | 1134 | CATCATCCCAAGTTGGAGAGAGAACCCGGACTTTCTGAAACCCGAGGACGCCGAGGCCCT | 1193 |
| Qy | 66 | GGATTTGCTTAAGAAGTTGCACAACCAATTCAAACTGCTGTAGAATGTATTTTGT | 125 |
| Db | 1194 | GGGTCCGCCCAAGAAAGCTGCGACCTCGACAAGACACCCGCAAGAACCTCATATTTCT | 1255 |
| Qy | 126 | GGGTGATGATGATGGGTGTTCCAACTGTACTGCTACTAGAAATTTTGAAGGCTCAATGAA | 185 |
| Db | 1254 | GGGCGATGGGAATGGGGGTGTCTACGGTGCACAGCTCCAGAGATCTTAAAGGGCAGAAAGA | 1313 |
| Qy | 186 | TGTTAAGTTGGGTCAGAAACCTCCATTGGCTATGATCAATTTCCATAGTTGCTTTGTC | 245 |
| Db | 1314 | GGACAAACCTGGGGCCTGAGATACCCCTGGCCATGACCGCTTCCATATGTGGCTCTGTTC | 1373 |
| Qy | 246 | TAAAGCTTACAATGTGTGATGACAAAGTTCCAGATTTCTGTGTACTGCGTACTGTTACTT | 305 |
| Db | 1374 | CAAAGCATACAAATGTGACAAACATGTGCAACAGTGAAGCCACAGCCACGGCTTACTT | 1433 |
| Qy | 306 | GTTGATGTGTTAAGGGTTAATTACAGAACTTTTGTGTTTCTGCTGTGCTAGATTAACAATCA | 365 |
| Db | 1434 | GTGCGGGGCTCAAGGGCACTTCCAGACCAATTTGGCTTGAATGACGCGCCGCTTTAACCA | 1493 |
| Qy | 366 | ATGTATACTACTAAGAGTAAATGAATTACTTCTGTATTATTAAGAAGCTTAAGAAAGCTGG | 425 |

| | | | |
|----|------|---|------|
| Db | 1194 | CTGCACACGACACGCGCGCAACGAGCTACTCTCGTATGAATCGGGCGCAAGAAAGCAGG | 1553 |
| Qy | 426 | TAAAGCTGTGTGTGTGTACTACTATGAGTTCAACATGCTTCTCCAGTGGTGTCTA | 485 |
| Db | 1554 | GAATCTCATGTGGAGATGTGTAAACACACACGAGTGCACACGCGCTCGCACGCGGCACCTA | 1613 |
| Qy | 486 | CGCTCATACTGTATTAATGAAATTGGTACTCGATGCTGATTTGGCAGCTGATGCTCAAA | 545 |
| Db | 1614 | CGCCCAACGCTGAACCGCAACTGTACTCGGAGCGCGAGCGTGCCTGCGGCGCGCA | 1673 |
| Qy | 546 | GAATGTTGTTCAGATATTGCTGCTCAATTGCTTTACATATGGAATATGATGTATTTT | 605 |
| Db | 1674 | GGAGGGGTGCACGAGACATCGCTACGACGCTCATCTCCAACTTGACATTTGACGTGATCTT | 1733 |
| Qy | 606 | GGGTGTGTGTGAATGTATCAATGTTTCCAGAAAGTATCCAGATCCAGATACAGATGA | 665 |
| Db | 1734 | AGGTGTAGAGCCGAAAGTACATGTTTTCGATGTGGAAACCCAGACCTTGATATCCAGATGA | 1793 |
| Qy | 666 | TGCTTCTGTATAGTGTGTAGAAAGATTAAGCAAAATTTGGTTCAAGATGGCAAGCTAA | 725 |
| Db | 1794 | CTACAGCCAAAGTGGAGACAGGCTGAGACGGGAAATCTGGTGCAGGAAATGGCTGGCCAA | 1853 |
| Qy | 726 | GCATCAAGAGCTCAATATGTTTGGAAATAGAATCGCTTGTGTGCAAGTGTGATATTC | 785 |
| Db | 1854 | GCGCCAGAGTGCCTCGATATGTGTGAACCGACATGAGCTATGCAAGCTTCTCCGAGACC | 1913 |
| Qy | 786 | TAGTGTACTCATTTGATGTGGTGTGTGTGGAACCACTGATATGAAGTATTAATGTTCAACA | 845 |
| Db | 1914 | GTCTGTAGCCATCTCATGGGTCTCTTTGACCTTGAGACATGAATATCGAGATCCACCG | 1973 |
| Qy | 846 | AGATCATATGAAGATCCAACTTTGGCTGAAATGACTGMAAGCTCTTTGCAGTTTGTCTC | 905 |
| Db | 1974 | AGACTCCACACTGAGACCCCTCCGTATGAGATATACAGAGCTCCCTCGCCCTGCTGAG | 2033 |
| Qy | 906 | TAGAATTCAGAGAGTTTTACTGTGTGTGGAAGTGTGTGAATTGATTCATGTGTCATCA | 965 |
| Db | 2034 | CAGGAAACCCCGCGGCTTCTTCTCTTCGTGAGAGGTGTGTGATTCACATATGGTCATCA | 2092 |
| Qy | 966 | TGATGTAGAGCTATATATGCTTTGACTGGAAGCTATTAATGTTTGATAATGCTATTTGCTTA | 1022 |
| Db | 2094 | TGAAGAAGCAGGCTTACCGGACACTGACATGACACATCATATGTTGACGACGGCATTTGAGAG | 2152 |
| Qy | 1026 | GGCTATGAATTTGAATTCTGAAATGAGATCTTGAATTTTGGTTACTGCTGATCATATGCA | 1086 |
| Db | 2154 | GCGGGGCGAGCTCACACGACGAGAGACACCTGAGCCTGCTACCTGCGACACACTCCCA | 2213 |
| Qy | 1086 | TGTTTTTCTTTTGTGTGTACACTTTGAGAGTACTTATATTTTGTGTGGCTCCAGG | 1145 |
| Db | 2214 | CGTCTTCTCTCGGAGGCTACCCCTCGAGGGGAGCTCAATCTTCGGGCTGGGCCCTGG | 2273 |
| Qy | 1146 | TAAAGCTTTGATATGTAAGTCTTACACTTCAATTTTGTATGATGTATGCTCAGGTTATGC | 1205 |
| Db | 2274 | CAGGCGCGGAGACAGAGAGGCTTACGAGTCTCTCTTAACGMAACGTTCCAGGCTATATGT | 2333 |
| Qy | 1206 | TTTGGGTGTGTCTTAGACCAATGTTAATGTATAGTACTATAGTAAAGCAATCTTAACG | 1265 |
| Db | 2334 | GCTACAGGACGGCGCGCGCGGATGTATCCGAGAGCAAGAGCGGGAACCCCGAGTATCG | 2392 |
| Qy | 1266 | ACACAAAGCTCTGTTCATTGTGCTAGTGAATCATATGAGTGTGAAGATGTGTGCTTTT | 1322 |
| Db | 2394 | GCAGAGTCAACAGTGCCTCTGACAGAAAGAACCCACAGGCGAGGACGTGGCGGTGT | 2452 |
| Qy | 1326 | TGCTTAGAGTCCACAAAGCTCAATTTGGTTTCAATGTGTTCMAAGAAACTTTTGTTCCTCA | 1388 |
| Db | 2454 | CGCGGGGCGCGAGCGACACTGTGTTCACGCGGTGACAGGACGACCTTCAATAGCGCA | 2511 |
| Qy | 1386 | TATTAATGCTTTTGTGTGTGTGTGAACATACATCAATATTTGTCAGCTCCAGC | 1444 |
| Db | 2514 | CGTATGAGCTTTCGCGGCTCTGAGACCTTACACGCGCTGCGACTGGCGCCCCCGCG | 2572 |

RESULT 15

US-09-693-011-11
 ; Sequence 11, Application US/09693011
 ; Patent No. 6632978
 ; GENERAL INFORMATION:
 ; APPLICANT: Kaelin, Edgar
 ; APPLICANT: Luyten, Marcel
 ; APPLICANT: Zewes, Hans-Gunter
 ; TITLE OF INVENTION: Transgenic Animals For Studying
 ; TITLE OF INVENTION: Regulation Of Genes
 ; FILE REFERENCE: 4-31176A
 ; CURRENT APPLICATION NUMBER: US/09/693,011
 ; NUMBER OF SEQ ID NOS: 12
 ; SOFTWARE: PasteSeq for Windows Version 4.0
 ; SEQ ID NO 11
 ; LENGTH: 5083
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: DNA CONSTRUCT
 US-09-693-011-11

Query Match 38.7%; Score 571.2; DB 4; Length 5083;
 Best Local Similarity 62.3%; Pred. No. 2e-141;
 Matches 897; Conservative 0; Mismatches 543; Indels 0; Gaps 0;

QY 6 CTGATTCGAGCTGAAGAAATCCAGCTTTTGGAAATGACAAAGCTCTCAAGTTT 65
 DB 1134 CATCATCCCGAGTGGAGAGAGAACCCGACTTCTGAAACCGAGGACACCGAGGCCCT 1193

QY 66 GAGTGTGCTAAGAAATGCAACCAATTCAGTCTGCTAAGAAATTTTGGTTTT 125
 DB 1194 GGGTCCGCCAAGAGCTGAGCTGACAGACAGCCGCCAAGAACTCATCTTCTCT 1253

QY 126 GGGTGTGCTAAGAAATGCAACCAATTCAGTCTGCTAAGAAATTTTGGTTTT 185
 DB 1254 GGGGATGGATGGGGGTGTCTACGGTGAAGCTGCGAGATCTTAAGAGGAGAA 1313

QY 186 TGGTAAGTGGGTCGAGAACTCCATTGCTATGATCAATTTCCATAGCTTGTCT 245
 DB 1314 GAGCAACCTGGGCTGAGATACCCCTGGCCATGAGACCGCTTCCATATGTGCTGTC 1373

QY 246 TAAGACTTACAAATGTTGATAGCAAGTTCAGATTCGCTGATCTACTGCTTACT 305
 DB 1374 CAAGACATACAAATGTTGATAGCAAGTTCGCTGATCTACTGCTTACTGCTTACT 1433

QY 306 GTGTGTGTTAAGGGATTAATTAAGAACTATGTGTTTCTGCTGCTGATTAACAATCA 365
 DB 1434 GTGCGGGGTCAAGGGCAATTCAGACCATTTGGCTTGAAGTGAAGCCGCCGCTTTAACCA 1493

QY 366 ATGTATATCTACAGAGTAAATGAATTAATTTCTGTTATTAATAGAGCTAAGAAAGCTGG 425
 DB 1494 GTGCAACACGACACGGGGCAAGGTCATCTCGTATGAATCGGGCCCAAGAAAGCAGG 1553

QY 426 TAAGGCTGTTGATGTTTACTACTAGTTCAACATGCTTCCAGCTGCTGCTTA 485
 DB 1554 GAAGTCAATGAGAGTGTAAACACACAGAGTGAAGACGCTTCCGCAAGCCGACCTTA 1613

QY 486 CGCTCACTACTGTTAATGAATTTGTAATCTGATGCTGATTTGCAAGCTGATCTCAAAA 545
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 Job time : 144.5 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 19, 2004, 14:44:42 ; Search time 753.5 Seconds

(without alignments)
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Perfect score: 1476

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Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysts of the total score distribution.

SUMMARIES

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| 1 | 1476 | 100.0 | 1476 | 10 | US-09-911-132a-5 |
| 2 | 1476 | 100.0 | 1476 | 16 | US-10-395-790A-3 |
| 3 | 1474.4 | 99.9 | 1476 | 16 | US-10-395-790A-8 |
| 4 | 1472.8 | 99.8 | 1476 | 16 | US-10-395-790A-9 |
| 5 | 1471.2 | 99.6 | 1476 | 16 | US-10-395-790A-10 |
| 6 | 1469.6 | 99.7 | 1476 | 16 | US-10-395-790A-11 |
| 7 | 845.6 | 57.3 | 1476 | 10 | US-09-911-132a-1 |
| 8 | 834.8 | 56.6 | 1464 | 16 | US-10-395-790A-1 |
| 9 | 572.8 | 38.8 | 1597 | 15 | US-10-053-637-9 |
| 10 | 572.8 | 38.8 | 1634 | 9 | US-09-006-298-22 |
| 11 | 572.8 | 38.8 | 1675 | 15 | US-10-053-637-11 |
| 12 | 572.8 | 38.8 | 1728 | 10 | US-09-908-943A-127 |
| 13 | 572.8 | 38.8 | 1748 | 15 | US-10-053-637-19 |

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| 14 | 572.8 | 38.8 | 1777 | 15 | US-10-053-637-15 | Sequence 15, Appl |
| 15 | 572.8 | 38.8 | 1915 | 15 | US-10-053-637-23 | Sequence 23, Appl |
| 16 | 572.8 | 38.8 | 1918 | 15 | US-10-053-637-5 | Sequence 5, Appl |
| 17 | 572.8 | 38.8 | 1975 | 15 | US-10-053-637-27 | Sequence 27, Appl |
| 18 | 572.8 | 38.8 | 2239 | 9 | US-09-747-419-18 | Sequence 18, Appl |
| 19 | 572.8 | 38.8 | 2239 | 15 | US-10-259-275-18 | Sequence 18, Appl |
| 20 | 572.8 | 38.8 | 7469 | 9 | US-09-776-167A-6 | Sequence 6, Appl |
| 21 | 572.8 | 38.8 | 13910 | 10 | US-09-919-901-1 | Sequence 1, Appl |
| 22 | 572.8 | 38.8 | 13910 | 10 | US-09-919-901-8 | Sequence 8, Appl |
| 23 | 572.8 | 38.8 | 13910 | 10 | US-09-919-901-15 | Sequence 15, Appl |
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| 25 | 572.8 | 38.8 | 13910 | 15 | US-10-191-966-8 | Sequence 8, Appl |
| 26 | 572.8 | 38.8 | 13910 | 15 | US-10-191-966-15 | Sequence 15, Appl |
| 27 | 572.4 | 38.8 | 1779 | 15 | US-10-071-645-4 | Sequence 4, Appl |
| 28 | 572.4 | 38.8 | 2051 | 16 | US-10-182-094-7 | Sequence 7, Appl |
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| 30 | 571.2 | 38.7 | 1558 | 17 | US-10-332-733-26 | Sequence 26, Appl |
| 31 | 571.2 | 38.7 | 1560 | 9 | US-09-965-697-10 | Sequence 10, Appl |
| 32 | 571.2 | 38.7 | 2645 | 17 | US-10-645-794-3 | Sequence 3, Appl |
| 33 | 571.2 | 38.7 | 2662 | 17 | US-10-645-883A-5 | Sequence 5, Appl |
| 34 | 571.2 | 38.7 | 2662 | 18 | US-10-645-187-5 | Sequence 5, Appl |
| 35 | 571.2 | 38.7 | 4260 | 16 | US-10-395-709-16 | Sequence 16, Appl |
| 36 | 571.2 | 38.7 | 4260 | 16 | US-10-315-907A-16 | Sequence 16, Appl |
| 37 | 571.2 | 38.7 | 4260 | 17 | US-10-281-067B-16 | Sequence 16, Appl |
| 38 | 571.2 | 38.7 | 4356 | 17 | US-10-655-702-2 | Sequence 2, Appl |
| 39 | 571.2 | 38.7 | 4677 | 15 | US-10-237-146-7 | Sequence 7, Appl |
| 40 | 571.2 | 38.7 | 4989 | 16 | US-10-620-627-12 | Sequence 12, Appl |
| 41 | 571.2 | 38.7 | 5083 | 16 | US-10-620-627-11 | Sequence 11, Appl |
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| 43 | 571.2 | 38.7 | 5928 | 10 | US-09-932-581-25 | Sequence 25, Appl |
| 44 | 571.2 | 38.7 | 5928 | 15 | US-10-338-294-25 | Sequence 25, Appl |
| 45 | 571.2 | 38.7 | 6314 | 16 | US-10-620-627-10 | Sequence 10, Appl |

ALIGNMENTS

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RESULT 1
US-09-911-132a-5
; Sequence 5, Application US/09911132A
; Publication No. US20030096341A1
; GENERAL INFORMATION:
; APPLICANT: Roche Diagnostics GmbH
; TITLE OF INVENTION: Expression of Alkaline Phosphatase in Yeast
; FILE REFERENCE: RDID 0073US
; CURRENT APPLICATION NUMBER: US/09/911,132A
; CURRENT FILING DATE: 2002-08-28
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 1476
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Codon-optimized DNA sequence
US-09-911-132a-5
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Query Match 100.0%; Score 1476; DB 10; Length 1476;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1476; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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| DB | 61 | GCTTGGATGCTGTAAGAGTTGCAACCAATTCACGCTGCTAGAAATGTTATTTG | 120 |
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RESULT 2
US-10-395-790A-3
; Sequence 3, Application US/10395790A
; Publication No. US20040072316A1
; GENERAL INFORMATION:
; APPLICANT: Roche Diagnostics Corp.
; TITLE OF INVENTION: Production of weakly active or inactive mutants of alkaline phosphatase
; FILE REFERENCE: RDID 02028US
; CURRENT APPLICATION NUMBER: US/10/395,790A
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: Patemlin version 3.1
; SEQ ID NO 3
; LENGTH: 1476
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: codon-optimized alkaline phosphatase sequence
US-10-395-790A-3

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1476; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 3
 US-10-395-790A-8
 ; Sequence 8, Application US/10395790A
 ; Publication No. US20040072316A1

; GENERAL INFORMATION:
 ; APPLICANT: Roche Diagnostics Corp.
 ; TITLE OF INVENTION: Production of weakly active or inactive mutants of alkaline phosj
 ; TITLE OF INVENTION: and their expression in yeast
 ; FILE REFERENCE: RDID 02028US
 ; CURRENT APPLICATION NUMBER: US/10/395,790A
 ; NUMBER OF SEQ ID NOS: 21
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO: 8
 ; LENGTH: 1476
 ; TYPE: DNA
 ; ORGANISM: artificial sequence
 ; FEATURE:
 ; OTHER INFORMATION: coding sequence for Ser92Ala mutant
 US-10-395-790A-8

Query Match 99.9%; Score 1474.4; DB 16; Length 1476;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 1475; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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 DB 1 GAATTTCTGATTCACGCTGAAGAGAAATCCAGCTTTTGGAAATGACAGCTGCTCA 60
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 QY 541 CAAAAGATGTTGTCAGATATTTGCTGCTCAATTTGTTTACAAATATGATATGATGTT 600
 DB 541 CAAAAGATGTTGTCAGATATTTGCTGCTCAATTTGTTTACAAATATGATATGATGTT 600
 QY 601 ATTTTGGTGGTGGTGAATGTATCATGTTCCAGAGGTATCTCAGATCCAGATCCCA 660
 DB 601 ATTTTGGTGGTGGTGAATGTATCATGTTCCAGAGGTATCTCAGATCCAGATCCCA 660
 QY 661 GATGATGCTTCTGTATATGTTAGTAAAGATTAAGCAAAATTTGGTTCAAGATGCGCA 720
 DB 661 GATGATGCTTCTGTATATGTTAGTAAAGATTAAGCAAAATTTGGTTCAAGATGCGCA 720
 QY 721 GCTAAGCATCAAGTGTCTCAATATGTTTGAATAGAACTGCTTTGTTGCAAGCTGCTGAT 780
 DB 721 GCTAAGCATCAAGTGTCTCAATATGTTTGAATAGAACTGCTTTGTTGCAAGCTGCTGAT 780

| | | | |
|----|------|--|------|
| OY | 781 | GATTCAGTGTACGATCATTTGATGGCTTGTTGAACAAGCGATAGAATAAAGTT | 840 |
| Dd | 781 | | |
| OY | 841 | CACACAGATCACTACTAGAGATCCAACTTGGCTGAATGACTGAAGCTGCTTGGCAGTT | 900 |
| Dd | 841 | CAACAGATCACTACTAGAGATCCAACTTGGCTGAATGACTGAAGCTGCTTGGCAGTT | 900 |
| OY | 901 | TTCGCTAGAAATCCAAAGGTTTTTACTTGTGTTGTAAGGTGGTAATTGATCAGT | 960 |
| Dd | 901 | | |
| OY | 961 | CATCATGATNGGAAGGCTTATATGGCTTGAAGTGAAGTATTAATGTAATGCTATT | 1020 |
| Dd | 961 | CATCATGATNGGAAGGCTTATATGGCTTGAAGTGAAGTATTAATGTAATGCTATT | 1020 |
| OY | 1021 | GCTAAGGCTAAATGAATGACTCTGAATTTGGATCTTGAATTTTGGTACTGCTGATCAT | 1080 |
| Dd | 1021 | GCTAAGGCTAAATGAATGACTCTGAATTTGGATCTTGAATTTTGGTACTGCTGATCAT | 1080 |
| OY | 1081 | AGTCATGTTTTCTTTTGGTGTTTACACTTTGAGAGGTAATCTTAATTTTGGTTGGCT | 1140 |
| Dd | 1081 | AGTCATGTTTTCTTTTGGTGTTTACACTTTGAGAGGTAATCTTAATTTTGGTTGGCT | 1140 |
| OY | 1141 | CCAGGTAGGCTTTGGATAGTAAGTCTTCACTTCTATTTTGTATNGTAATGTCACAGT | 1200 |
| Dd | 1141 | CCAGGTAGGCTTTGGATAGTAAGTCTTCACTTCTATTTTGTATNGTAATGTCACAGT | 1200 |
| OY | 1201 | TATGCTTTGGGTGGTGGTCTTAGACACAGATGTTAATGTTAGTACTAGTGAAGAACATCT | 1260 |
| Dd | 1201 | TATGCTTTGGGTGGTGGTCTTAGACACAGATGTTAATGTTAGTACTAGTGAAGAACATCT | 1260 |
| OY | 1261 | TACAGACAACAAGCTGCTGTTCCATTGGCTAGTGAACATCATGGTGTGAAGATGTTGCT | 1320 |
| Dd | 1261 | TACAGACAACAAGCTGCTGTTCCATTGGCTAGTGAACATCATGGTGTGAAGATGTTGCT | 1320 |
| OY | 1321 | GTTTTTGTCTAGAGTCCCAAGCTATTTGGTTCATGCTGTTCCAAGAAACCTTTTGTT | 1380 |
| Dd | 1321 | GTTTTTGTCTAGAGTCCCAAGCTATTTGGTTCATGCTGTTCCAAGAAACCTTTTGTT | 1380 |
| OY | 1381 | GCTCATATTATGAGCTTTGGTGGTGTGTGTAACCATCACATGATGTAAATTTGCCAGCT | 1440 |
| Dd | 1381 | GCTCATATTATGAGCTTTGGTGGTGTGTGTAACCATCACATGATGTAAATTTGCCAGCT | 1440 |
| OY | 1441 | CCAGTACTGCTACTAGTAATTCAGATTAAGGTACC | 1476 |
| Dd | 1441 | CCAGTACTGCTACTAGTAATTCAGATTAAGGTACC | 1476 |

RESULT 4
US-10-395-790A-9
; Sequence 9, Application US/10395790A
; Publication No. US20040072316A1
GENERAL INFORMATION:
APPLICANT: Roche Diagnostics Corp.
TITLE OF INVENTION: Production of weakly active or inactive mutants of alkaline phosphatase
FILE REFERENCE: RDID 02028US
CURRENT APPLICATION NUMBER: US/10/395,790A
NUMBER OF SEQ ID NOS: 21
SOFTWARE: PatentIn version 3.1
SEQ ID NO 9
LENGTH: 1476
TYPE: DNA
ORGANISM: artificial sequence
FEATURE:
OTHER INFORMATION: coding sequence for Gly322Phe mutant
US-10-395-790A-9

| | | | | |
|-----------------------|--------------|---------------|---------------|--------------|
| Query Match | 99.8% | Score 1472.8; | DB 16; | Length 1476; |
| Best Local Similarity | 99.9%; | Pred. No. 0; | | |
| Matches 1474; | Conservative | 0; | Mismatches 2; | Indels 0; |
| | | | Gaps | 0; |

| | | | |
|----|------|---|------|
| QY | 1 | GAATTCCTGATTCACAGCTGAAAGAAATATCCACCTTTTGGATATAGCAAGCTGCTCAA | 60 |
| Db | 1 | GAATTCCTGATTCACAGCTGAAAGAAATATCCACCTTTTGGATATAGCAAGCTGCTCAA | 60 |
| QY | 61 | GCTTGGATGTTGGCTAAGAAAGTTGCCAACCAATTCAACTGCTGCTAGAAATGTTATTTTG | 120 |
| Db | 61 | GCTTGGATGTTGGCTAAGAAAGTTGCCAACCAATTCAACTGCTGCTAGAAATGTTATTTTG | 120 |
| QY | 121 | TTTTTGGGTGATGGTATAGGGGTGTTCCAACTGTATCTGCTACTAGAAATTTTGAAGGTCAA | 180 |
| Db | 121 | TTTTTGGGTGATGGTATAGGGGTGTTCCAACTGTATCTGCTACTAGAAATTTTGAAGGTCAA | 180 |
| QY | 181 | ATGAATGGTAAAGTTGGGTCAGAAATCTCCATTTGGCTATGATCAATTTCCATAGCTTGCT | 240 |
| Db | 181 | ATGAATGGTAAAGTTGGGTCAGAAATCTCCATTTGGCTATGATCAATTTCCATAGCTTGCT | 240 |
| QY | 241 | TTTGCTAAGACTTACCAATGTTGATAGACAAGATTCAGATTTCTGCTGTAAGTCTACTGCT | 300 |
| Db | 241 | TTTGCTAAGACTTACCAATGTTGATAGACAAGATTCAGATTTCTGCTGTAAGTCTACTGCT | 300 |
| QY | 301 | TACTTGTTGGGTGTTAAGGGTAATTAAGAACTATAGGGTTTGTGCGTGCCTAGATAC | 360 |
| Db | 301 | TACTTGTTGGGTGTTAAGGGTAATTAAGAACTATAGGGTTTGTGCGTGCCTAGATAC | 360 |
| QY | 361 | AATCAATGTATATACTACTAGAGTAAATGAAATTACTTCTGTTATTAATAGAGCTAAGAG | 420 |
| Db | 361 | AATCAATGTATATACTACTAGAGTAAATGAAATTACTTCTGTTATTAATAGAGCTAAGAG | 420 |
| QY | 421 | GCTGTAAAGGCTTTGGGTGTGTTTACTACTATCTATAGATTCAAACATGCTTCTCCAGCTGCT | 480 |
| Db | 421 | GCTGTAAAGGCTTTGGGTGTGTTTACTACTATCTATAGATTCAAACATGCTTCTCCAGCTGCT | 480 |
| QY | 481 | GCTTACGCTCATCTGTTAATAGAAATTTGGTACTCTGATGCTGATTTTGGCAGCTGATGCT | 540 |
| Db | 481 | GCTTACGCTCATCTGTTAATAGAAATTTGGTACTCTGATGCTGATTTTGGCAGCTGATGCT | 540 |
| QY | 541 | CAAAAGATGTTGTCAAGATATTGCTGCTCAATTGTTTCAATATGATATTGATGTT | 600 |
| Db | 541 | CAAAAGATGTTGTCAAGATATTGCTGCTCAATTGTTTCAATATGATATTGATGTT | 600 |
| QY | 601 | ATTTTGGGTGTGTAGAAATGTAATGTTTCCAAAGATCTCAGATCCCAAGATTAACCA | 660 |
| Db | 601 | ATTTTGGGTGTGTAGAAATGTAATGTTTCCAAAGATCTCAGATCCCAAGATTAACCA | 660 |
| QY | 661 | GATGATGCTTCTGTTAATGTTAGAAAGGATTAAGCAAAATTTGTTCAAGAAATGCGAA | 720 |
| Db | 661 | GATGATGCTTCTGTTAATGTTAGAAAGGATTAAGCAAAATTTGTTCAAGAAATGCGAA | 720 |
| QY | 721 | GCTAAGCATCAAGTGTCTCAATATGTTTGGAAATGAACTGTTTGTTCGAAGCTGCTGAT | 780 |
| Db | 721 | GCTAAGCATCAAGTGTCTCAATATGTTTGGAAATGAACTGTTTGTTCGAAGCTGCTGAT | 780 |
| QY | 781 | GATTCATAGTTCATCAATTGATGGGTTTGTGTTAACAAGCTGATATGAATATATGTT | 840 |
| Db | 781 | GATTCATAGTTCATCAATTGATGGGTTTGTGTTAACAAGCTGATATGAATATATGTT | 840 |
| QY | 841 | CAACAAGATCATCTAAGATCCAACTTTGGCTGAAATGACTGAAGCTGCTTGCAGATT | 900 |
| Db | 841 | CAACAAGATCATCTAAGATCCAACTTTGGCTGAAATGACTGAAGCTGCTTGCAGATT | 900 |
| QY | 901 | TTTGCTAGAAATCCAAAGGTTTACTGTTGTTGTAAGGTGTAGAAATTTGATCAATGCT | 960 |
| Db | 901 | TTTGCTAGAAATCCAAAGGTTTACTGTTGTTGTAAGGTGTAGAAATTTGATCAATGCT | 960 |
| QY | 961 | CATCATGATGTTAAGGCTTATATGCTTTTGAAGCTATTAATGTTGATATATGCTATT | 1020 |
| Db | 961 | CATCATGATGTTAAGGCTTATATGCTTTTGAAGCTATTAATGTTGATATATGCTATT | 1020 |
| QY | 1021 | GCTAAGGCTAATGAATTCATCTTGAAATTTGATATCTTTGATTTTGGTTACTGCTGATCAT | 1080 |
| Db | 1021 | GCTAAGGCTAATGAATTCATCTTGAAATTTGATATCTTTGATTTTGGTTACTGCTGATCAT | 1080 |

| | | | |
|----|------|--|------|
| Oy | 1081 | AGTATGTTTTTTCTTTTGGTGGTTACCTTGAAGGTACTTTCATTTTTGGTTGGCT | 1140 |
| Db | 1081 | AGTCATGTTTTTTCTTTTGGTGGTTACCTTGAAGGTACTTTCATTTTTGGTTGGCT | 1140 |
| Oy | 1141 | CCAGTAAAGCTTTGGATAGTAAGTCTTACCTTCAATTTTGTATGTAAATGATCCAGT | 1200 |
| Db | 1141 | CCAGTAAAGCTTTGGATAGTAAGTCTTACCTTCAATTTTGTATGTAAATGATCCAGT | 1200 |
| Oy | 1201 | TATGTTTGGGTGGTGCTTTCTAGACCAAGTGTAAATGTAATGTAAGTAAGAACATCT | 1260 |
| Db | 1201 | TATGTTTGGGTGGTGCTTTCTAGACCAAGTGTAAATGTAATGTAAGTAAGAACATCT | 1260 |
| Oy | 1261 | TACAGACAACAAGCTGCTGTTCCATTTGCTAGTGAACATCAATGGGTGGAAGATGTTGCT | 1320 |
| Db | 1261 | TACAGACAACAAGCTGCTGTTCCATTTGCTAGTGAACATCAATGGGTGGAAGATGTTGCT | 1320 |
| Oy | 1321 | GTTTTTGGTAAAGGTCCACAAGCTCATTTGGTTCAATGCTGTTCAAGAAAGAACTTTGTT | 1380 |
| Db | 1321 | GTTTTTGGTAAAGGTCCACAAGCTCATTTGGTTCAATGCTGTTCAAGAAAGAACTTTGTT | 1380 |
| Oy | 1381 | GCTCATATTAAAGGCTTTTGGCTGGTTGTGTGAACATACATGATGTGAATTTGGCCAGCT | 1440 |
| Db | 1381 | GCTCATATTAAAGGCTTTTGGCTGGTTGTGTGAACATACATGATGTGAATTTGGCCAGCT | 1440 |
| Oy | 1441 | CCAGCTACTGCTACTAGTATTCAGATTCCAGATTAAAGGTACC | 1476 |
| Db | 1441 | CCAGCTACTGCTACTAGTATTCAGATTAAAGGTACC | 1476 |

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RESULT 5
US-10-395-790A-10
; Sequence 10, Application US/10395790A
; Publication No. US20040072316A1
; GENERAL INFORMATION:
; APPLICANT: Roche Diagnostics Corp.
; TITLE OF INVENTION: Production of weakly active or inactive mutants of alkaline phosphatase
; TITLE OF INVENTION: and their expression in yeast
; FILE REFERENCE: RDID 02028US
; CURRENT APPLICATION NUMBER: US/10/395,790A
; CURRENT FILING DATE: 2003-03-24
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 1476
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: coding sequence for His320Asn/Gly322Phe mutant
US-10-395-790A-10

Query Match          99.7%; Score 1471.2; DB 16; Length 1476;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1473; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Cy      1  GAATTTCTGATTTCCAGCTGAAGAGAAATTCAGCTTTTGGATAGACAACTGCTCA 60
      |||
Db      1  GAATTCCTGATTTCCAGCTGAAGAGAAATTCAGCTTTTGGATAGACAACTGCTCA 60

Cy      61  GCTTTGATGTTGCTAAGAGTTGCCAATTCCAATTCGAATGCTGCTAAGAAATGTTATTTG 120
      |||
Db      61  GCTTTGATGTTGCTAAGAGTTGCCAATTCCAATTCGAATGCTGCTAAGAAATGTTATTTG 120

Cy      121  TTTTGGGATGATGATGATGGGTGTTCCAACTGTTACTGCTACTAGAAATTTTGAAGGCTCA 180
      |||
Db      121  TTTTGGGATGATGATGATGGGTGTTCCAACTGTTACTGCTACTAGAAATTTTGAAGGCTCA 180

Cy      181  ATGAATGATGATGATGGGTCCAGAAATCTCAATGGCTATGATATCAATTTCCATACGTTGCT 240
      |||
Db      181  ATGAATGATGATGATGGGTCCAGAAATCTCAATGGCTATGATATCAATTTCCATACGTTGCT 240

Cy      241  TTGCTCAAGACTTACAAATGTTGATAGACAAAGTTCCAAATTTGCTGTTACTGCTACTGCT 300
      |||
Db      241  TTGCTCAAGACTTACAAATGTTGATAGACAAAGTTCCAAATTTGCTGTTACTGCTACTGCT 300

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| | | | |
|----|------|---|------|
| QY | 301 | TACTTGCTGGGTGTTAAGGCGTAATTAACAGACTATATGGTGTTCGTGCGCTGCAGTAATAC | 360 |
| Db | 301 | TACTTGCTGGGTGTTAAGGCGTAATTAACAGACTATATGGTGTTCGTGCGCTGCAGTAATAC | 360 |
| QY | 361 | AATCAATGTATTAATACTACTAGAGATATGAAGTTACTCTGTTATTAATATAGAGCTAAGAG | 420 |
| Db | 361 | AATCAATGTATTAATACTACTAGAGATATGAAGTTACTCTGTTATTAATATAGAGCTAAGAG | 420 |
| QY | 421 | GCTGGTAAGGCTGTGGTGTGTGTTACTACTACTAGAGTTCAACATGCTTCTCCAGCTGGT | 480 |
| Db | 421 | GCTGGTAAGGCTGTGGTGTGTGTTACTACTACTAGAGTTCAACATGCTTCTCCAGCTGGT | 480 |
| QY | 481 | GCTTAACGCTCACTACTGTTAATAGAAATTGGTACTCTGATGCTGATTTGGCCAGCTGATGCT | 540 |
| Db | 481 | GCTTAACGCTCACTACTGTTAATAGAAATTGGTACTCTGATGCTGATTTGGCCAGCTGATGCT | 540 |
| QY | 541 | CAAAAGAAATGGTGTGCAAGATATATGCTGCTCAATTTGGTTTCAATATGAGATATGATGTT | 600 |
| Db | 541 | CAAAAGAAATGGTGTGCAAGATATATGCTGCTCAATTTGGTTTCAATATGAGATATGATGTT | 600 |
| QY | 601 | ATTTTGGGTGTGTGATAGATATGATCATGTCTTCCAGAGATCTCCAGATCCAGAAATACCA | 660 |
| Db | 601 | ATTTTGGGTGTGTGATAGATATGATCATGTCTTCCAGAGATCTCCAGATCCAGAAATACCA | 660 |
| QY | 661 | GATGATGCTTCTGTTAATATGCTGTTAAGAAAGATATGACAAATTTGGTTCAAGAAATGCGAA | 720 |
| Db | 661 | GATGATGCTTCTGTTAATATGCTGTTAAGAAAGATATGACAAATTTGGTTCAAGAAATGCGAA | 720 |
| QY | 721 | GCTAAGCATCAAGGCTCAATATGTTTGGAAATGAACTGCTTGTGGCAAGCTGCAT | 780 |
| Db | 721 | GCTAAGCATCAAGGCTCAATATGTTTGGAAATGAACTGCTTGTGGCAAGCTGCAT | 780 |
| QY | 781 | GATTCTAGTGTACTCACTATTTGATGGGTTTGTTTAACCAGCTGATATGAATATATGTT | 840 |
| Db | 781 | GATTCTAGTGTACTCACTATTTGATGGGTTTGTTTAACCAGCTGATATGAATATATGTT | 840 |
| QY | 841 | CAACAAGATCACTAAGATCCAACTTTGGCTGAAATGACTGAAGCTGCTTTCCAAATT | 900 |
| Db | 841 | CAACAAGATCACTAAGATCCAACTTTGGCTGAAATGACTGAAGCTGCTTTCCAAATT | 900 |
| QY | 901 | TTGCTCTAGAAATCCAAAGGCTTTTACTGTGTTGTAAGGTGTGAATATGATCATGCT | 960 |
| Db | 901 | TTGCTCTAGAAATCCAAAGGCTTTTACTGTGTTGTAAGGTGTGAATATGATCATGCT | 960 |
| QY | 961 | CATCATGATGTGTAAGGCTTATATGCTTTGACTGAAGCTATATATGTTTGAATATGCTATT | 1020 |
| Db | 961 | CATCATGATGTGTAAGGCTTATATGCTTTGACTGAAGCTATATATGTTTGAATATGCTATT | 1020 |
| QY | 1021 | GCTAAGGCTAATGAATGACTCTTGAAATGTGATACCTTGATTTTGGTACTGCTGATCAT | 1080 |
| Db | 1021 | GCTAAGGCTAATGAATGACTCTTGAAATGTGATACCTTGATTTTGGTACTGCTGATCAT | 1080 |
| QY | 1081 | AGTCATGTTTTTCTTTTGGTGTACACTTTGAGAGTACTTATTTTTGGTTGGCT | 1140 |
| Db | 1081 | AGTCATGTTTTTCTTTTGGTGTACACTTTGAGAGTACTTATTTTTGGTTGGCT | 1140 |
| QY | 1141 | CCAGGTAAAGCTTTGGAATGAATCTTACCTCTATTTTTGTAATGTAATATGCTCAGCT | 1200 |
| Db | 1141 | CCAGGTAAAGCTTTGGAATGAATCTTACCTCTATTTTTGTAATGTAATATGCTCAGCT | 1200 |
| QY | 1201 | TATGCTTTGGGTGTGTTCTAGACCAAGATGTTAATGTAAGTACTAGTGAAGAACATCT | 1260 |
| Db | 1201 | TATGCTTTGGGTGTGTTCTAGACCAAGATGTTAATGTAAGTACTAGTGAAGAACATCT | 1260 |
| QY | 1261 | TACAGACAACAAGCTGCTGTTCCATTTGGCTAGTGAATCACTATGCTGTGTAAGATGTTGCT | 1320 |
| Db | 1261 | TACAGACAACAAGCTGCTGTTCCATTTGGCTAGTGAATCACTATGCTGTGTAAGATGTTGCT | 1320 |
| QY | 1321 | GTTTTTCTAGAGGTTCCAAAGCTCAATTTGGTCAATGCTGTTCAGAAAGAAACTTTTGGT | 1380 |
| Db | 1321 | GTTTTTCTAGAGGTTCCAAAGCTCAATTTGGTCAATGCTGTTCAGAAAGAAACTTTTGGT | 1380 |

SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 1
 ; LENGTH: 1476
 ; TYPE: DNA
 ; ORGANISM: Bovine
 US-09-911-132A-1

Query Match 57.3%; Score 845.6; DB 10; Length 1476;
 Best Local Similarity 73.3%; Pred. No. 1,1e-182;
 Matches 1082; Conservative 0; Mismatches 394; Indels 0; Gaps 0;

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QY 1 GAATCTTGAATTCAGCTGAAGAAAGAAATCCAGCTTTTGGAAATAGACAAGCTGCTCA 60
DB 1 GAATCTCTATCCAGCTGAGAGAGAAACCCGCTTTGGAACCCGACGAGGCCAG 60
QY 61 GCTTGGATGTGTGTAAGAGTTGCAACCAATTAACTGCTGTAAGAAATGTTATTTG 120
DB 61 GCCCTTGATGTAGCAAGAAAGTTGCAACCCGATCCAGACAGCTGCCAAGAAATGTCATCTC 120
QY 121 TTTTGGGATGATGGTATGGGTTTCAACTGTCTACTAGAAATTTTGAAGGGTCAA 180
DB 121 TTCTTGGGAGATGGGATGGGAGTCTTAAGGTACAGCTCGATCTTAAGGGGAG 180
QY 181 ATGAATGTAAGTTGGGTCAGAACTCAATGGCTATGATCAATTTCCATACGTTGCT 240
DB 181 ATGAATGGCAAACTGGGACCTGAGACACCCCTGGCCATGAGCCAGTTCCCATACGTGGCT 240
QY 241 TTGCTTAAGCTTAACAATGTTGATAGCAAGTTCAAGATTTGCTGTACTGCTACTGCT 300
DB 241 CTGTCCAAAGCATACAACTGAGACAGACAGGTGCACACAGCCGACCTGCTCCTGCT 300
QY 301 TACTGTGTGTGTAAAGGTAATTAAGAACTATGGTGTCTGCTGCTAGATAC 360
DB 301 TACTGTGTGTGTCAAGGGCACTACAGAACCTAGGTGTAGTGAAGCCGCTTAC 360
QY 361 AATCAATGTAATTAATTAAGTATGAATTAATTTCTGTATTAATTAAGTCAAGAG 420
DB 361 AATCAAGTCAACAGACAGTGGGATGAGGTGACGTGTGATCAACCCGGCCAAAGAA 420
QY 421 GCTGTAAAGCTGTGTGTGTGTTACTTAATTAATTAAGTCAATGCTTTCCAGCTGT 480
DB 421 GCAAGGAAAGCCGAGGAGTGTGACCAACAGGCTGAGCATGTCTCCAGCCGAG 480
QY 481 GCTTACGCTCATCTGTAAATTAAGAAATTTGTAATCTGATCTGATTTTCCAGCTGAT 540
DB 481 GCTTACGCTCATCTGTAAATTTGTAATCTGATCTGATCTGATCTGATGCA 540
QY 541 CAAAGAAATGTTGTCAAGATATTTGCTGCTCAATTTGTTTACAATATGATATGATGTT 600
DB 541 CAAAGAAATGCTGCAAGACATGCGGCAACGCTGCTTACAACATGATATGATGCTG 600
QY 601 ATTTGGGTGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 660
DB 601 ATCTGGGTGTGAGGCGCAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 660
QY 661 GATGATGCTCTGTGTAATGTTGTTAAGAAAGTAAAGAAATTTGTTCAAGATGCA 720
DB 661 GATGATGCTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 720
QY 721 GCTAAGCATCAAGGTGCTCAATATGTTTGGAAATGAAGCTGTTTGTGCAAGCTGCTGAT 780
DB 721 GCCAAGCAACAGGAGCCAGTATGTTGTAACCGCATGCTGCTTCAAGGCGCGAT 780
QY 781 GATTTAGTGTATCTCAATTTGATGAGTTGTTGAAACCAAGCTGATATGATATGTT 840
DB 781 GATCTCAGGTATCAACCTCAATGAGGCTTGTGAGCGGCAAGCATGATGATATGTT 840
QY 841 CAACAAGATCATCTAAGATCAACTTGGCTGAATGAAGTGAAGTGTGTTGCAAGT 900
DB 841 CACCAAGATCAACCAAGATCAAGATCAAGATCAAGATCAAGATCAAGATCAAGATCAAGAT 900
QY 901 TTGTCTAGAAATCAAGAGGTTTAACTGTTTGTGTAAGTGTAGAAATGATGATGAT 960
DB 901 TTGTCTAGAAATCAAGAGGTTTAACTGTTTGTGTAAGTGTAGAAATGATGATGAT 960

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DB 901 CTGAGCAGAAACCCCGGCTTCTACCTCTGCTGAGGAGGCGCCGATTTGACACAGCT 960
QY 961 CATCATGATGTAAGCTTATATGCTTTGACTGAAGCTATTAATGTTGATATGATAT 1020
DB 961 CACCATGACGCAAGGTTATATGCACTACGAGGCAATCATGTTTGAACAAATGCCATC 1020
QY 1021 GCTAAGGCTAATGAATGATCTTGAATGATGATGATGATGATGATGATGATGATGATGAT 1080
DB 1021 GCCAAGCTAACAAGCTCATGAGAACTGACACGCTGATCTTGTGCACTGACAGACAC 1080
QY 1081 AGTCATGTTTCTTCTTGTGTGTGATGATGATGATGATGATGATGATGATGATGATGAT 1140
DB 1081 TCCATGCTCTCTTCTTGTGTGTGATGATGATGATGATGATGATGATGATGATGATGAT 1140
QY 1141 CCAGTGAAGCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1200
DB 1141 CCGGCAAGGCTTGAACAAAGTCTTACACCTTCACTCTATGCAATGAGCCAGGC 1200
QY 1201 TATGCTTGGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1260
DB 1201 TATGCTTGGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1260
QY 1261 TACAGCAACAAAGCTGCTGCTTCAATGATGATGATGATGATGATGATGATGATGATGAT 1320
DB 1261 TACCGGACAGAGCGGCTGCTGCTTCAATGATGATGATGATGATGATGATGATGATGATGAT 1320
QY 1321 GTTTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1380
DB 1321 GTGTTGCGGAGGCGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1380
QY 1381 GCTCATATTAATGCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1440
DB 1381 GCGCATATTAATGCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1440
QY 1441 CCAGTGAAGCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1476
DB 1441 CCGGCAAGGCTTGAACAAAGTCTTACACCTTCACTCTATGCAATGAGCCAGGC 1476

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RESULT 8
 US-10-395-790A-1
 ; Sequence 1, Application US/10395790A
 ; Publication No. US20040072316A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Roche Diagnostics Corp.
 ; TITLE OF INVENTION: Production of weakly active or inactive mutants of alkaline phos.
 ; FILE REFERENCE: RDID 02028US
 ; CURRENT APPLICATION NUMBER: US/10/395,790A
 ; CURRENT FILING DATE: 2003-03-24
 ; NUMBER OF SEQ ID NOS: 21
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 1
 ; LENGTH: 1464
 ; TYPE: DNA
 ; ORGANISM: Bovine
 ; FEATURES:
 ; NAME/KEY: CDS
 ; LOCATION: (1)..(1464)
 ; OTHER INFORMATION:
 US-10-395-790A-1

Query Match 56.6%; Score 834.8; DB 16; Length 1464;
 Best Local Similarity 73.2%; Pred. No. 3,3e-180;
 Matches 1070; Conservative 0; Mismatches 392; Indels 0; Gaps 0;

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QY 8 TGAATCAGCTGAAGAAAGAAATCCAGCTTTTGAATATGACAAGGCTCAAGCTTTGG 67
DB 2 TCAATCCAGCTGAAGAAAGAAATCCAGCTTTTGAATATGACAAGGCTCAAGCTTTGG 61
QY 68 ATGTTCTAAGAAATGTAACCAATTAATCAATGCTGCTGATGATGATGATGATGATGAT 127
DB 62 ATGTACCAAGAAATGTAACCAATTAATCAATGCTGCTGATGATGATGATGATGATGAT 121

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QY 128 GTGATGTAATGGGTGTTCCAACTGTTACTGTAATGAAATTTTGAAGGCTCAATGAAG 187
 DB 122 GGGATGGGATGGGGGCTGCTACGGTGAACCACTCGAATCCTTAAAGGGGCAAGTGAAG 181
 QY 188 GTAAGTTGGGTCCAGAAATCCATTTGCTATGGAATTTTCCATATGCTGTTGCTTCTA 247
 DB 182 GCAACTGGGAACTGAGACACCCCTGCGATGAGACAGTTCCCATACGTGGCTGTGTCCA 241
 QY 248 AGACTTACAATGTTGATAGACAAAGTTCCAGATTTGCTGTAATCTGCTACTGTTACTTGT 307
 DB 242 AGACATACAAACGTGACAGACAGGTGCCAGACGCGGCACTGCCACTGCTACTCTGT 301
 QY 308 GTGGTGTAAAGGTAATTTACAGAACTATTTGCTGCTGCTGTGTAATTAATCAATCAT 367
 DB 302 GTGGGGTCAAGGGCACTACAGAACATGGGTAAAGTGAAGCGCCCTCATCAATCAAT 361
 QY 368 GTAAATCTACTAGAGGTAATGAAGTTACTTCTGTTAATTAAGAGCTAAGAAAGGCTGTA 427
 DB 362 GCACACGACACGTGGGAATGAGTCACTGTGTATCAACCGGGCCAGAAAGCAGGGA 421
 QY 428 AGGCTGTGGGTGTTGTTACTACTACTAGATTCAGATGCTTCTCAAGCTGTGCTTACG 487
 DB 422 AGGCGGTGGGAGTGTGACACACCAAGGGTGCAGCATGCTCCAGCGGGGCTTACG 481
 QY 488 CTCATCTGTTAATAGAAATTTGCTACTGATGCTGATTTGCAAGCTGCTCAAAAG 547
 DB 482 CGCACACGGTGAACCAAACTGGTACTCAGACCGCACTGCTGCTGATGACAGAAAG 541
 QY 548 ATGGTGTCAAGATATTGCTGCTCAATTGGTTTACATATGATATGATATTTATTTTGG 607
 DB 542 ATGGCTGCCAGACATGCGCGCACAGCTGCTTACAAATGATATTTAGATGATCTG 601
 QY 608 GTGGGTGTAAGATGATCATTTTCCAGAAAGTACTCAAGTCCAGAAATACCCAGATGAG 667
 DB 602 GTGGAGGCGCAATGATCATGTTTCTGAGGGGACCCAGACCTGTAATACCCAGATGAG 661
 QY 668 CTTCGTGTTAATGATTTAGAAAGATTAAGCAAAATTTGGTTCAAGATGGCAAGTAAAG 727
 DB 662 CCACTGTGAATGAGATCCGAGAGGACAGCAAGAACTGGTGCAGAAATGGCAGCCAGC 721
 QY 728 ATCAAGGTGCTCAATATGTTGGAATAGAACTGCTTGTGTAAGCTGTGATGATTTCTA 787
 DB 722 ACCAGGAGGCCAGTATGTGTGAACGCGCATGCGCTCTTCAAGCGCGCGATGATCTCCA 781
 QY 788 GTGTTACTCTTTGATGGGTTTGTGTAACCAAGTGAATGAAATGATATTAATTTCAAG 847
 DB 782 GTGTAAACACACTCATGGGCTCTTTGAGCGCGGACATGAAGTATTAATGTTCAAGCAG 841
 QY 848 ATGATCTAAGATCCAACTTTGGCTGAATGACTGAAGCTGCTTGGCAAGTTTGTCTA 907
 DB 842 ACCACACAGAGACCCGACCTTGGCGAGATGAGAGGGGGCCCTCGCAAGTGTGAGCA 901
 QY 908 GAAATCCAGAGGTTTACTTGTGTTGTAAGGTGTAAGTATGATCATGTCATCATG 967
 DB 902 GGAACCCCGGGGCTTCACTCTTGTGTAAGGGAGGCGCCATTTGACACAGGTCAACATG 961
 QY 968 ATGTGAAGGCTTAATAGGCTTTGATCTGAAGCTAATGTTGTAATGCTAATGCTAAG 1027
 DB 962 ACCGCAAGGCTTAATATGCACTGACTGAGGCAATGTTGACAAATGCAATGCCCCAAG 1021
 QY 1028 CTAAATGAATGACTTCTGAATTTGATCTTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1087
 DB 1022 CTAAACGAGTCACTAGAGAACTGACAGCTGATCTTGTGACAGGACCACTCCATG 1081
 QY 1088 TTTTCTTTTGTGTTGTTACCTTTGAGAGGTACTTCAATTTTGTGTTGTTGTTGTTGTT 1147
 DB 1082 TCTTCTCTTTTGTGTTGTTACCTTGTGAGGTACTTCAATTTTGTGTTGTTGTTGTTGTT 1141
 QY 1148 AGGCTTTGATAGTAAATGCTTCACTTATTTGTAATGTAATGCTCAAGGTTATGCTT 1207
 DB 1142 AGGCTTAAGACAGAAATGCTCACTTCACTTCTATGAGCAATGAGCCAGGCTATGCGC 1201

QY 1208 TGGGTGTGTTCTAGACACAGATGTTAATGTAAGTACTAGTGAAGAACATCTTACAGAC 1267
 DB 1202 TTGGGGGGGGCTCGAGGCGGATGTTAATGACACAAAGGAGAAACCTCATATCCGGC 1261
 QY 1268 AACAACTGCTGTTCCATTTGCTAGTGAATCTATGTTGTGTAAGATTTGCTTTTGG 1327
 DB 1262 AGCAGGCGCGGTGCTGCTGCTAGCGAGCCACCGGGGGGGAAGACGTGGCGGTGTGCG 1321
 QY 1328 CTAGAGGTCACAAGGCTATTGTTGTTCAATGTTGTTCAAGAAAGAACTTTGTTGCTCATA 1387
 DB 1322 CGCGAGGCGCGGACGACCTGTTGTCAGCGGCTGTCAGAGAGAGACCTTGTGGCGACCA 1381
 QY 1388 TTATGGCTTTTGTGTTGTTGTTGAACCAATCACTGATTTAATTTTGGCACTCAGCTA 1447
 DB 1382 TCATGGCTTTTGGGGCTGCGGTGAGCCCTACCGAATCTGCAATCTGCCAGCCCCCGCA 1441
 QY 1448 CTGCTACTAGTATTTCCAGATTA 1469
 DB 1442 CCGCACACGACATCCCGACTA 1463

RESULT 9
 US-10-053-637-9
 ; Sequence 9, Application US/10053637
 ; Publication No. US20030158132A1
 ; GENERAL INFORMATION:
 ; APPLICANT: KOVESDI, IMRE
 ; TITLE OF INVENTION: METHOD OF ENHANCING BONE DENSITY OR FORMATION
 ; FILE REFERENCE: 206211
 ; CURRENT APPLICATION NUMBER: US/10/053,637
 ; NUMBER OF SEQ ID NOS: 28
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 9
 ; LENGTH: 1597
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: SEAP/RGD fusion protein
 ; NAME/KEY: CDS
 ; LOCATION: (11)..(1585)
 ; OTHER INFORMATION:
 ; NAME/KEY: misc_feature
 ; LOCATION: (1538)..(1570)
 ; OTHER INFORMATION: RGD domain
 US-10-053-637-9

Query Match 38.8%; Score 572.8; DB 15; Length 1597;
 Best Local Similarity 62.4%; Pred. No. 2.2e-120; Indels 0; Gaps 0;
 Matches 898; Conservative 0; Mismatches 542;

QY 6 CTGATTCAGCTGAAAGAAATCCAGCTTTTGAATAGACAAAGTGTCAAGCTTT 65
 DB 61 CATATCCCAAGTTGAGAGAGAACCCGGACTTTGGAACCGCGAGGCGGAGCCCT 120
 QY 66 GGAATGCTTAAGAGAGTTCACCAATTTGAATCTGCTGTAAGATGTTATTTGTTTT 125
 DB 121 GGGTGGCGCAAGAAAGCTGACGCTGACAGACAGCCGCAAGAACCTCATATCTTCT 180
 QY 126 GGGTGAATGTAAGGGGTTCCAATGTTTACTGCTAATGAATTTTGAAGGGTCAATGA 185
 DB 181 GGGCGATGGATGGGGGTCTTACGGGTGACAGCTGCCAGATCTTAAAGGCGAAGAA 240
 QY 186 TGGTAAGTTGGGTCAGAAATCCATTTGCTATGATCAATTTCCATACGTTGCTTGTG 245
 DB 241 GGAACAACTGGGGCTCGAATATCCCTGCGCATAGAACCGCTTCCATATGTGGCTGTG 300
 QY 246 TAAACTTACATGTTGATAGACAAAGTTCAGATTTCTGCTGATCTGCTACTACTT 305
 DB 301 CAAGACATACATATGTAGACAAACATGTGCAACAGTGAAGCACAAGCGGCTTACCT 360
 QY 306 GTGTGTGTTAAGGGTAATTTACAGAACTATGTTGTTTCTGCTGCTGATATCAATCA 365

Db 361 GTGCGGGGTCAAGGCACTTCCAGACATTGGCTTGAGTGAGCCGCCGCTTTAAACA 420
Qy 366 ATGTAATACTAGAGTAATGAACTTCTGTTATTAATAGAGCTAAGAGCTGG 425
Db 421 GTGCAACAGACACGGGCAACAGGTCACTCCGTGATGAATCGGGCCAGAAAGGAG 480
Qy 426 TAAGCTGTGTGTTGTTACTACTAGAGTTCAACATGCTTCTCCAGCTGGTCTTA 485
Db 481 GAAGTAGTGGAGTGTAAACAACAGAGTGACAGACGGCTCCGACGCCGACCTTA 540
Qy 486 CGCTCATCTGTTAATGAATTTGTAATCTGATGCTGATTTGGCAGCTAGTCTAAA 545
Db 541 CGGCCACACGGTAAACGCAACTGTGTACTGAGACGGCAGAGTCTGCTCGGCCGCCA 600
Qy 546 GAATGTTGTCAAGATTTGCTGCTCAATGTTTACATATGGAATTAATGTTATTTT 605
Db 601 GAGGGGTGCGCAGACATCGCTTACGAGCTCACTCCACATGGAATTAAGTATCTCT 660
Qy 606 GGGTGTGTGTAAGATGATCATGTTTCCAGAAAGTATCCAGATCCAGAAATACCAGATGA 665
Db 661 AGGTGGAGGCGCAAGATCATGTTTCCATGGGAACCCAGACCTGAGTACCAATGA 720
Qy 666 TGTCTTCTGTTAATGCTTTGAAGAGTAAGCAAAATTTGTTCAAGATGGCAAGCTTA 725
Db 721 CTACAGCCAAAGTGGGACAGGCTGACGGGAAGATCTGTGACAGAAATGCTGGCGGA 780
Qy 726 GCATCAAGGTGCTCAATATGTTTGAATAGACGCTTTGTGCAAGCTGCTGATATTC 785
Db 781 GCGCCAGGGTGGCGGATATGTGGAACCGCACTGAGCTATGAGGCTTCCCTGGACCC 840
Qy 786 TAGTGTACTCATTTGATGAGTGTGTTTGAACAGCTGATATGATATGATTCACA 845
Db 841 GTCTGTGACCACTCATATGAGGTCTCTTGAAGCTGGAGACATGAATACAGATCCACG 900
Qy 846 AGATCATCTAAGATCAACTTTGGCTGAATGATGAAAGCTGCTTGGCAAGTTTGTTC 905
Db 901 AGATCACAACATGAGCCCTCCCTGATGAGATGACAGAGGCTCCCTGCGCTGTGAG 960
Qy 906 TAGAAATCCAAAGGTTTTTACTGTTTGTGAAGGTGAGAAATGATATGATGCTATCA 965
Db 961 CAGGAACCCCGGGCTTCTTCTCTTCTGAGAGGGTGGAGTCAATGACATGATCA 1020
Qy 966 TGAATGTAAGCTTAAATGAGCTTTGACTGAAGTATTAATGTTGATATGCTATTCCTAA 1025
Db 1021 TGAACAGAGGCTTACCGGCACTGACTGAGAGATCAITTTGACAGACCCATTTAGAG 1080
Qy 1026 GGTAAATGAATGACTTCTGAATTTGAACTTGAATTTGTTGTTACTGCTGATAGTCA 1085
Db 1081 GGGGGGCTCAGCTCAGCAGAGAGGACAGCTGAGCTGCTGCTGACCTGCGACCACTCCA 1140
Qy 1086 TGTCTTTTCTTTGGTGTGTTACATTTGAGAGTACTTCTAATTTTGGTTGGCTCAGG 1145
Db 1141 CGCTTCTCTCTGGAGGCTAACCCCTGCAAGGAGCTCATCTTGGGGTGGCCCTGG 1200
Qy 1146 TAAGCTTTGATAGTAACTTACATTTTGTATGTAATGTAATGTAATGTAATGTAATG 1205
Db 1201 CAAAGCCCGGAGAGAGAGGCTTACAGCTCTCTATAGAGAAAGGCTTCAAGCTATGT 1260
Qy 1206 TTTGGTGTGTGTTCTAGACCAAGATGTTAAATGTAATGTAATGTAATGTAATGTAATG 1265
Db 1261 GCTCAAGAGAGGCGCGCGGATGTTACGAGAGGAGAGGCGGAGCGCCGAGATGCG 1320
Qy 1266 ACAACAGAGCTGCTGTTCCATTTGGCTAGTAACTCATGTGTGTGAAGATGTGCTGTTT 1325
Db 1321 GAGCAGTCAAGAGTCCCTGAGCAAGAGACCCAGCAGGAGAGACCTGCGGTGTT 1380
Qy 1326 TGTAGAGGTCAAGAGCTATTTGTTCAATGTTTCAAGAGAACTTTGTTGCTCA 1385
Db 1381 CGGCGCGCGCGCGAGGAGGAGCTGTTTCAAGGCTGAGAGAGACACTTCAATGAGCA 1440
Qy 1386 TATTAATGCTTTTGTGTTGTGTTGAACATACATGATGTAATTTTGGCAAGCTCAAG 1445
Db 1441 CGTCATAGGCTTGGCGGCTGCTGAGAGCTTACACGCTGCGAGCTTGGCGGCCCGCG 1500

RESULT 10
US-09-006-298-22
Sequence 22, Application US/09006298
Patent No. US20020082224A1
GENERAL INFORMATION:
APPLICANT: Jolly, Douglas J.
APPLICANT: Moore, Margaret D.
APPLICANT: Chada, Sunil
TITLE OF INVENTION: NON-IMMUNOGENIC PRODRUGS AND SELECTABLE
TITLE OF INVENTION: MARKERS FOR USE IN GENE THERAPY
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED AND BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.10
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/006,298
FILING DATE: 13-JAN-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: McMaister, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 930049,459
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 1634 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 13..1617
US-09-006-298-22
Query Match 38.8%; Score 572.8; DB 9; Length 1634;
Best Local Similarity 62.4%; Pred. No. 2,2e-120;
Matches 898; Conservative 0; Mismatches 542; Indels 0; Gaps 0;
Qy 6 CTGATTCAGCTGAAGAAATTCAGCTTTTGGAAATGACAAAGCTGCTCAGCTTT 65
Db 78 CATCATCCAGATGAGAGAGAACCCGAGCTTGGAAACCGGAGGCGAGGCCCT 137
Qy 66 GGAATGTTGTAAGAGTTGCAACCAATTCAACTGCTGTAGAAATGTAATTTGTTT 125
Db 138 GGGTCCGCAAGAGCTCAGCTGACAGACAGCGCCAGAACTTATCTATCTTCT 197
Qy 126 GGGTATGATGAGGTTGTTCCAACTGTTACTGCTACTAGAAATTTTGAAGGTCAAATGA 185
Db 198 GGGCAGATGAGATGGGGGTCTTACGCTGACAGCTGCAAGATCTTAAAGGAGAAAGA 257
Qy 186 TGTAAAGTTGGGCTCAGAAATCTCATGGCTATGATCAATTTCCATACGTTGCTTGTTC 245
Db 258 GGAACAACTGGGGCTGAGATATCCCTGGCCATGAGACCCCTTCCATATGTGCTGTGTC 317
Qy 246 TAAGACTTCAATGTTGATAGCAAGTTCCAGATTCGTGTGATCTGACTAGCTTACTT 305
Db 318 CAAAGATCAATATGAGCAAACTGTGCAACAGTGAAGCAGACAGCGCTTACCT 377
Qy 306 GTGTGTGTTAAGGTAATTAAGAACTATTTGTTGCTGCTGCTAGATACAAATCA 365

Db 378 GTGCGGGGTCAAGGCGAACTTCAGACCAATTGGCTGAGCCGCCCTTAAACA 437
Qy 366 ATGTATATCTACTAGAGGTATGAAATTCTTGTATTATTAATAGATAAGAGCTGG 425
Db 438 GTGCACACGACACCGGCGACAGAGGTCTATCCGTGATGAATCGGCCAAGAAAGCAGG 497
Qy 426 TAAAGCTGTGGTGTGTGTACTACTAATAAGATTCAACATGCTTCTCCAGCTGTGCTTA 485
Db 498 GAAAGTCAGTGGAGTGTATACCAACACAGATGACAGCCGCTCGCCGCGGACCTTA 557
Qy 486 CCTCATATCTGTTAATAGAAATTTGTACTCTGATGCTGTTTGGCAGCTGATGCTCAAA 545
Db 558 CCGCCACAGGTGAACCGCACTGTGATCGACGCGGAGCTGCTGCTCGGCCGCCA 617
Qy 546 GAATGGTTTCAAGATATTGCTGCTCAATTGGTTTCAAAATATGATATTGATTTT 605
Db 618 GGAAGGGTCCAGAGATCGCTACGAGCTCATCTCAACATGGAATTTGATGATCTCT 677
Qy 606 GGGTGTGTAGATATGATATGATTTTCCAGAGGATCTCCAGATCCGAATACCCAGATGA 665
Db 678 AGGTGAGGCCGAAATGATATGTTTCCATGGGAACCCAGACCTGAGATCCAGATGA 737
Qy 666 TGGTCTGTATATGTGTATAGAAAGATAGCAAAATTTGTTTCAAGATGGCAAGCTTA 725
Db 738 CTACAGCCAAAGTGGACCAAGCTGACGGAAGAAATCTGTGCAAGAAATGGCTGGCAA 797
Qy 726 GCATCAAGGTGCTCAATATGTTTGAATAGAACTGCTTGTGCAAGCTGTGATGATTC 785
Db 798 GCGCCAGGGGTGCCGGTATGTGTGAACGCACTGAGCTCATGCAAGTCTCCCTGAGACC 857
Qy 786 TACTGTACTATTGATGGGTGTGTTTGAACCAAGCTGATATCAATATTAATTTCAACA 845
Db 858 GTCTGTGACCACTCATAGGGTCTCTTGAAGCTGAGATGAATGAATACAGATCCACCG 917
Qy 846 AGATCACTACTAAGATCCAACTTGGCTGAATGATCAAGAGCTGCTTGTGCAAGTGTGTC 905
Db 918 AGACTCACTGACGACCCCTCTGTATGAGATGACAGAGGCTGCCCTGCGCTGTGAG 977
Qy 906 TAGAAATCCAAAGAGTTTACTTGTGTTTGAAGGTGTGAATTTGATATGATGTCATCA 965
Db 978 CAGAAACCCCGGGGCTTCTCTCTGAGAGGGGTGCGCATGACATGATGTCATCA 1037
Qy 966 TGAATGTAAGGCTTATATGCTTGTGCTGAGCACTATTTGATTAATGTAATGCTATTGCTAA 1025
Db 1038 TGAAGAGAGGCTTACCGGCACTGACTGAGATCATGTGACGACCCATTGAGAG 1097
Qy 1026 GGTAAATGAATGACTTCTGAATTTGATCTTGAATTTGTTGTTGTTGTTGTTGTTGTTGTT 1085
Db 1098 GGGGGGCACTCACCAGAGAGAGACAGCTGAGCCTGTCATGCTCGACCACTCCCA 1157
Qy 1086 TGTATTTTCTTTGGTGTGTTACACTTTGAAGGTACTTCAATTTTGGTGTGCTCCAGG 1145
Db 1158 CGTCTTCTCTCGAGAGCTTACCCCTGCGAGGAGCTCATCTTGGGGTGGCCCTGG 1217
Qy 1146 TAAAGCTTTGGATGTAAGCTTACCTTCAATTTTGTATGTTAATGTCAGGTTATGC 1205
Db 1218 CAAAGGCCCCGACAGAGGCTTACACGTCCTCTTATGGAAGAGCTTCAAGCTATGT 1277
Qy 1206 TTTGGGTGTGTGTTCTAGACCAAGATGTTAATGTAGTACTAGTGAAGAACCATTTTACG 1265
Db 1278 GCTAAGAGAGGGGCGCGCGGAGATGTTAACGAGAGAGAGCGGAGCCCGAGTATCG 1337
Qy 1266 ACAACAGCTGCTTTCATTTGCTAGTGAATCTCATGTGTGTGAATGTTGTTGTTT 1325
Db 1338 GCAACAGTCAAGCAATGCCCCCTGAGAGAAAGCCACGACAGCGAGGCGGGGGTGT 1397
Qy 1326 TGTAGAGGTCCAAAGCTCATTTGTTTCAATGTTTCAAGAAAGAACTTTTGTGCTCA 1385
Db 1398 CGCGCGGGGCGCGAGCGACCTGTGTTCAAGGGGTGAGAGAGACCTTCAATAGGCA 1457
Qy 1386 TATTATGGCTTTTCTGTGTGTGTGAACATACATGATGTTAATTTTCCAGCTCCAGC 1445
Db 1458 CGTATGGCTTTCGCGCGCTGCGAGCCCTTACACGCGCTGCAACCTGGGCGCCCGCGC 1517

RESULT 11
US-10-053-637-11
; Sequence 11, Application US/10053637
; Publication No. US20030158132A1
; GENERAL INFORMATION:
; APPLICANT: KOWESDI, IMRE
; TITLE OF INVENTION: METHOD OF ENHANCING BONE DENSITY OR FORMATION
; FILE REFERENCE: 206211
; CURRENT APPLICATION NUMBER: US/10/053,637
; CURRENT FILING DATE: 2002-01-22
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 1675
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: SEAP/Decorin fusion
; NAME/KEY: CDS
; LOCATION: (11)..(1663)
; OTHER INFORMATION:
; NAME/KEY: misc feature
; LOCATION: (1545)..(1663)
; OTHER INFORMATION: decorin domain
US-10-053-637-11

Query Match 38.8%; Score 572.8; DB 15; Length 1675;
Best Local Similarity 62.4%; Pred. No. 2.3e-120;
Matches 898; Conservative 0; Mismatches 542; Indels 0; Gaps 0;

Qy 6 CTGTATCCAGCTGAGAAAGAAATCCAGCTTTTGGAAATGACAAAGCTGCTCAAGCTTT 65
Db 61 CATCATCCAGTGTGAGAGAAACCCGACTTCTGAAACCGAGAGCCGAGCCCT 120
Qy 66 GGATGTCTTAAGAAAGTTGCAACCAATTCAACTGCTGCTAAGAAATGTTATTTGTTT 125
Db 121 GGGTCCCGCAAGAAAGTGTGACGCTGACACAGAGCCGCCAAGAACTCATCATCTTCT 180
Qy 126 GGTATGATGATGGGTGTTCCAACTGTACTGTACTAGAAATTTGAAGGGTCAAAATGA 185
Db 181 GGGCATGGGAAGGGGGTGTCTACGTTGACAGCTGCGCAGGATCTTAAAGGAGAGAA 240
Qy 186 TGTAAATGGGTCCAGAACTCCATGGCTATGATCAATTTCCATGATGTTGCTTGTG 245
Db 241 GACAAACTGGGGCTTGAGATACCCCTGGCATGAGACCGCTTCCATATGTGGCTGTG 300
Qy 246 TAAAGCTTACATGTTGATAGCAAGATTCCAGATTCTGCTGTACTGTACTGTTACTT 305
Db 301 CAAAGATTCATATGTAGCAAAACATGTGCCAGACAGTGGAGCCACAGCCGCTTACT 360
Qy 306 GTGTGTGTTAAGGTAATTAAGAACTTATGATGTTTCTGTGCTGTGCTAGTACATCA 365
Db 361 GTGCGGGTCAAGGGCACTTCCAGACATTTGCTTGAATGACGCGCCGCTTTAAACA 420
Qy 366 ATGTATATCTACTAGAGGTATGAAATTCTTCTGTTATTAATAGCTTAAGAGGCTGG 425
Db 421 GTGCACACGACACCGGGAAGAGATATCTCCGTATGAATTCGGGCGAAAGAGCAGG 480
Qy 426 TAAAGCTGTGTGTTGTTTACTACTAGTGAATGATGTTCAATGCTTCTCCAGCTGTGCTTA 485
Db 481 GAAATCAGTGGAGTGTATACCAACACAGATGAGACCGCTCGCCACGCGGACCTTA 540
Qy 486 CGCTCATCTGTATTAAGAAATTTGGAATCTGATGCTGATTTGGCAGCTGATGCTCAAA 545
Db 541 CCGCCACAGGTGAACCGCACTGTACTGAGCGCCAGCGCTGCTCGGCCGCCA 600
Qy 546 GAATGGTTTCAAGATATTGCTGCTCAATTTGTTTCAATATGATGATGATGTTT 605
Db 601 GGAAGGGTCCAGAGATCGCTACGAGCTCATCTCAACATGAGCATTTGATGATCTCT 660
Qy 606 GGGTGTGTAGATATGATATGTTTCCAGAAAGTACTCCAGATCCAGAAATACCAAGATGA 665

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Db 661 AGGTGAGGCGGAAAGTACATGTTCCCATGGGAAACCCGACGCTGATGACCAAGTGA 720
Qy 666 TCGTCTCTGTTAATGCTGTTGAAAGGATAAGCAAAATTTGGTTCAGATGAGCAAGTAA 725
Db 721 CTACAGCCAAAGGTGGGACCGAGCTGGACGGGAAATCTGTGTCAAGAAATGGCTGGGAA 780
Qy 726 GCATCAAGGTGCTCAATATGTTTGAATAGAACTGCTTTGTGCAAGCTGTGATGATTC 785
Db 781 GCGCCAGGGTGCCCGGATGTGTGGAACCGCACTGAGCTCATGACGCTTCCCTGGACCC 840
Qy 786 TAGTGTACTCAATTGATGGGTTGTTGAACCAAGCTGATGATGAAGTAAATGTTCAACA 845
Db 841 GTCTGTGACCCATCTCATGAGGTCTCTTGAAGCTGAGACATGAATAACAGATCCACCG 900
Qy 846 AGATCATCTAATAGATCCAACTTGGCTGAATGACTGAAGCTGCTTTCGAAGTTTGTCT 905
Db 901 AGACTCCACATGGAACCCCTCCCTGATGAGATGACAGAGCTGCCCTGGCTGCTGAG 960
Qy 906 TAGAAATCCAAAGAGTTTACTTGTGTTGTTGAAGGTGATGAATTGATGATGATCA 965
Db 961 CAGGAACCCCGGGGCTTCTTCTCTTCTGAGAGGTGTGCGATGACATGATGATCA 1020
Qy 966 TGAATGTAAGCTTATATGCTTGAAGCTTGAAGCTATATGTTGATATGCTATTTGCTAA 1025
Db 1021 TGAAGAGAGGCTTACCGGACACTGACAGATGATGATGATGATGATGATGATGATG 1080
Qy 1026 GGTAAATGAATGATCTTGAATGATGATGATGATGATGATGATGATGATGATGATG 1085
Db 1081 GGGGGGCAAGCTCAGCAGCAGGAGGACAGCTGAGCTGCTGCTGCTGCTGCTGCTGCT 1140
Qy 1086 TGTATTTCTTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 1145
Db 1141 GCTCTCTCTCTGAGAGCTACCCCTGCGAGGAGCTTCCATCTTGGGCTGGCCCTGG 1200
Qy 1146 TAAAGCTTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1205
Db 1201 CAGAGCCCGGAGACAGGAGGCTACACGCTCTCTATACGAAACGCTCAAGCTATGT 1260
Qy 1206 TTTGGGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 1265
Db 1261 GCTCAAGAGCGGCGCGCGCGGATGTACCGAGAGGAGCGGAGCCCGCAGATATCG 1320
Qy 1266 ACAACAGCTGCTGTTCCATGCTAGTGAAGTCACTGATGTTGTTGTTGTTGTTGTTG 1325
Db 1321 GCGAGCTGACAGTGGCTCTGAGCAAGAGACCCGACGAGGAGGAGGAGGAGGAGGAG 1380
Qy 1326 TGCTAAGGTCCAAAGCTCATTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 1385
Db 1381 CCGGCGCGCGCGCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1440
Qy 1386 TATTATGCTTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 1445
Db 1441 CGTCATGCGCTTGCGCGCTGCTGAGAGCCCTACACGCGCTGCGACCTGGCGCCCCGCG 1500

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RESULT 12

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US-09-908-943A-127
; Sequence 127, Application US/09908943A
; Publication No. US20030017991A1
; GENERAL INFORMATION:
; APPLICANT: Yan, Riqiang
; APPLICANT: Tomasek, Alfred G.
; APPLICANT: Gurney, Mark E.
; APPLICANT: Emmons, Thomas L.
; APPLICANT: Bienkowiak, Mike J.
; APPLICANT: Heinrikson, Robert L.
; TITLE OF INVENTION: SUBSTRATES AND ASSAYS FOR BETA-SECRETASE ACTIVITY
; FILE REFERENCE: 29915/00281A.US1
; CURRENT APPLICATION NUMBER: US/09/908, 943A
; PRIOR FILING DATE: 2001-07-19
; PRIOR FILING DATE: 2000-07-19

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; NUMBER OF SEQ ID NOS: 197
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 127
; LENGTH: 1728
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: nucleic acid
US-09-908-943A-127

Query Match 38.8%; Score 572.8; DB 10; Length 1728;
Best Local Similarity 62.4%; Pred. No. 2,3e-120;
Matches 898; Conservative 0; Mismatches 542; Indels 0; Gaps 0;

Qy 6 CTGATATCCAGCTGAAGAAAGAAATCCAGCTTTTGGATATGACCAAGCTGCTCAAGCTTT 65
Db 51 CATCATCCAGATTGAGAGAGAGAACCCGACCTTCTGAAACCGGAGGACAGCCGAGGCTT 110
Qy 66 GATGTTGCTAAGAGTTGCAACCAATTCAAATGCTGCTAAGATGTTATTTGTTT 125
Db 111 GGGTCCCGCCAGAGAGCTGACGCTTCAACAGACAGCCGCGAGAACTTCAATCTTCT 170
Qy 126 GGGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 185
Db 171 GGGCATGAGGATGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 230
Qy 186 TGGTAATGTTGGTCCAGAAATTCATGCTATGATGATCAATTTCCATAGCTGCTTGTCT 245
Db 231 GGCACAACTGGGGCTGAGATACCCCTGGCATTGACCCCTTCCATATGTGCTGCTGTC 290
Qy 246 TAAAGCTTCAATGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 305
Db 291 CAGACATCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 350
Qy 306 GTGTGTTGTTAAGGTTAATTAACAGAACTATGTTGTTGTTGTTGTTGTTGTTGTTGTTG 365
Db 351 GTGCGGGGTCAAGGAGCAATTCACAGACATTTGGCTTGAATGAGACCGGCGGCTTTAAC 410
Qy 366 ATGTAATCTACTAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 425
Db 411 GTGCAACAGACACGCGGCAAGAGGTCACTCCGATGATGATGATGATGATGATGATGATG 470
Qy 426 TAAAGCTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 485
Db 471 GAAATGATGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 530
Qy 486 CGCTCATCTGTTAATAGAAATTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 545
Db 531 CCGCCACAGGTGACCGCACTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 590
Qy 546 GAAATGTTGTCAGATATTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 605
Db 591 GAGAGGATGACAGAGATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 650
Qy 606 GGGTGTGTTGTTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 665
Db 651 AGGTGAGGCGCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 710
Qy 666 TCGTCTGTTAATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 725
Db 711 CTACAGCCAAAGGTGGACAGGCTGAGCGGAGAAATCTGTGTCAAGAAATGGCTGGCGAA 770
Qy 726 GCATCAAGGTGCTCAATATGTTTGAATAGAACTGCTTTGTGCAAGCTGCTGATATTC 785
Db 771 GCGCCAGGGTGCCCGGATGTGTGGAACCGCACTGAGCTCATGAGGCTTCCCTGGACCC 830
Qy 786 TAGTGTACTCAATTGATGGGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 845
Db 831 GTCTGTGACCCATCTCATGAGGTCTCTTGAAGCTGAGACATGAATAACAGATCCACCG 890
Qy 846 AGATCATCTAAGATCCAACTTTGGCTGAATGATGATGATGATGATGATGATGATGATGAT 905

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1201 CAAGGCCCGGAGCAGGAAGGCTTACAGGTCCTCTTATACGAAACCGTCAGGCTATGT 1260
1206 TTTGGGTGGTGTCTTACAGATGTTATGTAGTACTAGTGAAGAACCATTTTACAG 1265
1261 GCTCAAGAGACGGGCGCGCGGATGTACCGAAGGAGAGCGGAGCCCGAGTATCG 1320
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RESULT 14

US-10-053-637-15
Sequence 15, Application US/10053637
Publication No. US20030158132A1
GENERAL INFORMATION:
APPLICANT: KOVESDI, IMRE
TITLE OF INVENTION: METHOD OF ENHANCING BONE DENSITY OR FORMATION
FILE REFERENCE: 206211
CURRENT APPLICATION NUMBER: US/10/053,637
NUMBER OF SEQ ID NOS: 28
SOFTWARE: PatentIn version 3.1
SEQ ID NO 15
LENGTH: 1777
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: SEAP HBNF fusion
NAME/KEY: CDS
LOCATION: (11)..(1765)
OTHER INFORMATION:
NAME/KEY: misc feature
LOCATION: (1538)..(1762)
OTHER INFORMATION: HBNF domain
US-10-053-637-15

Query Match 38.8%; Score 572.8; DB 15; Length 1777;
Best Local Similarity 62.4%; Pred. No. 2,3e-120;
Matches 898; Conservative 0; Mismatches 542; Indels 0; Gaps 0;

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QY 66 GAGATGTTGCTAAGAGTTGCAACCAATTCAACCTGCTAGAGATTTTATTTTGTGTTT 125
DB 121 GGGTCCGCGCAAGAGCTGAGCTGCAAGACAGCCGCGCAAGAACTTCACTTCTCT 180
QY 126 GGGT 185
DB 181 GGGCGATGGGATGGGGGTGTCTACGGTGACAGCTGCGAGATCTTAAAGGGCAGAAAG 240
QY 186 TGTAGTGTGGGTTCAGAAACTCATTTGGCTATGATCAATTTTCATAGCTTGTGTTTC 245
DB 241 GAGCAAACTGGGCGCTGAGATACCCCTGGCCATGAGACCGCTTCCCATATGTGCTGTGC 300
QY 246 TAAGACTTACATGTTGATAGACAAAGTTCTGCTGTATGCTGTATGCTGTATGCTTACT 305
DB 301 CAAGACATACATGTAGACAAACATGTGCAAGACAGTGGAGCCAGCCAGCCGCTTACT 360
QY 306 GT 365
DB 361 GTGCGGGGTCAAGGGAATTTCCAGACCATTTGGCTTGTGAGCAGCCGCGCTTTAAACA 420

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US-10-053-637-23
; Sequence 23, Application US/10053637
; Publication No. US20030158132A1
; GENERAL INFORMATION:
; APPLICANT: KOWESDI, IMRE
; TITLE OF INVENTION: METHOD OF ENHANCING BONE DENSITY OR FORMATION
; FILE REFERENCE: 206211
; CURRENT APPLICATION NUMBER: US/10/053,637
; CURRENT FILING DATE: 2002-01-22
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Patentin version 3.1
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; FEATURE:
; OTHER INFORMATION: SEAP/VEGF121 fusion
; NAME/KEY: CDS
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; NAME/KEY: misc feature
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QY      186  TGTGATGTTGGGTCCAGAACTCCATTGGCTATGATGATCAATTCATAGSTTGTTC 245
DB      241  GGCACAACTGGGCTGTGATGATCCCTGSCCATGAGCCGCTTCCATATGTGCTCTGTC 300
QY      246  TAAGACTTACAAATGTTGATAGACAAGTTCAGATTCTGTGATGCTACTGCTTACTT 305
DB      301  CAAGACATCAATATGTAGACAAACATGTGCCAGACAGTGGACAGCCAGCCGCTTACCT 360
QY      306  GTGTGTGTTAAGGGTATTTACAGAACTATTTGTTTCTGCTGCTGCTGATGATCAATCA 365
DB      361  GTGCGGGGTCAAGGGCAACTTCCAGACATTTGGCTTGAGTCAAGCCGCGCTTTTAAACA 420
QY      366  ATGTAAATCACTAGAGCTATGAAGTTACTTCTGTTATTAATAGAGCTAAGAGGCTG 425
DB      421  GTGCAACACAGACGCGGCAACGAGTCTCTCGTATGAATCGGGCCAAAGAAAGCAGG 480
QY      426  TAAGGCTGTGTTGTTGTTACTACTACTAGAGTTCAACATGCTTCTCCAGCTGGTGT 485
DB      481  GAAGTCAGTGGAGTGTGTAACACACACAGAGTGCACACGCGCTGCGCACGGCACCTA 540
QY      486  CGCTCATACTGTTAATAGAAATGTGTACTGTGATGCTGATTTGCCAGCTGATGTCAAAA 545
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QY      546  GAATGTTGTCAAGATATGCTGCTCAATTGGTTTACATATAGGATATGATGTTATTTT 605
DB      601  GGAAGGGTGCAGGACATCGTACGACGTCATCTCCAAATGACATTTAGCGTGAATCCT 660
QY      606  GGGTGTGTGTAAGATGTACATGTTTCCAGAAAGTACTCCAGATCCAGAAATACCAATGA 665
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DB      721  CTACAGCCCAAGGTGGGACCAAGCTGACGGGAAATCTGTGTGAGAAATGCTGGCGAA 780
QY      726  GCATCAAGTGTCTCAATATGTTTGAATAGAACTGCTTGTGTCAGACTGCTGATGATTC 785
DB      781  GCGCCAGGATGTCGGGATGTGTGTGAACCGGACCTGAGCTCATGACGGCTTCCCGAACCC 840
QY      786  TAGTGTACTCATTTGATGAGGTTTGTGTTGAACCACTGATATGAAATGATTAATGTTCA 845
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Search completed: October 19, 2004, 23:49:31
Job time : 758.5 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 19, 2004, 10:20:22 : Search time 5049.5 Seconds
(without alignments)
10651.558 Million cell updates/sec

Title: US-09-911-132A-5

Perfect score: 1476

Sequence: 1 gattcttcgattccagctga.....gtattccagattaagttacc 1476

Scoring table: IDENTITY_NUC

Gapop 10.0, Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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1: gb_est1:*
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8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| 3 | 350.6 | 23.8 | 950 | 5 BX458398 | BX458398 BX458398 |
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| 40 | 229.2 | 15.5 | 653 | 7 CN788362 | CN788362 4122694 B |
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ALIGNMENTS

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| LOCUS | AK076459 | | | | |
| DEFINITION | Mus musculus 0 day neonate head cDNA, RIKEN full-length enriched library, clone:4833407E05 product:alkaline phosphatase 2, liver, full insert sequence. | | | | |
| ACCESSION | AK076459 | GI:26096820 | | | |
| VERSION | AK076459.1 | | | | |
| KEYWORDS | HTC; CAP trapper. | | | | |
| SOURCE | Mus musculus (house mouse) | | | | |
| ORGANISM | Mus musculus | | | | |
| REFERENCE | Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. | | | | |
| AUTHORS | Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Komno, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y. | | | | |
| TITLE | Normalization and subcloning of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes | | | | |
| JOURNAL | Genome Res. 10 (10), 1617-1630 (2000) | | | | |
| MEDLINE | 20499374 | | | | |
| PUBMED | 11042159 | | | | |
| AUTHORS | 3 Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Komno, H., Akiyama, J., Nishi, K., Kisanui, T., Tashiro, H., Itoh, M., Sumi, N., Itoh, Y., Nakamura, S., Hazama, M., Nishibe, H., Hatada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watanabe, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsumura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kita, A., and Hayashizaki, Y. | | | | |
| TITLE | RIKEN integrated sequence analysis (RISA) system-384-format | | | | |
| JOURNAL | sequencing pipeline with 384 multicapillary sequencer | | | | |
| MEDLINE | Genome Res. 10 (11), 1757-1771 (2000) | | | | |
| PUBMED | 20530913 | | | | |
| AUTHORS | 4 The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium. | | | | |
| TITLE | Functional annotation of a full-length mouse cDNA collection | | | | |
| JOURNAL | Nature 409, 685-690 (2001) | | | | |
| REFERENCE | 5 The FANTOM Consortium and the RIKEN Genome Exploration Research | | | | |
| AUTHORS | | | | | |

Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 2459)
Aachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P.,
Hayashida,K., Hayatsu,N., Hiramoto,K., Hirooka,T., Hirozane,T.,
Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W.,
Kawachi,K., Kawai,J., Kojima,Y., Kondo,S., Kono,H., Kouda,M.,
Koyama,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M.,
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Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N.,
Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T.,
Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S.,
Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,
Muraetsu,M. and Hayashizaki,Y.
Direct Submission
Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
Kanagawa 230-0045, Japan (E-mail:genome-res@gs.riken.jp,
URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222,
Fax:81-45-503-9216)
CDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Please visit our web site for further details.
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URL:http://fantom.gsc.riken.jp/.
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QY 539 CTCAAAAGATGTTGTCAAGATTTGCTCTCAATTGGTTTACATAT--GATATTG 595
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QY 596 ATGTTATTTTGGTGTGTGTAATGTAATGATGTTTCCAGAAAGGTCTCCAGATCCAGAT 655
DB 825 AGCTATCTGAGTGTGCGCGCGGAAATGATTTACCGAAGAACGAATGATGTGAT 884
QY 656 ACCCAGATGATCTTCTGTTAATGATGTTAGAAAGATGAGCAATTTGGTTCAAGAT 715
DB 885 ACGAATGATGAGAAAGCGAGGGGTACAAAGGCTGATGCGCTGATCTCATCAGATATT 944
QY 716 GG-----CACTAAGCATCAAGTGTCTCAATATGTTTGAATGAACTGCTTGT 766
DB 945 GGAAAGCTTTAAACCCAGACACAAACATCTCCATATGTCTGAAACCGCATGAATCTGC 1004
QY 767 TGCAAGCTCGATGATTTCTATGTTTACTCAATTTGATGGGTTTGGTAAACAGCTGAT 826
DB 1005 TG--GCCCTGACCCCTCCAGGAGTGAATCTTGAAGTCTCTTTGAGCCGGGAGACA 1061
QY 827 TGAAGTATATGTTCAACAGATCATCTACTAAGATCCAACTTTGGCTGAATGATGTAAG 886
DB 1062 TGCACTTAATGAAATGAAATGGAACCAACCTGACCTGCTCCGAGATGATGAGG 1121
QY 887 CTGCTTTGCAAGTTTGTCTGAAGAAATCCAGAGGTTTACTTCTTTGTTGAAGTGTGA 946
DB 1122 TGGCCCTCCGATCTCGACCAAAAACCTCAAAAGGCTCTTCTGCTGGTGAAGAGGCA 1181
QY 947 GAAATGATCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1006
DB 1182 GGAATGACACGACATCATGAGGTGAAGGCCAAGCAAGGCTCTGATGAAGAGAGAGACA 1241
QY 1007 TTGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1066
DB 1242 TGGAACAGGCAATTTGCAAGGAGGCGCATGACATCCAGAAAGACCTTGAAGTGTGG 1301
QY 1067 TTACTGCTGATCATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1126
DB 1302 TTACTGCTGATCATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1361
QY 1127 TTTTGTGTGTGCTCA---GGTAAAGCTTTGATGATGATGATGATGATGATGATGAT 1183
DB 1362 TCTTTGTGTGTGCTCAAGTGAAGGACGACGAGACAGAAAGGCTTCAAGGCAATCTAT 1421
QY 1184 ATGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1243
DB 1422 ATGATATGAGGCGCTGCTGCAAGAGTGTGAAGAGGGAAGAAATGCTTCATAGGTAG 1481
QY 1244 CTAGTGAAGAACATCTTACAGACAAAGAGCTGCTGTTCCATGTGCTGAGAACTCATG 1303
DB 1482 ATTAAGCTCAACAACAATACAGAGGCCAGTCCGCTGTTCCTGCGCATAGAGACCAAG 1541

QY 1304 GGTGTAAGATGTCGTGTTTGTCTAGAGCTCCACAGCTCATTTG-GTTCAATGCTGT 1362
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 DB 1542 GTGAGAGACGCGGGGCTTGTGCGCAAGGCCGAGACACCTGCTTCAAGGGGTC 1601
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 QY 1363 CAAAGAAAGAACTTTGTTGCTCATATTAATGCTTTGCTGTTGTGTTGAACATACACT 1422
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 DB 1602 CATGACAGAACTAATCATCCCGCATGTATGCGTATGCTCTGATGAGGGGCAACCTT 1661
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 QY 1423 GA 1424
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 DB 1662 GA 1663
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RESULT 2
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 LOCUS 4096346 BARC 10BOV Bos taurus cDNA clone 10BOV35_H01 5', mRNA
 DEFINITION
 CK956273
 CK956273
 CK956273.1 GI:45470653
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Bos taurus (cow)
 Bos taurus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 Bovinae; Bos.
 1 (bases 1 to 733)
 REFERENCE
 AUTHORS
 Somtegard, T.S., Van Tasseil, C.P., Matukumalli, L.K., Harhay,
 G.P., Bosak, S., Rubenfield, M. and Gasbarre, L.C.
 TITLE
 Production of EST from cDNA libraries derived from immunologically
 activated bovine gut
 JOURNAL
 unpublished (2004)
 COMMENT
 Contact: Ted S. Somtegard
 Bovine Functional Genomics Laboratory
 Animal and Natural Resources Institute
 Bldg. 200 Rm2A BARC-East, Beltsville, MD 20705, USA
 Tel: 3015048416
 Fax: 3015048414
 Email: tadesant@barc.usda.gov
 Single pass sequencing. Bases called and trimmed with phred
 0.000925 using options -trim alt -trim fasta. Vector identified
 by cross match using options -mismatch 12 -mismatch 18
 Plate: 35 row: H column: 01
 Seq primer: CCCAGTCACGACGTTGTAACG
 High quality sequence stop: 733.
 Location/Qualifiers
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 /organism="Bos taurus"
 /mol_type="mRNA"
 /strain="Holstein"
 /db_xref="taxon:9913"
 /clone="10BOV35_H01"
 /sex="Male"
 /tissue_type="Pooled"
 /dev_stage="Multiple"
 /lab_host="DH10B T1 phage resistant"
 /clone_1lb="BARC 10BOV"
 /note="Organ: Small Intestine; Vector: pagen-1; Site: 1;
 EcorV; Site 2: NotI; Equimolar amounts of mRNA extracted
 from proximal jejunums of 18 and 21 wk old steers, and
 distal ileums of 14 day old calves. Proximal jejunum
 exposed to C. concophora for 3 and 6 weeks, and distal
 ileum exposed to C. parvum for 7 days"

ORIGIN
 Query Match 24.2%; Score 357.6; DB 7; Length 733;
 Best local Similarity 70.6%; Pred. No. 5.6e-78;
 Matches 477; Conservative 0; Mismatches 199; Indels 0; Gaps 0;
 QY 791 TTAATCTATTTGATGGTTTGTGAAACGAGCTATGAAATATATGTTCAACAGATC 850
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 DB 12 TAAACACCTCATGGGCTCTTGTAGCGCGCAGACATGAATATATGTTCAACAGATC 71
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QY 851 ATACTAAGATCCAACTTTGGCTGAATGATGATGAGCTGTTGCAAGTTTGTCTAGAA 910
 |||||
 DB 72 ACACCAAGAGCCGACCTCTGACAGGAATGACAGAGGTGCGCTCGAGGTCTAAGACGA 131
 |||||
 QY 911 ATCAAAGAGTTTAACTTGTGTTGTTGAGAGGTGTAATGATCATGTCATCATGATG 970
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 DB 132 ACCCCAGGGGCTTCTACCTCTTGTGTGAGGAGGAGCGGCATATGACACAGGTACCATGATG 191
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 QY 971 GTAAAGCTTATATAGGCTTTGACATGAGCTATTAATGTTGTAATGATTTGTAAGGCTA 1030
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 DB 192 ACAAGCTTATATATGACATGACCGAGCGGTCAATGTTGCAATGATCCATGACCAAGGCTA 251
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 QY 1031 ATGAATGACTTCTGATATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1090
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 DB 252 ATGAGCTCACTACGACACTGACACCGCTATCTTGTGACGACGACCTGATCTCTATGCT 311
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 QY 1091 TTTCTTTTGGTGTGTTACCTTTGAGAGTACTTCTAATTTTGGTTGGCTCCAGTAAAG 1150
 |||||
 DB 312 TCTCTTTTGGTGTGTTACCTTTGAGAGTACTTCTAATTTTGGTTGGCTCCAGTAAAG 371
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 QY 1151 CTTTGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1210
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 DB 372 CTTTGAACAGCAAGTCTTACCTCACTCTTATGCAATGAGCCCTGAGCTTATGCGCTTG 431
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 QY 1211 GTGCTGTTCTAGACCAAGATGTTAATGATGATGATGATGATGATGATGATGATGATG 1270
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 DB 432 GCGGGGCTGAGGCGCCGATGTTAATGACAGCAACAGAGACCCCTGCTACAGAGC 491
 |||||
 QY 1271 AAGCTGCTGTTCCATGCTAGTGAATCTCATGATGATGATGATGATGATGATGATGATG 1330
 |||||
 DB 492 AGCGGCGCGTCCCTGCTAGAGACCAACGAGGCGGAGAGTGGCGGTGTCGCGC 551
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 QY 1331 GAGTCCACAAAGCTATTTGTTGTTGATGATGATGATGATGATGATGATGATGATGATG 1390
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 DB 552 GCGGCGCGAGGCGACCTGAGTGCAGCGCTGAGAGAGGAGACCTTGTGGCCACATYCA 611
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 QY 1391 TGGCTTTTGGTGTGTTGTTGAAACATACATGATGATGATGATGATGATGATGATGATG 1450
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 DB 612 TGGCTTTTGGGCTGCTGCTGAGACCTTACACGACATGCAATCTGCCAGCCCAACACCG 671
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 QY 1451 CTACTAGTATTCAGA 1466
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 DB 672 CCACGACATCCCGA 687
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RESULT 3
 BX458398 950 bp mRNA linear EST 05-MAY-2004
 LOCUS BX458398 Homo sapiens PLACENTA Homo sapiens cDNA clone CSDB002YN21
 DEFINITION
 5-PRIME mRNA sequence.
 ACCESSION
 BX458398
 BX458398.2 GI:47053565
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Homo sapiens (human)
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 950)
 REFERENCE
 AUTHORS
 Li, W.B., Gruber, C., Jessee, J. and Polyes, D.
 TITLE
 Full-length cDNA libraries and normalization
 JOURNAL
 Unpublished (2001)
 COMMENT
 On May 22, 2003 this sequence version replaced gi:31023009.
 Contact: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 EVRY cedex - France
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
 end enriched, double-strand cDNA was digested with Not I and cloned
 into the Not I and EcorV sites of the pCMVSPORT 6 vector. Library
 was not normalized. Library was constructed by Life Technologies, a
 division of Invitrogen.
 This sequence belongs to sequence cluster 1699.f
 For more information about this cluster, see

FEATURES <http://www.genoscope.cns.fr/cdna?c=CS0DE002CG110P1&c=1699.f>.
Location/Qualifiers
1. 950

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DE002YN21"
/issue_type="PLACENTA"
/clone_lib="Homo sapiens PLACENTA"
/note="Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized."

ORIGIN

Query Match 23.8%; Score 350.6; DB 5; Length 950;
Best Local Similarity 63.5%; Pred. No. 3.3e-76;
Matches 533; Conservative 1; Mismatches 305; Indels 0; Gaps 0;

6 CTTGATTCAGCTGAAGAAATCCAGCTTTTGGAAATAGACAGCTGCTCAAGCTTT 65
112 CATCATCCAGTTGAGAGAGAGACCCGACCTTCTGAAACCGAGAGCGAGCCGCTT 171
66 GGATGTGCTAAGAAAGTTGCAACCAATTCGCTGCTAAGAAATGTTATTTGTTTT 125
172 GGGTCCGCGCAAGAAAGCTGAGCTGCAACAGACGGCCGCAAGAACTCATCTTCT 231
126 GGGTATGATGATGGGTTTCCAACTGTTACTGTTACTAGAAATTTGAAGGTCAAATGA 185
232 GGGCGATGGATGGGGGTGTCTACGGTGACAGCTGCAGAGATCTTAAAGGCGAAGAA 291
186 TGGTATGTTGGGTCAGAAACCTCATTTGGTATGATGATTCATTCATGAGTCTTTC 245
292 GACAAACCTGGGCTGAGTACCTCGGCTGACGACCGCTTCCATATGGCTCTGTC 351
246 TAAGACTTCAATGTTGATAGACCAAGTTCCAGATTGCTGCTACTGCTTACTT 305
352 CAAGACATACATGTAGACAAACATGTGCAGACATGTGAGCCAGCCAGCCGCTTACCT 411
306 GTGTGTGTTAAGGTTAATTAACAACTATTTGTTTCTGCTGCTGCTGATATACATCA 365
412 GTCCGGGTGCAAGGGGACCTTCCAGACCAATGGCTTGAAGTGCAGCCGCGCTTTAACCA 471
366 ATGTAATACCTAGAGATGATGAAGTTACTTCTGTTATTAATAGAGCTAAGAAAGCTGG 425
472 GTGCACACGACACGCGGCGACGAGTCACTTCGATGATGATCGGCGCAAGAAACAGG 531
426 TAAGCTGTGTGTTGTTACTACTACTAGAGTTCAACATGCTTCTCCAGCTGGTCTTA 485
532 GAAGTCAGTGGAGTGTAAACCAACAGATGACAGACGGCTGCGCAGCCGCGACCTTA 591
486 CGCTCATCTGTTAATAGAAATTTGGTACTCTGATGCTGATTTGGCAGCTGATGCTTAAA 545
592 CCGCCACAGCGTGAACCGCAACATGTAATCGGACGCGGCGGAGCTGCGCCGCGCA 651
546 GAATGGTGTCAAGATATTGCTGCTCAATTTGTTCAATATGATGATGATTTT 605
652 GAGAGGGTCCAGAGATCGCTACGAGCTCATCTCCAAACATGGAATGACCTGATCTCT 711
606 GGGTGTGTAGAAATGATAGTTTCCAGAAAGTACTCCAGATCCAGAAATACCAAGATGA 665
712 AAGTGAAGCCGAAATGATAGTTTTCGATGGAAACCCAGAACCTGAGATACCCAGATGA 771
666 TCGTTCTGTTAATGTTTGAAGAGATAGCAAAATTTGGTCAAGAAATGGCAAGCTTA 725
772 CTACAGCCAAAGGTGGAGCAGGCTGAGACGGAAATCTGTGTCAGAAATGGCTGGAG 831
726 GCATCAAGGTGCTCATATGTTTGAATAGAACTGTTTGGCAAGCTGCTGATGATTC 785
832 GGCACAGGGTGGCCGCTAGCTGTGGAACGCACTGATGACAGGCTTCCCTGGAGCC 891
786 TAGTGTACTCATTTGATGGGTTTGTGAACAGCTGATATAGTATATATGTTTCAAC 844

Db 892 GTGTGATGACATTCATGATGGTCTCTTTGAGCTGAGACATGAATACGATCCACC 950

RESULT 4
BX439339
LOCUS BX439339 1027 bp mRNA linear EST 05-MAY-2004
DEFINITION BX439339 Homo sapiens PLACENTA Homo sapiens cDNA clone CS0DE009YD10
5-PRIME. mRNA sequence.
ACCESSION BX439339
VERSION BX439339.2 GI:47036618
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS Li, W.-B., Gruber, C., Jessee, J., and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT On May 15, 2003 this sequence version replaced gi:30789748.

Contact: Genoscope - Centre National de Sequencage
Genoscope - BP 191 91006 Evry cedex - France
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized. Library was constructed by Life Technologies, a division of Invitrogen.
This sequence belongs to sequence cluster 1699.f
For more information about this cluster, see
<http://www.genoscope.cns.fr/cdna?c=CS0DE009B09Q1&c=1699.f>.

FEATURES

source

1. .1027
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DE009YD10"
/issue_type="PLACENTA"
/clone_lib="Homo sapiens PLACENTA"
/note="Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized."

ORIGIN

Query Match 23.5%; Score 346.6; DB 5; Length 1027;
Best Local Similarity 62.6%; Pred. No. 3.3e-75;
Matches 577; Conservative 6; Mismatches 335; Indels 3; Gaps 3;

6 CTTGATTCAGCTGAAGAAATCCAGCTTTTGGAAATAGACAGCTGCTCAAGCTTT 65
104 CATCATCCAGTTGAGAGAGAGACCCGACCTTCTGAAACCGAGAGCGAGCCGCTT 163
66 GGATGTGCTAAGAAAGTTGCAACCAATTCGCTGCTAAGAAATGTTATTTGTTTT 125
164 GGGTCCGCGCAAGAAAGCTGAGCTGCAACAGACCGCCGCAAGAACTCATCTTCTCT 223
126 GGGTATGATGATGGGTTTCCAACTGTTACTGTTACTAGAAATTTGAAGGTCAAATGA 185
224 GGGCGATGGATGGGGGTGTCTACGGTGACAGCTGCCAGATCTTAAAGGCGAAGAA 283
186 TGGTATGTTGGTCCAGAAATCCATTTGGCTATGATGATCAATTTCCATACGTTGCTT 245
284 GACAAACCTGGGGCTGAGTTAACCTCGGACATGACCGCTTCCATATGTTGGCTGTC 343
246 TAAGCTTCAATGTTTGAATAGCAAGTTCAGATTCGCTGATGATGCTACTGCTTACTT 305
344 CAAGACATACATGTAGCAAAACATGTGTCAGACAGTGGAGCCAGACGCGCTTACTCT 403
306 GTGTGTGTTAAGGTTAATTAACAACTATTTGTTGTTGCTGCTGCTAGATACATCA 365

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Db 404 GTCCGGGTCAGAGGCACTTCCAGACATTTGGCTTAGTGACCCCGCTTAAACA 463
Qy 366 ATGTAATACACTAGAGAGTAATGAAGTACTCTGTTATTAATAGAGCTAAGAGCTGG 425
Db 464 GTCCACACACACACCGCGCAACGAGTCACTCCGTATGATCGGGCCAAAGAGAGG 523
Qy 426 TAAGCTGTGTGTTGTTTACTACTACTAGAGTTCAACATGCTTCTCCAGCTGGTCTTA 485
Db 524 GAAGTCAGTGGAGTGTAAACACACACAGTGACAGCTTCGCCACGCCGACCTTA 583
Qy 486 CGCTCACTACTGTTAATAGAAATTTGTACTGTGATGCTGATTTGCCAGCTGATCTAAA 545
Db 584 CGCCACACAGGTGACCGCAACTGTACTGACGCGGAGCTGCTCCCGCCGCCCA 643
Qy 546 GAATGCTGTTCAGATATTTCTGCTCAATTTGTTTACATATGATATTTGATTTATTT 605
Db 644 GAGGGGTGTCAGACATCCCTACGCACTCATCTCCAGATGACATTCAGCTGATCCT 703
Qy 606 GGGTGTGTAGATGATGATGATTTCCAGAGGATCCAGATCCAGATATCCAGATGA 665
Db 704 AGGTGAGGCCGAAAGTACATGTTT-CGATGGGAAACCCAGACCTTATGATCCAGATGA 762
Qy 666 TGCTTCTGTTAATGTTTGAAGATAGAAATTTGTTCAAGATGCGAAGCTAA 725
Db 763 CTACAGCGAAGGTGG-GACAGGCTGACGCGGAGAAATCTGTGAGGAAATGGCTGGAG 821
Qy 726 GCATCAAGTGTCTCATATTTTGGAAATAGAACTGCTTTGTCAGCTGCTGATGATTC 785
Db 822 GCCCAGGGGGTCCCGGTACGTGTGAACCCGACCTGACCTCATGACGCTTCCCTGAGCC 881
Qy 786 TAGTGTACTCATTTGATGAGTGTGTTTGAACAGCTGATATGAGATATATGTTCA-AC 844
Db 882 GTTGTGACCCATCTCATGGGTCTCTTGTAGCTTGAGACATGAAAMAGATCCACCC 941
Qy 845 AAGATCATATTAAGATTCACAACTTTGCTGAATTTGACTGAAGCTGCTTTCAGATTTGT 904
Db 942 GAACTCTCMACCTGACGCCCTCCCTGATGATGAGATGACAGAGGCTGCTGCTGCTGTA 1001
Qy 905 CTAGAAATCCAAAGGTTTTT 925
Db 1002 GCAGGAACCCCGCGCTTTT 1022

RESULT 5
BX379970 LOCUS 991 bp mRNA linear EST 26-APR-2004
BX379970 DEFINITION Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
clone CS0D1042YG09 5-PRIME, mRNA sequence.
BX379970 ACCESSION BX379970.2 GI:46573405
BX379970.2 KEYWORDS
EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 991)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On May 8, 2003 this sequence version replaced gi:30448840.
COMMENT
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 Evry cedex - France
Email: sequef@genoscope.cns.fr, Web: www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
1699.f
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?S=CS0D1042AD05QP1&c=1699.f.

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FEATURES
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                /issue_type="PLACENTA COT 25-NORMALIZED"
                /clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
                /note="1st strand cDNA was primed with a NotI-oligo(dT)
                primer. Five prime end enriched, double-strand cDNA was
                digested with Not I and cloned into the Not I and EcoR V
                sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN
Query Match 23.3%; Score 343.6; DB 5; Length 991;
Best Local Similarity 63.3%; Pred. No. 1.0e-74;
Matches 557; Conservative 1; Mismatches 320; Indels 2; Gaps 2;

Qy 6 CTGATTCCAGCTGAAGAAATCCAGCTTTTGGAAATAGCAAGCTCTCAAGCTTT 65
Db 106 CATCATCCCGATTGAGAGAGAAACCCGACTTCTGAAACCGGAGCCAGGCCCT 165
Qy 66 GATGTTGCTAAGAGTTCAGCAATTCAACTGCTCTAAGATGTTATTTTCTTTT 125
Db 166 GGGTCCGCGCAAGAGCTGACGCTGACACAGCGCGCAAGAACTCATCATCTTCT 225
Qy 126 GGGTATGATATGGGTGTTCCACTGTACTGTAAGAAATTTGAAGGTCAATGAA 185
Db 226 GGGCATGGGATGGGGGTGCTACGGTGAAGCTGCCAGGATCTTAAAGGGCAAGAA 285
Qy 186 TGGTATGGTGGTCCAGAAACTCATTTGGCTATGATCAATTTCCATACGTTGCTG 245
Db 286 GGAACAACGTGGGCTGAGTACCTTGGCAGTACGACCGCTTCCATATGTGCTGTC 345
Qy 246 TAAGACTTACATGTTGATAGACAAAGTTCCAGATTCGTGTACTGCTACTGTTACT 305
Db 346 CAAGACATACATGTTAGACAAACATGTGCGACAGTGGACCAAGCCAGCGCTACT 405
Qy 306 GTGTGTGTTAAGGTATTAACGAATCTATGGTGTTCGTCTGCTGTATGATCA 365
Db 406 GTGCGGGGTCCAGGGCACTTCAGACATTTGCTGAGTGACGCGCGCTTTAAACA 465
Qy 366 ATGTAATACACTAGAGATGATGAAGTACTTCTGTTATTAATAGAGCTAAGAGCTGG 425
Db 466 GTCCACACACACACCGCGCAACGAGTCACTCCGTATGATTCGGGCCAAAGAGAGG 525
Qy 426 TAAGCTGTGTGTTGTTTACTACTACTAGAGTTCAACATGCTTCTCCAGCTGGTCTTA 485
Db 526 GAAGTCAGTGGAGTGTAAACACACACAGATGACAGCGCTCGCCAGCCGACCTTA 585
Qy 486 CGCTCACTACTGTTAATAGAAATTTGTACTGTGATGCTGATTTGCCAGCTGATGCTC-AAA 544
Db 586 CGCCACACAGGTGACCGCAACTGTGATCTGAGCGCGAGTCTGCTCCGCCGCCCA 645
Qy 545 AGAATGTTGTCAAGATTTGCTGCTCAATTTGTTTACAATATGATGATGATTTATTT 604
Db 646 GAGGGGGGTGCCAGACATGCTACGAGCTCATCTTCAACATGAGACATTTGAGTATCC 705
Qy 605 TGGTGTGTGTAGATGATGATGATTTTCCAGAGTACTCCAGATCCAGAAATACCAAGATG 664
Db 706 TAGTGTGAGGCGCAAGATCATGTTTCGATGTGAACCCAGACCTCGAATACCAAGATG 765
Qy 665 ATGCTTCTGTTAATGTTGTTGAAGATGACAAATTTGTTCAAGATGCGCAAGCTTA 724
Db 766 ACTACAGCCAAAGTGTGACACGAGCTGACCGGAAGATCGTGCGAGATGCTGCGGA 825
Qy 725 AGCATCAAGTGTCTCAATATGTTTGAATGAACTGCTTGTGTCAGAGCTGATGATTT 784
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Qy 785 CTAGTGTACTCATTTGATGGGTTTGTGTAACCACTGATATGAAATGATGTTCAAC 844
Db 885 CGTCTGACCATCTCATGGGTCTCTTGAAGCTGGAAGMATGAAATAGAGATCCACC 944

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QY 845 AGATCATCTAAGATCCACTTTGGCTGAAATGACTGA 884
DB 945 GAGACTCCACACTGGAMCCCTCCCTGATGAGATGACARA 984

RESULT 6
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LOCUS
DEFINITION
MUS MUSCULUS ALPPL2 gene, VIRIDAL TRANSCRIPT, partial sequence,
AY404255 1587 bp DNA linear GSS 15-DEC-2003
ACCESSION
AY404255
VERSION
AY404255.1 GI:39760232
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 1587)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
Todd, M.A., Tanenbaum, D.M., Civeille, D.R., Lu, F., Murphy, B.,
Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Shtinsky, J.J.,
Adams, M.D. and Cargill, M.
Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL
Science 302 (5652), 1960-1963 (2003)
PUBMED
14671302
TITLE
2 (bases 1 to 1587)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
Todd, M.A., Tanenbaum, D.M., Civeille, D.R., Lu, F., Murphy, B.,
Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Shtinsky, J.J.,
Adams, M.D. and Cargill, M.
Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT
This sequence was made by sequencing genomic exons and ordering
them based on alignment.
FEATURES
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/mol_type="genomic DNA"
/db_xref="taxon:10090"
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ORIGIN
Query Match 22.7%; Score 334.6; DB 9; Length 1587;
Best Local Similarity 35.6%; Pred. No. 3.6e-72;
Matches 512; Conservative 0; Mismatches 921; Indels 6; Gaps 1;

QY 8 7GATTCGAGCTGAAGAAATCCAGCTTTTGGAAATGACAGCTGCTCAAGCTTTGG 67
DB 59 TCATTCGAGTGAAGAGGAAACCCGCTCTGGAACAAGAGCGAGCCCTGG 118
QY 68 ATGTGCTAAGAGTTGCAACCAATCAACTGCTCTAGAAGTGTATTTGTTTGG 127
DB 119 ATGTGCTAAGAGTTGCAACCAATCAACTGCTCTAGAAGTGTATTTGTTTGG 178
QY 128 GTGATGTAATGGGTGTTCCAACTGTTACTGCTAAGAAATTTGAAGGTCAAATGATG 187
DB 179 G-----GATGGGGGTAACCAAGTGAACAGCACCGAGATCTTAAAGGGGAGTGAAG 232
QY 188 GTAAGTGGGTGCAAGAACTCCATTGGGCTATGATCAATTCCTATCGTTGCTGTA 247
DB 233 GCACATCGAGACCGGAGACACCCCTAGCATGGAACCTTCCATACATGCTCTGTCA 292
QY 248 AGACTTACATGTTGATAGACAAGTTCCAGATTGCTGCTAGTCTGCTACTTGT 307
DB 293 AGACATACAGTGTGACACAGGTTCCAGACAGTGAACACGCGCAACGCTTACTGT 352
QY 308 GTGTGTTAAGGTAATTAACAATACTATTGTTGTTTCTGCTGCTAGATCAATCAAT 367

DB 353 GTGGGGTCAAGACCAACTACAGACCATCGGGTGAGCGCAGCGGAGATTGCACCACT 412
QY 368 GTAATATCTAGAGTAATGAATTACTTCTGTTATTAATGAGTAAGAGCTGGTA 427
DB 413 GCACACCAACATTTGGCAATGAGGCTTCTCAGTATGATACGTCGCAAGAAAGACGGA 472
QY 428 AGGCTGTTGGTGTGTTACTACTAGAGTTCACATGCTTCTCAGCTGCTGCTTAC 487
DB 473 AGTCTGTGGAGTGGTGACACGACGAGGTGACAGATGCTTCTCAGCGGACCTTAC 532
QY 488 CTCATACCTGTTAATGAAAATTTGTACTGATGCTGATTTGGCAGCTGCTCAAGA 547
DB 533 CACACACGGTGAACCGTAAATTTGTAAGATGAGATGCTGCTGCTGCTGCTGCTG 592
QY 548 ATGTGTTCAAGATATTGCTGCTCAATTTGTTTACAAATATGATATTGATTTTGG 607
DB 593 ACGGCTGCAAGACATCGCACTCACTATCTCAACATGACATGATGATGATGATG 652
QY 608 GTGTGTGTAAGATGATAGTGTTCAGAAAGTACCAAGATCCAGATGATG 667
DB 653 NNN 712
QY 668 CTTCTGTTAATGCTGTGTAAGAAAGATTAAGCAAAATTTGCTCAGAAATGCAAG 727
DB 713 NNN 772
QY 728 ATCAAGGCTCTCAATATGTTGGAATAGAACTGCTTTGTGCAACTGCTGATTTCA 787
DB 773 NNN 832
QY 788 GTGTACTACTATTGATGGGTTGTTGGAACAGCTGATGATGATATGTTCAACAAG 847
DB 833 NNN 892
QY 848 ATCATATCTAAGATCAACTTTGCTGTAAGTACTGAAGCTGCTTGCAGATTGCTCTA 907
DB 893 NNN 952
QY 908 GAAATCCAAAGGTTTACTTCTGTTGTTGAAGTGTGTAAGTATGATGCTATCATG 967
DB 953 NNN 1012
QY 968 ATGTAAAGCTTATATGCTTTGACTGAAGTATATGTTGATATGCTATGCTAAAG 1027
DB 1013 NNN 1072
QY 1028 CTAATGAATGACTCTGAAATGATGACTTGAATTTGCTTACTGCTATCATG 1087
DB 1073 NNN 1132
QY 1088 TTTTCTTTTGGTGTGTTACACTTTGAGAGTACTTCTATTTTGGTTGGCTCAGGTA 1147
DB 1133 NNN 1192
QY 1148 AGGCTTGGATAGTAACTTCACTTATTTGTATGTATGTTGTCAGGTTATGCTT 1207
DB 1193 NNN 1252
QY 1208 TGGGTGGTCTTCAAGCAAGTGTAAATGCTAGTCAAGTCAATCTTCAAGC 1267
DB 1253 NNN 1312
QY 1268 AACAGCTGCTGTTCACTGCTAGTAAATCATGAGTGAAGATGTTGCTTTTGG 1327
DB 1313 AGCAGGCTGCTGATCCCTGTGTCAGAGACCCACAGCGGGAGACGTGGCAATATTCG 1372
QY 1328 CTAGAGTTCACAAGCTCATTTGTTTCAAGTGTTCAGAAAGAACTTTTGTCTATA 1387
DB 1373 CGCGTGGCCACAGGCGGACCTGCTGTCAGAGACCCAGAGTTCAAGAGCAAACTACGCGCAG 1432
QY 1388 TTATGCTTTTGGTGTGTTGTTGAACATACATGATTTGTAATTTGCAAGCTCAGCT 1446
DB 1433 TCATGCGCTTGGCAGCTGCTGAGCCCTTACATGACTGCGGCGCTGCAATCCCTGCT 1491

RESULT 7
AL552555
LOCUS
DEFINITION
AL552555 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA
clone CSODI067YC24 5-PRIME, mRNA sequence.
AL552555
ACCESSION
AL552555.3 GI:45857340
VERSION
EST.
KEYWORDS
Homo sapiens (human)
SOURCE
Homo sapiens
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 984)
REFERENCE
Li, W.B., Gruber, C., Jesse, J. and Polayes, D.
Full-length CDNA libraries and normalization
Unpublished (2001)
On Feb 15, 2001 this sequence version replaced gi:31274370.
COMMENT
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
1699.f
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?cs=CSODI067BBI2QP1&c=1699.f.

FEATURES
source
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODI067YC24"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized." sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Query Match 22.4%; Score 330.4; DB 1; Length 984;
Best Local Similarity 63.2%; Pred. No. 3.6e-71;
Matches 556; Conservative 0; Mismatches 321; Indels 3; Gaps 3;
QY 6 CTGATTCGACGAGAGAAATCCAGCTTTTGGATAGACAGCTGCTCAAGCTT 65
DB 106 CATCATCCCGATTGAGAGAGAAACCGGACTCTGAGACCGGAGGACCCGAGCCCT 165
QY 66 GGATGTTGCTAGAGAGTGGCAACCAATTCAACTGCTGCTAGAGATTTTGGTTT 125
DB 166 GGGTGGCGCAAGAGCTGACGCTGCACAGACGCGCAAGAACTTATCTTCTCT 225
QY 126 GGGTATGATGAGGCTTCCAACTGTTACTGCTACTGAGATTTTGAAGGCTCAATGAA 185
DB 226 GGGCGATGGAGTGGGGGTGCTCTACGTCAGACGCTGCAGATCTTAAAGGAGAA 285
QY 186 TGGTAGTGGGGTCCAGAACTCCATGGTATGATGATTTCCATAGCTGCTTTC 245
DB 286 GGGCAAACTGGGGCTGAGTTACCCCGGCAAGACCGCTTCCCATATGCTGCTGTC 345
QY 246 TAAGACTTCAATGTTGATAGACAAAGTTCCAGATTCTGCTGCTACTGCTACTTACT 305
DB 346 CAAGACATCAATGATGACAAACATGTCAGACAGTGGAGCCACAGCCGCTTACT 405
QY 306 GTGTGTTTAAGGCTTATTAAGAACTATTGTTGCTGCTGCTGCTGCTGCTGCTGCT 365
DB 406 GTGGGGGTTCAGGGGCACTTCCAGACCATTTGCTGAGTGCAGCGCGCTTTTAAACA 465

QY 366 ATGTAATACTACTAGAGTATGAGTATCTTCTGTTATTAATAGAGCTAGAGGCTGG 425
DB 466 GTCCAAACAGACACGGGGCAAGAGGTCACTCCGATGATATCGGGCCAAAGAAAGG 525
QY 426 TAAGCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 485
DB 526 GAAGTCAAGTGGGAGTGGTAAACCAACACAGAGTGCAGACGCTCCGACCCGCACT 585
QY 486 CGCTCATCTGTTAATAGAAATTTGTAATCTGTAATGCTGTAATTTCCAGCTGATCTC-AAA 544
DB 586 GGGCCACACGGTGAACCGCACTGTGATCTGAGCGCGAGTGTGCTGCGCCGCCA 645
QY 545 AGAATGTTGTTCAAGATTAATTTGCTGCTCAATTGGTTTACATATGATATGATATTT 604
DB 646 GAGAGGGGTGCCAGACATCGTACGACGTATCTTCCAAATGACATTTGATGATGATCS 705
QY 605 TGGGTGTTGTTAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 664
DB 706 TAGGTGAGGCGCAAGATCATGTTTCCGATGGGAACCCGAGACCTGAGTACCCAGATG 765
QY 665 ATGCTTCTGTTAATGTTGTTAGAAAGATTAAGCAAAATTTGTTCAAGATGGCAAGT 724
DB 766 ACTACAGCCAAAGTGGGACCGAGCTGACGGAGAAATCTGTGACAGAAATGGCTGGCA 825
QY 725 AGCATCAAGTGTCTCAATATGTTTGAATAGACCTGTTGTTGTTGTTGTTGTTGTTGTT 784
DB 826 CGC-CAGGGGTGCCGCTACGTGTGATGATGATGATGATGATGATGATGATGATGATGAT 884
QY 785 CTAGTGT-TACTGATTTGATGAGTGTGTTTGAACGAGCTGATGATGATGATGATGAT 843
DB 885 CGTCTGTAACCATCTCATGAGGTCTTTTGAAGCTGAGACATGAAATGAGATTCAC 944
QY 844 CAAGATCATATCAAGATCAACTTGGCTGAAATATCAG 883
DB 945 CGAGACTCCACACTGAGACCTTCTCTGATGAGATGACAG 984

RESULT 8
CF591568
LOCUS
DEFINITION
AGENCOURT 15681730 NICHD_XGC_Swlin Xenopus tropicalis CDNA clone
CF591568
IMAGE:7023090 5', mRNA sequence.
VERSION
CF591568.1 GI:36343216
KEYWORDS
EST.
SOURCE
Xenopus tropicalis (western clawed frog)
ORGANISM
Xenopus tropicalis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
Xenopodidae; Xenopus; Silurana.
1 (bases 1 to 888)
REFERENCE
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
CONTACT: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgaabs-remail.nih.gov
Tissue Procurement: Rob Granger, University of Virginia
CDNA Library Preparation: Open Biosystems
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L14M14750 row: f column: 16
High quality sequence stop: 621.

FEATURES
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1..888
/organism="Xenopus tropicalis"
/mol_type="mRNA"
/db_xref="taxon:8364"

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/clone="IMAGE:7023090"
/clone_type="whole body"
/clone_lib="NICHID XGC SwbIN"
/notes=Vector: pEXpress-1; Site 1: EcoRV; Site 2: NotI;
Bulk tissue was collected from a whole 10 month old male
from the P6 strain. 1st strand cDNA was primed with a Not
I - oligo (dT) primer, double-stranded cDNA was cloned into
the Not I and EcoRV sites of pEXpress-1. Library was
size-selected for >1.5 kb fragments for an average insert
size of 1.92 kb. Library was normalized to Cots with a
180-fold reduction of actin. A non-normalized version of
this library is also available (NICHID XGC SwbI). Library
was constructed by Open Biosystems (Huntsville, AL).
PLEASE NOTE: This library contains high level of
contamination by tubifex"

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ORIGIN

Query Match 20.9%; Score 308; DB 7; Length 888;

Best Local Similarity 63.2%; Pred. No. 1.3e-65;

Matches 473; Conservative 0; Mismatches 275; Indels 0; Gaps 0;

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QY 10 ATTCCAGCTGAAGAAAGAAAATCCAGCTTTTGGAAATAGACAAGCTCTCAAGCTTGAT 69
DB 61 ATTCCAGCGGAAGAGAGCCAGCCTGAATTTGGAAACAAAGATGATCCAGATTAAT 120
QY 70 GTTGCTAAGAGTGGCAACCAATTCCTGCTAGAGATGTTATTTTGGGT 129
DB 121 GAAGCCCTAAGACTAAGCCATTCAGCAGAGCTTAAACCTGATCTCTTTAGGT 180
QY 130 GATGTATGGGTGTTCCAACTGTTACTAGATTAAGATTTGAAGGTCAATGAATGAT 189
DB 181 GATGGATGGAGTTCCACAGCTCAGCCACAGAGATCTTAAGTGGCAGATGAAGAGA 240
QY 190 AAGTGGGTCCGAACCTCATTTGCTATGATCATTTCCATCTTCTTGTCTAG 249
DB 241 ATGCTGGGAAGAAATAGCTGGCAATGACAAATCTCCCTACCGGACTCTTAAAG 300
QY 250 ACTTCAATGTTGATAGACAAGTTCCAGATTCGCTGATCTACTCTTACTTGTGT 309
DB 301 AATACAAATGTGATGCGCAAGTCTCTGACAGCGCGGATCTGCAACTGTTAATGT 360
QY 310 GGTGTTAAGGGTAAATTAACAACATATGTGTTCTGCTGCTAGATTAACAATCAAT 369
DB 361 GGAGTGAAGAACCAATATGAAACAGTCGAGTGAATGCTGTCTCAAGTTCAACTGC 420
QY 370 AATACTACTAGAGTAATAGTTACTTCTGTTAATTAAGAGCTTAAGAGCTGTAG 429
DB 421 AACCAATATGAAGCAATAGGTTGATGCTTCTCAAGAAAGCAAGGACAGAGAAA 480
QY 430 GCTGTGTGTTGTTACTACTACTAGAGTTCAACATGCTTCTCAGCTGTGCTTACGT 489
DB 481 TGGGTAGGAATTTTACTACACAGAGTCCAGACAGCTTCCCTCTTGCACTTAGCT 540
QY 490 CATACTGTTAATAGAAATTTGTAATCTGTAATGCTGATTTGCCAGCTGATCTCAAA 549
DB 541 CACATCTCTGACCGGGATTTGTAATGATGATGATGATGATGATGATGATGATGAT 600
QY 550 GGTTCGAGATATTTGCTCTCAATTTGTTTCAATATGATTAATTTTGGGT 609
DB 601 GGGGTGAAGATATTTGCCAGCAGCTGATTTCAAAAGTGAACATATGATCTTGTGT 660
QY 610 GGTGTAGATATGATGTTTCCAGAGGTAATCCAGATCCAGAAATCCAGATGATGCT 669
DB 661 GGGGGGGGGAATATATGACACCAAGTGGAACTTCTGATCTGAGTACCTTCAATAG 720
QY 670 TCTGTTATGTGTTAGAAAGATAGCAAAATTTGTTCAAGATGGAAGCTAAGCAT 729
DB 721 AAGCAAAATGCGATTAAGAAAGATGAAGAACTTATAGATGAATGCTTTGAAAAC 780
QY 730 CAAGGTCTCATATCTTTGGAATAGA 757
DB 781 AGGGGGGCTCAGTATGTGTGAATAAA 808

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RESULT 9
AY04253
LOCUS
DEFINITION
AY04253
ACCESSION
AY04253
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
PUBMED
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
FEATURES
source
gene
locus_tag="HOM1829"

1593 bp DNA linear GSS 15-DEC-2003
Homo sapiens ALPL2 gene, VIRTUAL TRANSCRIPT, partial sequence.
Homo sapiens survey sequence.
AY04253
GSS
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 1593)
Clark A.G., Gianowski S., Nielson R., Thomas P., Kejariwal A.,
Todd M.A., Tanenbaum D.M., Civello D.R., Lu F., Murphy B.,
Fertiera S., Wang G., Zheng X.H., White T.J., Sinsky J.J.,
Adams M.D. and Cargill M.
Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
Science 302 (5652), 1960-1963 (2003)
14671302
2 (bases 1 to 1593)
Clark A.G., Gianowski S., Nielson R., Thomas P., Kejariwal A.,
Todd M.A., Tanenbaum D.M., Civello D.R., Lu F., Murphy B.,
Fertiera S., Wang G., Zheng X.H., White T.J., Sinsky J.J.,
Adams M.D. and Cargill M.
Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering
them based on alignment.

Location/Qualifiers
1..1593
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
<1..>1593
/gene="ALPL2"
/locus_tag="HOM1829"

ORIGIN

Query Match 20.6%; Score 303.6; DB 9; Length 1593;

Best Local Similarity 34.2%; Pred. No. 1.9e-64;

Matches 493; Conservative 0; Mismatches 941; Indels 6; Gaps 1;

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QY 6 CTTGATCCAGCTGAAGAAAGAAATCCAGCTTTTGAATAGACAAGCTGCTCAAGCTTT 65
DB 57 CATCATCCAGTGAAGAGAGAAACCCGACTTCTGGAACCGCCAGCGAGCCCT 116
QY 66 GGATGTGCTAAGAGTGGCAACCAATTCAAAGCTGCTGAAGATGTTATTTGTTT 125
DB 117 GGGTCCGCAAGAGCTGACGCTGCAAGACAGCCGCAAGAACTCATCATTTCTT 176
QY 126 GGGTATGATGATGGGTGTTCCAACTGTTACTGCTACTAGAAATTTGAAGGTCGAATGA 185
DB 177 G-----GGATGGGGGTGTCTACGGTGACAGCTGCCAGATTCCTAAAGGCAAGAA 230
QY 186 TGTATGTTGGGTCCAGAACTCAATTTGCTATGATCAATTTCCATAGCTTTGCT 245
DB 231 GGACAAACTGGGGGCTTGAGACTTCTCGGCATGACCGCTTCCGTACGTGCTCTG 290
QY 246 TAAGCTTACAATGTTGTAAGACAAGTCCGATTTGCTGCTGTAATGCTTACTGCTTACT 305
DB 291 CAGACATACAGTGTAGCAAGCATGTGCGACAGAGTGAGCCACAGCCAGCGCTTACT 350
QY 306 GTGTGTGTTAAGGTTAATTAACAACTATTGTTGTTCTGCTGCTGCTAGATCAATCA 365
DB 351 GTGGGGGTCAAGGCAACTTCCAGACATTTGGCTGTAGTGCAGCGCGCTTTAAACA 410
QY 366 ATGTATATCTACTAGAGTAAATGAATTTCTGTTATTAATAGAGTAAAGAGCTGG 425
DB 411 GTGCACACGACAGCGGCAAGAGTATCTCGGTATGATGATGATGATGATGATGATGAT 470

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| | | | |
|----|------|---|------|
| Qy | 426 | TAAGCGTGGTGTGTTTACTACTACGAGGTTCAACATGCTTCTCAGGTGGTCA | 485 |
| Db | 471 | AAAGTCACTGGAGTGTAAACCAACACGGGTGACGATCTCTGCCAGCCGGCGCTTA | 530 |
| Qy | 486 | CGCTCATCTCTTATATAGAAATGGTACTGTATGCTGATTTGGCCAGCTGATGCTCAAA | 545 |
| Db | 531 | CGCCACACGGGTGAACCGCAACTGGTACTCGGATGCGCAGCTGCTGCGCCCGCA | 590 |
| Qy | 546 | GAATGCTTGTCAAGATATTTGCTGCTCAATTGGTTTCAATATGATATATGATATTTT | 605 |
| Db | 591 | GGAGGGGGTGCAGGACATCGCACGACACTCATCTCCAAACATGACATTTGATNNNNNNN | 650 |
| Qy | 606 | GGGTGGTGTGAATGTATGATGTTTCCAGAAAGTACTCAGATCCAGAAATCCAGATGA | 665 |
| Db | 651 | NN | 710 |
| Qy | 666 | TGCTTCTGTTAATGGTGTAAAGAGATTAAGCAAAATTTGGTTCAGAATGGCAAGCTAA | 725 |
| Db | 711 | NN | 770 |
| Qy | 726 | GCATCAAGGTGCTCAATATGTTTGGAAATGAACCTGCTTTGTCAGCTGCTGATGATTC | 785 |
| Db | 771 | NN | 830 |
| Qy | 786 | TAGTGTACTCATTTGATGGGTTGTTTGAACAGCTGATATGAAGTATTAATGTTCAACA | 845 |
| Db | 831 | NN | 890 |
| Qy | 846 | AGATCATATCTAAGGATCCAACTTGGCTGGAATGACGAACTGCTTTGCAAGTTTGTCTC | 905 |
| Db | 891 | NN | 950 |
| Qy | 906 | TAGAAATCCAAAGAGTTTCTTGTGTTGTTGGAAGTGTGAATGTATCATGTGATCA | 965 |
| Db | 951 | NN | 1010 |
| Qy | 966 | TGATGGTAAGCTTATATATGCTTTGACTGAAGCTATATGTTGATATATGCTATTGTA | 1025 |
| Db | 1011 | NN | 1070 |
| Qy | 1026 | GGCTAATGAATGACTTCTGGAATTGGATACTTGTATTTGGTTACTGCTGATCATAGTCA | 1085 |
| Db | 1071 | NN | 1130 |
| Qy | 1086 | TGTTTTTCTTTGGTGTACACTTGAAGACTCTTATTTTGGTTGGCTCCAGG | 1145 |
| Db | 1131 | NN | 1190 |
| Qy | 1146 | TAAAGCTTGGATAGTAGTACTTACACTTATTTGTATGTGTAATGCTCAGGTTATGC | 1205 |
| Db | 1191 | NN | 1250 |
| Qy | 1206 | TTTGGGTGGTGTCTAGACAGATGTTAATGTAGTACTAGTGAAGAACCATCTTACAG | 1265 |
| Db | 1251 | NN | 1310 |
| Qy | 1266 | ACAACAACTCTGTTCATTTGGCTAGTGAAGTATCATGTGTGTGAAGATTTTGGCTTTT | 1325 |
| Db | 1311 | GCAGACAGTACACAGTGCCTCTGGACGAGAGAACCCACGACGACGAGCGTGGCGGT | 1370 |
| Qy | 1326 | TGCTAGAGGTCCACAAAGCTCAATTTGGTTCATGTTTCAAGAAGAACTTTTGGTGTCTCA | 1385 |
| Db | 1371 | CGCGGCGGGCCCGACGAGCGCACCTGTCTTCACGGCGTGCAGAGACGACCTTCATAGCGCA | 1430 |
| Qy | 1386 | TATTATGGCTTTTGTCTGTGTGTGAACATATCACTGATTGTAAATTTGCCAGCTCAGC | 1445 |
| Db | 1431 | CGTATGCTTTCGCGCTGCTGAGAGCCCTACACCGCTGCGACTGGCGCCCGCGC | 1490 |

| DEFINITION | EX417625 Homo sapiens PLACENTA Homo sapiens cDNA clone CS0DE011YC1 |
|---------------------------|--|
| ACCESSION | EX417625 |
| VERSION | EX417625.2 |
| KEYWORDS | EST. |
| SOURCE | Homo sapiens (human) |
| ORGANISM | Homo sapiens |
| REFERENCE | Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo. |
| AUTHORS | Li, W. B., Gruber, C., Jesse, J. and Polayes, D. |
| TITLE | Full-length cDNA libraries and normalization |
| JOURNAL | Unpublished (2001) |
| COMMENT | On May 15, 2003 this sequence version replaced gi:30767760. Contact: Genoscope Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - France Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five primed end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 1699.f For more information about this cluster, see http://www.genoscope.cns.fr/cdna?cs=CS0DE011AB09Q1&c=1699.f . Location/Qualifiers |
| FEATURES | 1..936 |
| source | /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon.9606" /clone="CS0DE011YC1" /issue_type="PLACENTA" /clone_id="Homo sapiens PLACENTA" /note="Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized." |
| ORIGIN | |
| Query Match | 20.5%; Score 303.2; DB 5; Length 936; |
| Beet Local Similarity | 63.4%; Pred. No.2.1e-64; |
| Matches 458; Conservative | 3; Mismatches 261; Indels 0; Gaps 0; |
| OY | 6 CTGATTCACGACTAAGAAAGAAATCCAGCTTTTGGATATGACAACTGCTCAAGCTT 65 |
| DB | 142 CATATCCCACTTGAGAGAGAACCCGACTTCTGAAACCGCAGCAGCCGAGGCCCT 201 |
| OY | 66 GGATGTTGCTAAGAGTTGGCAACCAATTCAACTGCTGCTAAGATGTATTTGTTTT 125 |
| DB | 202 GGGGCGCCCAAGAACTGACAGCTGCACAGACAGCCGCAAGAACTCATCTTCCCT 261 |
| OY | 126 GGGGATGAGTATGGGTGTTCCAACTGTTACTGCTACTAGAAATTTGAAGGTCAAAGAA 185 |
| DB | 262 GGGGATGAGTATGGGTGTTCTAGGGTGAAGCTGCAGGATCTTAAAGGGCAGAAAGAA 321 |
| OY | 186 TGTAAATGGGGTCCAGAAACTCCATGGGCGATGAGTCAATTTCCATACGTTGGCTTGC 245 |
| DB | 322 GGACAACTGGGGCTTAGTTATCCCTGGCCATGAGACCGCTTCCCATATTTGGCTCTKTC 381 |
| OY | 246 TAAGACTTACATGTTGATAGACAAAGTTCAGATTCGTGCTACTGCTACTGCTTACTT 305 |
| DB | 382 CAAACATTAACATGTTAACAACAATGTGCCAGACAGTGAAGCCACAGCAGCGGCTACCT 441 |
| OY | 306 GTGTGTGTTAAGGGTATTTACAGAACTATTTGTGTTTCTGCTCTGCTAGATACATCA 365 |
| DB | 442 TTTCGGGGGTCAAGGGCAACTTCCAGACCAATTTGGCTTTATTTACGCCGCCCTTTAACA 501 |
| OY | 366 ATGTAATATCACTAGAGTATGAAAGTTACTCTCTGTTATTAATAGACTAAGAGGCTGG 425 |
| DB | 502 GTGCAACGACGACGGGCAACGAGTCACTTCCTGATGATGATGGGCTCAAGAAACGAG 561 |

QY 426 TAAGCTGTGGTGTGTTACTACTAGATTCAACAGTCTTCCAGCTGGCTTA 485
DB 562 GAAAGTACGTGGAGTGTGTAACCAACAGAGTGCAGACGCTCCCGCAGCGGACCTA 621
QY 486 CGCTCACTACTGTTAATAGAAATTGGTACTCTGATGCTGATTGCCAGCTGATGCTAAA 545
DB 622 CCCCCACAGGTGAACCGCAACTGTGATCTGACGCGCGACGTCCTCGCCGCCGCCA 681
QY 546 GAATGTTTCAAGATATTGCTGCTCAATTGTTTCAATATGATATGATGTTT 605
DB 682 GGAAGGGGTCCAGAGATATGCTACGAGCTCATCTCAACATGACATTTGACCTGATCT 741
QY 606 GGGTGTGTAGATATGATATGTTTCCAGAGTACTCCAGATCCAGAAATACCAATGA 665
DB 742 AGGTGAGGCGCAAAATACATGTTTGCATGGAACCCASACCTGAGATACCAATGA 801
QY 666 TGCCTTCTGTTAATGTTGTTAGAAAGATTAAGCAAAATTTGTTCAAGAAATGCGAAGCTTA 725
DB 802 CTACAGCCCAAGGTGGAGCAGCGCTGGACGGGAAGATCTGTGACAGAAATGCTGCGAC 861
QY 726 GC 727
DB 862 GC 863

RESULT 11

AL553521 902 bp mRNA linear EST 30-MAR-2004
LOCUS AL553521 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
DEFINITION clone CS0D1076YD24 5-PRIME, mRNA sequence.
ACCESSION AL553521
VERSION AL553521.3 GI:45858290
KEYWORDS EST.

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

Li W.B., Gruber C., Jessee J. and Polyes D.
Full-length cDNA libraries and normalization

Unpublished (2001)
On Feb 15, 2001 this sequence version replaced gi:31275335.

COMMENT Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France

Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr

1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime

end enriched, double-strand cDNA was digested with Not I and cloned

into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library

was normalized. Library was constructed by Life Technologies, a

division of Invitrogen. This sequence belongs to sequence cluster

1699.f
For more information about this cluster, see
http://www.genoscope.cns.fr/cdnas?CS0D1076B120P1ec=1699.f.

FEATURES

source location/Qualifiers

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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0D1076YD24"
/issue_type="PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Query Match 20.4%; Score 301.6; DB 1; Length 902;
Best Local Similarity 63.6%; Pred. No. 5.2e-64;
Matches 476; Conservative 8; Mismatches 262; Indels 2; Gaps 2;
6 CTTGATTCAGCTGAAGAAATCCAGCTTTTGGATAGACAAGTGTCAAGCTTT 65

DB 106 CATCATCCAGTTGAGAGAGAAACCGGACCTTCTGGAAACCGGACGCGAGCCCT 165
QY 66 GATGTTGCTAAGAAAGTTGCAACCAATTCAACTGCTGTAAGAAATGTTATTTT 125
DB 166 GGTCCCGCCAGAAAGCTGACAGCTGCAACAGACCGCCCAAGAAACCTCATCTTCT 225
QY 126 GGGTATGGTATGGGTGTTCCAACTGTTACTAGTCTAGTAATTTGAAGGGTCAATGTA 185
DB 226 GGGCATGGATGGGGGTGTCTACGGTGACAGCTCCAGATCTTAAAGGGCAGAA 285
QY 186 TGGTAAGTTGGGTCCAGAACTCCATGGCTATGATCAATTTCCATAGTTGCTTGT 245
DB 286 GGAACAAGTGGGGCTGAGATACCCCTGGCATGAGACCGCTTCCATATGTTGCTGT 345
QY 246 TAAAGCTTAACAATGTTGATAGACAAGTTCCAGATTTCTGTTACTGTTACTT 305
DB 346 CAAGCATACATATGTAGACAACAATGTCAGACAGTGAAGCCACAGCCAGCTTACT 405
QY 306 GTGTGTGTTAAGGTTAATTAACAGAACTATTGTTGTTCTGCTGCTAGATACATCA 365
DB 406 GTGCGGGTCAAGGGCACTTCCAGACCAATTTGCTTGTAGTGCAGCCGCCCTTTAAC 465
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DB 466 GTGCAACACGACAGCGGCAACGAGTCACTCGGTATGATGCGGCAAGAAAGCAG 525
QY 426 TAAGCTGTGGTGTGTTACTACTAGATTCAACAGTCTTCCAGCTGGTCTTA 485
DB 526 GAAAGTCAATGGAGGTGTAACCAACAGAGTGCAGACCGCTCCAGCGGACCTTA 585
QY 486 CGCTCACTGTTAATAGAAATTTGTTACTCTGATCTGATTTGCCAGCTGATGCTC-AA 544
DB 586 CGCCCAACGTTGAACCCCACTGTTACTCGAGCCGACAGCTGCTGCCGCCGCA 645
QY 545 AGAATGTTGTTCAAGATATTGCTGCTCAATTGTTTCAATATGATATGATGTTATT 604
DB 646 GAGAGGGGTGCAGACATCGTACGAGCTCATCTCAACATGACATTCGATGATCC 705
QY 605 TGGGTGTGTGTAAGATGTAATGTTTCCAGAAAGTACTCCAGATCCAGAAATCCAGATG 664
DB 706 TAGGTGAGGGCCGAAGTACATGTTTCCATGAGGAACCCACACCTTGAATACCCATATG 765
QY 665 ATGCTTCTGTTAATGTTGTTAAGAAAGATTAAGCAAAATTTGTTCAAGATGCAAGCTTA 724
DB 766 AATTAAAGCCAGAGTGGACCAACCTGAGCGGAGAAATCTGTGAGAAATKGTGCGCA 825
QY 725 AGCATCAAGGTGCTCAATATGTTTGA 752
DB 826 CGC-CAGGGTGGCCCGTATGTGTGAA 852

RESULT 12

BX343739

LOCUS BX343739

DEFINITION BX343739 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
clone CS0D1017YB14 5-PRIME, mRNA sequence.

ACCESSION BX343739

VERSION BX343739.2 GI:46270510

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

Li W.B., Gruber C., Jessee J. and Polyes D.
Full-length cDNA libraries and normalization

Unpublished (2001)

On May 2, 2003 this sequence version replaced gi:30336211.

Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France

Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr

1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 1699.f

For more information about this cluster, see <http://www.genoscope.cns.fr/cdna?cs=1A10052B08QP1&c=1699.f>.

Location/Qualifiers

FEATURES

source

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/clone="CS01017B14"
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/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."
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Query Match      20.2%; Score 298.4; DB 5; Length 1125;
Best Local Similarity 63.5%; Pred. No. 3,5e-63;
Matches 517; Conservative 1; Mismatches 292; Indels 4; Gaps 4;

QY 6 CTGATTCCAGTCGAGAAAGAAATCCAGCTTTTGGAAATAGACAGCTGCTCAAGCTT 65
DB 211 CATCATCCCGATTGAGAGAGAAACCGGACTTGTGAACCGGAGGACCCGAGGCGCT 270
QY 66 GGAATGTTCTAGAGATGTCACCAATTCAGTGTCTAGTAAGATGTTTGTGTTT 125
DB 271 GGGTGGCGCCAAAGATGAGCTGACAGACAGCGCCGCAAGACTATCATCTTCT 330
QY 126 GGGTATGATGATGGGTTTCAACTGTACTGCTACTAGATTTTGAAGGTCAAATGA 185
DB 331 GGGCGATGGATGGGGGTCTCTCGGTGACAGCTGCAGATCTTAAAGGCGAAGAA 390
QY 186 TGGTAATGGGTCCAGAACTCATTTGGTATGATGATCAATTCATAGCTTGTTC 245
DB 391 GGAACAATGGGGCTGAGTACCCCTGGGCAAGACCGCTTCCAAATGTGCTGTG 450
QY 246 TAAAGCTTCAATGTTGATAGCAAGTTCAGATTCGTGTGACTGCTACTCTTACT 305
DB 451 CAAGACATCAATGTAAGACAAATATGTCAGACAGTGGACCAAGCCAGCCCTTAC 510
QY 306 GTGTGTGTTAAGGGTAATTACAACTATTTGTTTCTGTCTGTCTAGATATCAATCA 365
DB 511 GTGCGGGGTCAAGGGCAACTTCAGACCAATTTGGCTTGAAGTGCAGCCGCTTTAACCA 570
QY 366 ATGTAATCTACTAGAGTAATGAATTTACTTCTGTTTATTAATAGAGTAAGAGCTG 425
DB 571 GTGCAACAGACACGGGGCAACAGGTCTCTCCGATGAATCGGGCCAAAGAACAG 630
QY 426 TAAAGCTGTGTTGTTTACTACTACTAGAGTTCAACATGCTTCCAGCTGGTCTTA 485
DB 631 GAAGTAGTGGAGGTGTAACCAACAGAGTGCAGACGCTCCGACAGCCGACCTTA 690
QY 486 CGCTACTACTGTTAATGAATTTGTAAGTCTGATGCTGATTTGCCAGCTGATCTC-AAA 544
DB 691 CGGCCACACGGTGAAACCGCACTGTACTCGAGCGCGAGCTGCTCGCCCGCGCA 750
QY 545 AGAATGTTTCTCAAGATTTGCTGCTCAATTTGTTTACATATGATATTTGATTTT 604
DB 751 GAGAGGGGGTCCAGGACATCGCTACAGCTCACTTCCAAATGAGCATTTGAGTATCC 810
QY 605 TGGGTGTGTAGATGATGATGATGTTCCAGAAAGTCTCCAGATCCAGATACCCGATG 664
DB 811 TAGGTAGAGCCCAAGATCATTTT-CGATGTGGAAACCAAGACCTTGATGATCCAGATG 869
QY 665 ATGCTTCTGTTAATGTTTGAAGAGATGAAGCAATTTGTTTCAAGATGGCAGC-T 723
DB 870 ACTACAGCAAGGTGGGACAGGCTGAGCGGAAAGATCTGGTGCAGGAATGCTGGCG 929
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QY 724 AACCATCAAGTGTCTCATATATGTTTGAATAGAACTTGTGTCAGAGCTGATGAT 783
DB 930 AGCCCAAGGGGTCCCGGTAAGTGTGACCCGACTGAGCTATGACAGCTTCCAGAC 989
QY 784 TCTAGTGTACTCATTTGATGGGTTTGTGAAC 817
DB 990 CGGTCTGTGAC-CATCTCATAGGCTCTTTGAGC 1022
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RESULT 13

BY732148

LOCUS

DEFINITION

BY732148

KEYWORDS

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

REFERENCE

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AUTHORS

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TITLE
JOURNAL
MEDLINE
PUBMED
COMMENT

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The Institute of Physical and Chemical Research (RIKEN)
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Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.jp, URL: <http://genome.gsc.riken.jp/>
Adachi, J., Aizawa, K., Akimura, T., Aizawa, K., Hirazawa, T., Hori, F.,
Fukuda, S., Hasehizume, M., Hayashizaki, K., Hirozane, T., Itoh, Y.,
Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kawai, J., Kojima, Y.,
Kondo, S., Kono, H., Koya, S., Miyazaki, A., Murata, M., Nakamura, M.,
Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Saito, R., Sakazume, N.,
Sano, H., Sasaki, D., Sato, K., Shibata, K., Shiraki, T., Tagami, M.,
Takeda, Y., Waki, K., Watahiki, A., Yamazaki, M., and Hayashizaki, Y.
Computational Analysis of Full-length Mouse cDNAs Compared with
Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)

Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
 RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)

Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
 cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken Division of Experimental Animal Research in Riken contributed to prepare mouse cDNAs.
 Please visit our web site (<http://genome.gsc.riken.go.jp>) for further details.

FEATURES

Location/Qualifiers
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 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="B860129L22"
 /cell_type="8 cells"
 /dev_stage="8 cells embryo"
 /clone_lib="RIKEN full-length enriched, 8 cells embryo"

ORIGIN

Query Match 20.4%; Score 297; DB 6; Length 724;
 Best Local Similarity 63.4%; Pred. No. 7e-63;

Matches 453; Conservative 0; Mismatches 262; Indels 0; Gaps 0;

59 AACCTTGGATGTTGCTAAGAACTTGCACCACTTCAAACTGCTGTAAGATGTTATT 118
 2 AGGCGCTGGATGCTGCAGAACCTGAAGCCCATTCAGATCACTAAGAACTCTGTTA 61
 119 TGTGTTGGGTGATGATGGGTGGTTCACATCTGCTGCTAGTAAGATTTGAAGGTC 178
 62 TCTCTATGGAGATGGGATGGGGGTCTTACAGTAACCGTACCCGGATCTTAAAGGGC 121
 179 AATGATGATGATGTTGGGTTCAGAACTTCATTTGGCTATGATCAATTTCCATACGTT 238
 122 AGAGCAAGCCATCTGGGACCTGAGACACAGCTAGTATGATCGCTTCCACACATGG 181
 239 CTGTTGCTAAGACTTACATGTTGATGACAACTTCCAGTTCTGCTGATCTGCTACG 298
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 299 CTGACTTGGTGGTGTAAAGGTAATTACAGAACTATTGGTGTCTGCTGCTAGAT 358
 242 CTTTCTCTGGGGGTCAAAACCAACATGAAAGTCATTGGCTTGATGACGCTGACGCT 301
 359 ACAATCAATGTAATACTACTAGAGATGATGAAAGTACTTCTGTTATTAATGAGCTAAG 418
 302 TCAACAGATGCAACAGACATGGGGTAAAGAGTCGCTCGATGACACCGTAAAG 361
 419 AGCTGTAAAGCTGTTGGTGTGTTACTACTACTAGAGTTCACATGCTTCTCCAGCT 478
 362 AACACAGAAAGTCTGGAGAGTGGTGCACACAGTCGAGCAGATCTTCTCCGCG 421
 479 GTGCTTACGCTCACTGTTAATAGAAATTGATCTGATCTGATGCTGATTTGCCAGCTGAT 538
 422 GCACCTACGCGCACCTGTAAACCGTGGTGGTGTGATCTGATGACAAATGCTGCTCAG 481
 482 CGCTACAGATGGCTGCAAGACATCTTACTAGCTCATCTCCACATGATGATGATG 541
 539 CTCAAAAGATGTTGTCAAGATATGCTGCTCAATTTGTTTCAATATGATATTTGATG 598
 599 TTTATTTGGGTGGTGTGATGATGATGATTTTCCAGAAAGTATCCAGATCCAGATACC 658
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 659 CAGATGATGCTTGTGTTAATGTTGTTAAGAAAGTAAAGCAAAATTTGGTTCAAGATGCG 718

|||||
 602 CAATGACACCAAGACAGGCTGGAACACAGCTGATGACCGCAACTGTTCAAGATGCGC 661
 719 AAGCTAAGCATCAAGAGTGTCTCAATATGTTTGAATAGAACTGCTTTGTTGTAAC 773
 662 TGGCANAACACACAGGAGCCCGTATGTTTGAACCCCTCAGAGCTCATTCANCG 716

RESULT 14

LOCUS CK453205 772 bp mRNA linear EST 12-JAN-2004
 DEFINITION 908900 MARC 4P1G Sus scrofa cDNA 5', mRNA sequence.
 ACCESSION CK453205
 VERSION CK453205.1 GI:40800419

KEYWORDS EST.
 SOURCE Sus scrofa (pig)
 ORGANISM Sus scrofa

REFERENCE 1 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 TITLE Smith,T.P.L., Freking,B.A., Ford,J.J., Vallet,J.L., Wise,T.A., Nomenan,D.J., Wray,J.B. and Keeler,W.
 JOURNAL Porcine EST collection using a normalized library constructed from embryos representing early developmental stages
 COMMENT Unpublished (2003)
 Contact: Smith TPL
 USDA, ARS, US Meat Animal Research Center
 PO Box 166, Clay Center, NE 68933-0166, USA
 Tel: 402 762 4366
 Fax: 402 762 4390
 Email: smith@email.marc.usda.gov

Single pass sequencing. Bases called with phred v0.020425.c and trimmed with the aid of the trim_alc option. Vector identified with cross_match v0.990329.
 Plate: TMW8024 row: H column: 10
 Seq primer: GTAATACGATCACTATATGAGG.
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 /tissue_type="pooled"
 /lab_host="DH10B"
 /clone_lib="MARC 4P1G"
 /note="Vector: pcDNA3.1; Site 1: Scori; Site 2: NoCI; Library made with combined RNA from day-10, day-13, day-15, day-25, and day-30 whole embryos."

FEATURES

Location/Qualifiers
 1..772
 /organism="Sus scrofa"
 /mol_type="mRNA"
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 /note="Vector: pcDNA3.1; Site 1: Scori; Site 2: NoCI; Library made with combined RNA from day-10, day-13, day-15, day-25, and day-30 whole embryos."

ORIGIN

Query Match 19.8%; Score 292; DB 7; Length 772;
 Best Local Similarity 61.4%; Pred. No. 1.2e-61;

Matches 469; Conservative 0; Mismatches 295; Indels 0; Gaps 0;

627 GTTTCAGAAAGTACTCCAGATCCAGATATGCTGTTAATGCTTTAG 686
 1 GTTCTCAGAGAGATCTCCGACCTGAAATACCCAGACATCCAGACAGAAACGGAGTTCG 60
 687 AAAGATTAAGCAAAATTTGTTTCAAGATGCAAGCTAAGCATCAAGGTGCTCAATATGT 746
 61 GAAGACAAAGCGGAACCTGTGACAGAGTGGAGCCAAAGACCGGAGACCCGTAATGT 120
 747 TTGAATAGAACTGCTTTGTTGCAAGCTGATGATTTCTAGTGTACTCAATTTGATGGG 806
 121 GTGAACCGCAGCGGCTCATTCAGGCGTCCAGAACCCAGCCCTAACACACCTCATGGG 180
 807 TTTGTTGAACCAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 866
 181 CCTTTTGAAGCGGAGACATGAAGTATGAAGAAAGAGAGAGAGAGAGAGAGAGAGAG 240
 867 TTTGCTGAATAGATGAACTGCTTTGCTGCAAGTTTGTCTGAATTCAGAGGTTTGA 926
 241 CTTGGTGAAGATGACGAGGTGGCCCTGCGCTGAGACAGAAACCCCGGCTTCTT 300

| | | | |
|----|------|--|------|
| Oy | 927 | CTGTGTTGTGTAAGGTGTGTAAGTAATGATCATATGATCATATGATGTAAGGTAAGCTTATATGGC | 986 |
| Db | 301 | CCTCTTCGTGGAAGGAGGCCGCAATTGACCAAGCAACCTATGGAACATGCTTTATATAGGC | 360 |
| Oy | 987 | TTTGACTGAAGCTATTAATGTTTGTATTAATGCTATTAAGGCTTAATGAATTAAGCTTCTGA | 1046 |
| Db | 361 | GCTGATCAGAGGCGTCATGTTTGAACACGCGCATTCACAAGGCTGGCCAGCTCATTAGCGA | 420 |
| Oy | 1047 | ATTGATATCTTGGATTTTGGTACAGCTGATCATATAGTCAATGTTTTTCTTTGGTGGTGA | 1100 |
| Db | 421 | AGAGGACACACTGACCCTGGTACAGGCGGACCACTCTCATATGCTTTCACCTAATGGTGGCTA | 480 |
| Oy | 1107 | CACTTTGAAGAGTACTTCTATTTTGGTTGGCTCCAGGTGAAGGCTTTGATATGTAATGAC | 1166 |
| Db | 481 | CCCGCTGGGTGAAGCTCCGTTTTGGGCTGGCTATGGCAAGGCTTTGATATGGCAAGC | 540 |
| Oy | 1167 | TTACACTTCTATTTTGTATGTGTAATGTGTCAAGTATATGTTTGGTGTGGTTCTTAGACC | 1222 |
| Db | 541 | CTACACCTTCACCTTTATATGGCAATGGCCCGGGAATACAAGCTCACAGCAAGGGGCAAGGCG | 600 |
| Oy | 1227 | AGATGTATATGTATAGTACTAGTGAAGAACATCTTACAGACAAACAAGCTGCTGTTCATTT | 1286 |
| Db | 601 | TGATTTTATGAACCAAGAGAGGAGGCCGCAATACGTGACGACAGGCGGCGCTGTCCCTT | 660 |
| Oy | 1287 | GGCTATGTAAACTCATGTGTGTGAAGATGTGCTGTTTTTGTAGAGGTCCACAAGCTCA | 1346 |
| Db | 661 | GGGTGCCAGAACCCACGGCGGGCGAAGACGTGGCGGTGTTCGGCGCCGCGCCCTGGGCGGA | 720 |
| Oy | 1347 | TTTGGTTCATGCTGTTCAAAGAAACATTTTCTTCTCATATTA | 1390 |
| Db | 721 | CTGTGTGACCGCGCTGCAAGAACATGCTTCTGTGCGACCGTGA | 764 |

RESULT 15

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|------------|--|--------|------|--------|-----------------|
| LOCUS | CR834465 | 681 bp | mRNA | linear | EST 04-MAR-2004 |
| DEFINITION | 4058791 BARC 8BOV Bos taurus CDNA clone 8BOV_6003 5', mRNA sequence. | | | | |
| ACCESSION | CR834465 | | | | |
| VERSION | CR834465.1 | | | | |
| DATE | 04-MAR-2004 | | | | |

ORGANISM

| | |
|-----------|--|
| REFERENCE | 1 (bases 1 to 681) |
| AUTHORS | Baumann, R.G., Baldwin, R.L., Sonstegard, T.S., Van Tassel, C.P. and |

TITLE

JOURNAL Unpublished (2004)
COMMENT Contact: Richard G. Baumann

ANRI

Tel: 3015048604

Fax: 3015048744

Email: rbaumann@anrl.barc.usda.gov
Single pass sequencing bases only

0.000925 using options -trim all - - -trim faata Vector identified
change pass sequencing. bases called and eliminated with pined

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by cross match using options -minmatch 12 -minscore 18
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Plate: 6_row: 3_column: 03

Seq primer: CCTATTAGTGACACTATAGAAC

High quality sequence stop: 681

| FEATURES | LOCATION/QUALIFIERS |
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/clone="8BOV_6J03"
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/sex="female"
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ORIGIN

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|-----------------------|-----------------|--------------------|-----------|-------------|
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| Best Local Similarity | 71.0%; | Pred. No. 9.6e-61; | | |
| Matches 382; | Conservative 0; | Mismatches 156; | Indels 0; | Gaps 0; |

| | | | |
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| Qy | 929 | TGTTTGTTGAAGGTGTGAATATGATCATGGTCTCATGATGTGAAGGCTTATATGCTT | 988 |
| Dp | 2 | TCCTTTGTGGAGGGAGGCCGCAATTGCACCGGTTCACATGATGACAAAGCTTATATGGCAC | 61 |
| Qy | 989 | TGACTGAAAGCTATTTATGTTTGATATAGCTATATGCTTAAAGGCTTAAATGAATTCCTCTAAT | 1048 |
| Dp | 62 | TGACCCGAGCGCGTCATGTTTGACATATCCATTCGCCAAAGGCTTAAATGAGCTCACTAGCCGAAC | 121 |
| Qy | 1049 | TGATATACCTTGATTTTGTGTAAGTCTGATCATAGTCAATGTTTTTCTTTTGGTGGTACA | 1108 |
| Dp | 122 | TGGACAGCGTATCTCTGTCTACGTCAAGACACACTCTCATGTCTTCTCTTTTGGTGGCTATA | 181 |
| Qy | 1109 | CTTTGAGAGGTACTTCTATTTTTTGGTTTTGGCTCCAGGTAAAGCTTTGGATAGTAATCTT | 1168 |
| Dp | 182 | CACGTGCTGGGAGCCTCCATTTTTTGGTCTGGGCCCCACACAAGGCTTATGACAGCAAGTCTCT | 241 |
| Qy | 1169 | ACACTTCTATTTTGTATGTATATGTCATGTCACAGGTTATGCTTTGGGTGGTCTCTGACACAG | 1228 |
| Dp | 242 | ACACTCTCATCTCTTATGTGCATATGCCCTTGGCTATATGGCTTGGCGGGGGCTCTGAGGCCCG | 301 |
| Qy | 1229 | ATGTTTAAATGGTAGTACTAGTGAAGAACATCTTATCAGACACAAGAGCTGTTCATATGG | 1288 |
| Dp | 302 | ATGTTTATATGACAGACACAAGCGAGGACCCCTGTATCCAGCAGCAGGCGGCGCTGCCCCCTGG | 361 |
| Qy | 1289 | CTAGTGAACATCATNGTGTGTGAAGATATCTGCTGTTTTTGTCTAGAGGTCCCAACTCATTT | 1348 |
| Dp | 362 | CTAGCCGAGACCCAGGGGGGGCGAGGACGTGGGGGTTTCGGCGCGGCCCGCAGGCGCACCC | 421 |
| Qy | 1349 | TGCTTCATGTGTTGTCAAGAAAGAACTTTTGTGTCTCATATTAATGACTTTTGTCTGTGTGTG | 1408 |
| Dp | 422 | TGGTGACAGGCGTGTACAGGAGGAGACCTTCGTGGGCGACATCATATGACTCTTTGGGGGTGCG | 481 |
| Qy | 1409 | TTGAAACCATACACTGATGTTTAAATTTTGGCAGCTCCAGTACTGCTATCTATATTTCTCAGA | 1466 |
| Dp | 482 | TGGAGCCCTTACCCGATCTGCATATCTGCGACGCCCCACACCGCCACCAAGCATCTCCCA | 539 |

Search completed: October 19, 2004, 17:33:09
Job time : 5053.5 secs

Page Blank (uspto)

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 19, 2004, 07:43:22 ; Search time 6521 Seconds

(without alignments)
10703.818 Million cell updates/sec

Title: US-09-911-132A-1

Perfect score: 1476
Sequence: 1 gcatcccatccagctga.....gcatcccgactagagttacc 1476

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 2364849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl: *
1: gb_ba: *
2: gb_hgt: *
3: gb_in: *
4: gb_om: *
5: gb_ov: *
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8: gb_pl: *
9: gb_pr: *
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11: gb_sca: *
12: gb_sy: *
13: gb_un: *
14: gb_vi: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| 1 | 1476 | 100.0 | 1476 | 6 | BD175591 |
| 2 | 1476 | 100.0 | 1476 | 6 | AX356645 Sequence |
| 3 | 1476 | 99.12 | 1464 | 6 | AX840884 Sequence |
| 4 | 1462 | 99.1 | 1798 | 6 | ES9950 Highly acti |
| 5 | 1462 | 99.1 | 1798 | 6 | AR214214 Sequence |
| 6 | 1462 | 99.1 | 1798 | 6 | AX012341 Sequence |
| 7 | 1454.2 | 98.5 | 1650 | 6 | AX741748 Sequence |
| 8 | 1338.2 | 90.7 | 2460 | 4 | AF052226 |
| 9 | 1338.2 | 90.7 | 2460 | 6 | ES9951 |
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| 11 | 1338.2 | 90.7 | 2460 | 6 | AX012343 Sequence |
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| 17 | 1032.6 | 70.0 | 1587 | 6 | E08258 |
| 18 | 1032.6 | 70.0 | 1587 | 6 | E10970 |
| 19 | 1032.6 | 70.0 | 1587 | 9 | HUMALPHB |

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| 21 | 1018.2 | 69.0 | 3076 | 6 | E10977 |
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| 24 | 1008.8 | 68.3 | 2484 | 6 | E10972 |
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ALIGNMENTS

RESULT 1
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LOCUS
BD175591
DEFINITION
Expression of alkaline phosphatase in yeast.
ACCESSION
BD175591
VERSION
BD175591.1 GI:29121289
KEYWORDS
JP 2002253269-A/1.
SOURCE
Bos sp.
ORGANISM
Bos sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.

REFERENCE
1 (bases 1 to 1476)
Wueller, R., Thalhoffer, J. P., Geipel, F., Hoelke, W., Glaeser, S., Eckstein, H., Kirschaum, T. and Ribbel, B. N.
Expression of alkaline phosphatase in yeast
Patent: JP 2002253269-A 1 10-SEP-2002.
JOURNAL
F. HOFMANN LA ROCHE AG
COMMENT
OS Bos sp. (bovine)
PN JP 2002253269-A/1
PD 10-SEP-2002
PF 23-JUL-2001 JP 2001222153
PR 25-JUL-2000 DE 10036491.8
PI RAINER MOELLER, JOHANN PETER THALHOFER, FRANK GEIPEL, WERNER PI HOELKE,
PI STEPHAN GLASER, HELMUT ECKSTEIN, THOMAS KIRSCHBAUM, PI BETTINA BOMMARIUS NEE RIEBEL
PC C12N15/09, C12N1/19, C12N9/16//C12N1/19, C12R1:645), (C12N1/19, PC C12R1:78),
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Expression of alkaline phosphatase in yeast
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FT source
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ORIGIN

Query Match 100.0%, Score 1476, DB 6, Length 1476.

Best Local Similarity 100.0%; Pred. No. 9,1e-270;
Matches 1476; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2

AX356645 LOCUS AX356645 1476 bp DNA linear PAT 13-FEB-2002
DEFINITION Sequence 1 from Patent EP1176205.
ACCESSION AX356645
VERSION AX356645.1 GI:18673986

KEYWORDS
SOURCE
ORGANISM
Bos taurus (cow)
Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.

REFERENCE
1 Mueller, R., Thalhofer, J.P., Geipel, F., Hoelke, W., Glaser, S.,
Eckstein, H., Kirchbaum, T. and Bommaritus, B.
Expression of alkaline phosphatase in yeast
Patent: EP 1176205-A 1 30-JAN-2002;
Roche Diagnostics GmbH (DE) ; F. HOFMANN-LA ROCHE AG (CH)
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Location/Qualifiers
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Matches 1476; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 LOCUS Sequence 1 from Patent EP1348760.
 DEFINITION AX840884
 ACCESSION AX840884
 VERSION AX840884.1 GI:39979031
 KEYWORDS
 SOURCE Bos taurus (cow)
 ORGANISM Bos taurus
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 Bovinae; Bos.
 REFERENCE
 1 Mueller, R., Thalhofer, J. P., Geipel, F., Hoelke, W., and Kirschbaum, T.
 AUTHORS Production of inactive mutants or mutants with a low activity of an
 TITLE alkaline phosphatase and their expression in yeast
 JOURNAL Patent: EP 1348760-A 1 01-OCT-2003;
 Roche Diagnostics GmbH (DE) ; F.HOFFMANN-LA ROCHE AG (CH)
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RESULT 4
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LOCUS Highly active alkaline phosphatase.
DEFINITION E59950
ACCESSION E59950
VERSION E59950.1 GI:13017720
KEYWORDS JP 1999332586-A/1.
SOURCE JP 1999332586-A 1 07-DEC-1999;
ORGANISM Bos taurus (cow)
Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
REFERENCE 1 (bases 1 to 1798)
Werner,H., Reina,M., Herumuto,B. and Jose,L.M.
TITLE Highly active alkaline phosphatase
JOURNAL Patent: JP 1999332586-A 1 07-DEC-1999;
ROCHE DIAGNOSTICS GMBH
COMMENT OS Bovidae
PN JP 1999332586-A/1
PD 07-DEC-1999
PF 06-MAY-1999 JP 1999126494
PR 05-MAY-1998 DE 19819962:7
PT WERNER HOERKU,REINA MÜLLER,HERUMUTTO BURUTOSHA, PI JOSE
LOUIS MILAN
PC C12N15/09,C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12N9/16,PC
C12N15/00,C12N5/00
CC

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FT source location/Qualifiers
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Qy 246 CAAGCATACACGTTGACAGACAGTGTCCAGACAGCGGACGCACTGCTCACTGCTTACT 305
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LOCUS AR214214 1798 bp DNA linear PAT 25-SEP-2002
DEFINITION Sequence 1 from patent US 6406899.
ACCESSION AR214214
VERSION AR214214.1 GI:23311768
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
1 (bases 1 to 1798)
AUTHORS Hoelke, W., Muller, R., Burtcher, H. and Millan, J.L.
TITLE Highly active alkaline phosphatase
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Query Match 99.1%; Score 1462; DB 6; Length 1798;
Best Local Similarity 100.0%; Pred. No. 4e-267;
Matches 1462; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 426 GAAAGCCGTGGGAGTGTGACACACACAGGGTGCAGCATGCTCCCGAGCCGGGGCTTA 485
DB 527 GAAAGCCGTGGGAGTGTGACACACACAGGGTGCAGCATGCTCCCGAGCCGGGGCTTA 586
QY 486 CCGGCACACAGTGAACCGAAACTGTGTACTCAGACGCCGACTCTGCTGTATCAGAGAA 545
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| | | | |
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| QY | 606 | GGGTGGAGGCGGAATGTATCATGTTTCTGTAGGGGAGCCCGAGACCTGAATACCATGATGA | 665 |
| DB | 707 | GGGTGGAGGCGGAATGTATCATGTTTCTGTAGGGGAGCCCGAGACCTGAATACCATGATGA | 766 |
| QY | 666 | TCCCAATGTGAATGAGTCCGGAAGAGCAAGAGAACTGTGACAGAAATGGCAGGCCAA | 725 |
| DB | 767 | TCCCAATGTGAATGAGTCCGGAAGAGCAAGAGAACTGTGACAGAAATGGCAGGCCAA | 826 |
| QY | 726 | GCAACCAAGGAGCCCAATATGTGTGAAACCGCACTGGGCTCTTCAAGGGCCGAGATGATC | 785 |
| DB | 827 | GCAACCAAGGAGCCCAATATGTGTGAAACCGCACTGGGCTCTTCAAGGGCCGAGATGATC | 886 |
| QY | 786 | CAGTGAACACACCTCATGAGGCTCTTGTAGCCGGGAGCATGATGATATATGTTTACGA | 845 |
| DB | 887 | CAGTGAACACACCTCATGAGGCTCTTGTAGCCGGGAGCATGATGATATATGTTTACGA | 946 |
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| QY | 906 | CAGGAACCCCGGGGCTTCTACCTCTTGTGAGAGGAGCCGCACTTGAACAGGTTACCA | 965 |
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| QY | 966 | TGACGCAAAAGCTTATATGAGCACTGAGGCGATCATGTTTGAACATGSCATGSCCAA | 1025 |
| DB | 1067 | TGACGCAAAAGCTTATATGAGCACTGAGGCGATCATGTTTGAACATGSCATGSCCAA | 1126 |
| QY | 1026 | GAGTAAAGAGCTCATAGGAACTGAGCAAGCTGATCTTGTCTACTGACAGCACTCCCA | 1085 |
| DB | 1127 | GAGTAAAGAGCTCATAGGAACTGAGCAAGCTGATCTTGTCTACTGACAGCACTCCCA | 1186 |
| QY | 1086 | TGTCTTCTCTTTTGTGTGCTTACACATGTGTGTGAGAACTTCAATTTTGTGTGCTGCTG | 1145 |
| DB | 1187 | TGTCTTCTCTTTTGTGTGCTTACACATGTGTGTGAGAACTTCAATTTTGTGTGCTGCTG | 1246 |
| QY | 1146 | CAAGGCTTGAACAGCAAGTCTTACACTCTCTTATGGAATGAGCCAGGCTATGC | 1205 |
| DB | 1247 | CAAGGCTTGAACAGCAAGTCTTACACTCTCTTATGGAATGAGCCAGGCTATGC | 1306 |
| QY | 1206 | GCTTGGCGGGGCTCGAGGCGCCGATGTAAATGAGCAGACAAAGCAGAAACCTCATACCG | 1265 |
| DB | 1307 | GCTTGGCGGGGCTCGAGGCGCCGATGTAAATGAGCAGACAAAGCAGAAACCTCATACCG | 1366 |
| QY | 1266 | GGAAGAGGCGGCGCTGCGCTGCTGAGAGACCCAGCGGGGAGAGAGTGGCGGTGT | 1325 |
| DB | 1367 | GGAAGAGGCGGCGCTGCGCTGCTGAGAGACCCAGCGGGGAGAGAGTGGCGGTGT | 1426 |
| QY | 1326 | CGCGCAGAGCCCGCAGAGGCACTGTGTGACGCGCTGAGAGAGAACCTTGTGTGCGCA | 1385 |
| DB | 1427 | CGCGCAGAGCCCGCAGAGGCACTGTGTGACGCGCTGAGAGAGAACCTTGTGTGCGCA | 1486 |
| QY | 1386 | CATCATGAGCTTTTGGCGGCTGCGTGAAGCCCTTACACCGACTGCAATCTGCGAGCCCGC | 1445 |
| DB | 1487 | CATCATGAGCTTTTGGCGGCTGCGTGAAGCCCTTACACCGACTGCAATCTGCGAGCCCGC | 1546 |
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| DB | 1547 | CACCGCACCAGCATCCCGAC 1568 | |

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LOCUS AX012341
DEFINITION Sequence 1 from Patent EP0955369.
ACCESSION AX012341
VERSION AX012341.1 GI:9998390
KEYWORDS
SOURCE Bos taurus (cow)
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.

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| DB | 167 | TGATGTAGCCAAAGATTGACAGCCGATCCAGACAGCTGCGCAAGATGATCTTCTT | 226 |
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| DB | 767 | TCCCAATGTGAATGAGTCCGGAAGAGCAAGAGAACTGTGACAGAAATGGCAGGCCAA | 826 |
| QY | 726 | GCAACCAAGGAGCCCAATATGTGTGAAACCGCACTGGGCTCTTCAAGGGCCGAGATGATC | 785 |
| DB | 827 | GCAACCAAGGAGCCCAATATGTGTGAAACCGCACTGGGCTCTTCAAGGGCCGAGATGATC | 886 |
| QY | 786 | CAGTGAACACACCTCATGAGGCTCTTGTAGCCGGGAGCATGATGATATATGTTTACGA | 845 |
| DB | 887 | CAGTGAACACACCTCATGAGGCTCTTGTAGCCGGGAGCATGATGATATATGTTTACGA | 946 |
| QY | 846 | AGACCAACCAAGAGCCCGACCTGTGAGAGATGACGAGAGCGGCCCTTCAAGTGTGAG | 905 |

Db 947 AGACCAACCAAGAGACCCGACCTCGGAGGATGAGGAGCGGCGCTCGAATGGCTGAG 1006
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 LOCUS AX741748
 DEFINITION Sequence 26 from Patent WO03002736.
 ACCESSION AX741748
 VERSION AX741748.1 GI:30524393
 KEYWORDS
 SOURCE
 ORGANISM
 Bos taurus (cow)
 Bos taurus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 Bovinae; Bos.
 REFERENCE
 1 Shao, Z., Kratzsch, P., Schmuck, R., von der Eltz, H. and Kenklee, J.
 A walk-through technique for in vitro recombination of
 polynucleotide sequences
 Patent: WO 03002736-A 26 09-JAN-2003;
 Roche Diagnostis GmbH (DE) ; F. HOFMANN-LA ROCHE AG (CH)
 FEATURES
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AF052226
LOCUS AF052226 2460 bp mRNA linear MAM 03-SEP-1998
DEFINITION Bos taurus intestinal alkaline phosphatase III mRNA, complete cds.
ACCESSION AF052226
VERSION AF052226.1 GI:3510650
KEYWORDS
SOURCE Bos taurus (cow)
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
1 (bases 1 to 2460)
Mames,T., Hoylaerts,M.F., Muller,R., Lottspeich,F., Hoelke,W. and
William,J.L.
Bovine alkaline phosphatases
Unpublished
2 (bases 1 to 2460)
Mames,T., Hoylaerts,M.F., Muller,R., Lottspeich,F., Hoelke,W. and
William,J.L.
Direct Submission
Submitted (05-MAR-1998) Medical Genetics, Umea University, S-901 85
Umea, Sweden
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ORIGIN
Query Match 90.7%; Score 1338.2; DB 4; Length 2460;
Best Local Similarity 94.4%; Pred. No. 1.1e-243;
Matches 1388; Conservative 0; Mismatches 83; Indels 0; Gaps 0;
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DEFINITION
ACCESSION E59951
VERSION E59951.1 GI:13017721
KEYWORDS JP 199332586-A/2.
SOURCE Bos taurus (cow)
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
1 (bases 1 to 2460)
REFERENCE
AUTHORS Werner,H., Reina,M., Herumuto,B. and Jose,L.M.
TITLE Highly active alkaline phosphatase
JOURNAL Patent: JP 199332586-A 2 07-DEC-1999;
ROCHE DIAGNOSTICS GMBH
COMMENT
OS Bovidae
PN JP 199332586-A/2
PD 07-DEC-1999
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PR 05-MAY-1998 DE 19819962.7
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FEATURES
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Query Match 90.7%; Score 1338.2; DB 6; Length 2460;
Best Local Similarity 94.4%; Pred. No. 1.1e-243;

Matches 1388; Conservative 0; Mismatches 83; Indels 0; Gaps 0;
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DEFINITION Sequence 3 from patent US 6406899.
ACCESSION AR214215
VERSION AR214215.1 GI:23311769
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 2460)
AUTHORS Hoelke, W., Muller, R., Burtcher, H. and Millan, J. L.
TITLE Highly active alkaline phosphatase
JOURNAL Patent: US 6406899-A 3 18-JUN-2002;
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Query Match 90.7%; Score 1338.2; DB 6; Length 2460;
Best Local Similarity 94.4%; Pred. No. 1.1e-243;
Matches 1388; Conservative 0; Mismatches 83; Indels 0; Gaps 0;

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LOCUS AX012343 2460 bp DNA linear PAT 06-SEP-2000
DEFINITION Sequence 3 from Patent EP0955369.
ACCESSION AX012343
VERSION AX012343.1 GI:9998391
KEYWORDS
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ORGANISM Bos taurus (cow)
Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Bovinae; Bos.

REFERENCE
1 Burtscher, H.D., Mueller, R.D., Hoelke, W.D. and Millan, J.L.
AUTHORS
TITLE High active alkaline phosphatase
JOURNAL Patent: EP 0955369-A 3 10-NOV-1999;
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Best Local Similarity 94.4%; Pred. No. 1.1e-243;
Matches 1388; Conservative 0; Mismatches 83; Indels 0; Gaps 0;

QY 6 CCTCATCCCGACGAGGAGGAAAACCCGCTCTGGAAACCGGACGAGCCGAGCCCT 65
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DB 1442 CCGGACAGGCGCCGACAGCGCACCTGTTGACCGGCTGACAGAGAGACCTTCTGTGCGCA 1501
QY 1386 CATCATGCGCTTTGCGGGCTGCGTGAGCCCTTACACCGACTGCAATCTGCGAGCCCCG 1445
DB 1502 CGTCATGCGCTTTGCGGGCTGCGTGAGCCCTTACACCGACTGCAATCTGCGAGCCCCC 1561
QY 1446 CACCGCCACCGACGATCCCGACTAGGGTACC 1476
DB 1562 TGGCTCTCCGACGCGCGCCTGCGGGCC 1592

RESULT 12
AF052227 2536 bp mRNA linear MAM 03-SEP-1998
LOCUS AF052227
DEFINITION Bos taurus intestinal alkaline phosphatase IV mRNA, complete cds.
ACCESSION AF052227
VERSION AF052227.1 GI:3510652
KEYWORDS
SOURCE Bos taurus (cow)

ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
REFERENCE 1 (bases 1 to 2536)
AUTHORS Manes,T., Hoylaerts,M.F., Muller,R., Lottspeich,F., Hoelke,W. and
Millan,J.L.
TITLE Bovine alkaline phosphatases
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 2536)
AUTHORS Manes,T., Hoylaerts,M.F., Muller,R., Lottspeich,F., Hoelke,W. and
Millan,J.L.
TITLE Direct Submision
JOURNAL Submitted (05-MAR-1998) Medical Genetics, Umea University, S-901 85
Umea, Sweden
FEATURES
source location/Qualifiers
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Query Match 89.9%; Score 1327; DB 4; Length 2536;
Best Local Similarity 93.9%; Pred. No. 1.5e-241;
Matches 181; Conservative 0; Mismatches 90; Indels 0; Gaps 0;

QY 6 CCTCATCCAGCTGAGAGAAACCCGCTTCTGAAACCGCCAGGACCGCAGGCTT 65
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QY 246 CAAGAATATCAACGTTGACAGACAGGTCGACAGCGAGGCACTGCACTGCTTACCT 305
DB 361 CAAGAATATCAACGTTGACAGACAGGTCGACAGCGAGGCACTGCACTGCTTACCT 420
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QY 366 GTGCAACAAGACCTGGGATGAGTCACTGTGTGATCAACCGGCGCAAGAAAGCAGG 425
DB 481 GTGCAACAAGACCTGGGATGAGTCACTGTGTGATCAACCGGCGCAAGAAAGCAGG 540
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DB 601 TGCACACACGGTGAACCGAAACTGGTACTGACAGCGCGACCTGCTGCGATGACAGAC 660
QY 546 GAATGGCTGCCAGACATCGCGACAGCTGGTCTTACAACTGATATGATGACGATCT 605
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DB 721 GGGTGAAGCGGATGTATGATGTTCTTCTGAGGGGACCCCGGATCTTGAATACCTCATACGA 780
QY 666 TGGCATGTGAATGAGTCCGGAAAGAGAGAACTGGTGACAGGATGGCAGGCCAA 725
DB 781 TGTCAATCAAGATGAGTCCGGAAAGAGAGAACTGGTGACAGGATGGCAGGCCAA 840
QY 726 GCACCGAGGAGCCAGTATGTGTGAAACCGGACCTGCTCTTCAAGCGCGCGATGATCTC 785
DB 841 GCACCGAGGAGCCAGTATGTGTGAAACCGGACCTGCTCTTCAAGCGCGCGATGATC 900
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QY 906 CAGGAACCCCGGGGCTTCTACCTCTTGTGTGAGGAGGCGGACATTGACACAGCTACCA 965
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QY 1446 CACGCGACAGCAATCCCGGACTAGGGTACC 1476
DB 1561 TGGCTCTCGAGCGCGGACCTGCGGCGC 1591

RESULT 13
E59952

LOCUS E59952 2542 bp DNA linear PAT 13-AUG-2002
DEFINITION Highly active alkaline phosphatase.
ACCESSION E59952
VERSION E59952.1 GI:13017722
KEYWORDS JP 199332586-A/3.
SOURCE
ORGANISM Bos taurus (cow)
Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
REFERENCE 1 (bases 1 to 2542)
AUTHORS Werner,H., Reina,M., Herumutto,B. and Jose,L.M.
TITLE Highly active alkaline phosphatase
JOURNAL Patent: JP 199332586-A 3 07-DEC-1999;
ROCHE DIAGNOSTICS GMBH
COMMENT OS Bovidae
PN JP 199332586-A/3
PD 07-DEC-1999
PE 06-MAY-1999 JP 1999126494
PR 05-MAY-1998 DE 19819962:7
PI WERNER HOERUKU, REINA MÜLLER, HERUMUTTO BURUTOSHA, PI JOSE
LOUIS MILAN
PC C12N15/09, C12N1/15, C12N1/19, C12N1/21, C12N5/10, C12N9/16, PC
C12N15/00, C12N5/00
FH Key Location/Qualifiers
FT source 1. 2542
FT 1. 2542 /organism='Bovidae'.
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source Location/Qualifiers
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ORIGIN
Query Match 89.3%; Score 1327; DB 6; Length 2542;
Best Local Similarity 93.3%; Pred. No. 1.5e-241;
Matches 1381; Conservative 0; Mismatches 90; Indels 0; Gaps 0;
QY 6 CCTCATCCCGAGTGGAGAGAGAAACCCCGCTTCTGGAAACCGGACAGCCAGGCGCT 65
DB 121 CTTTCATCCCGAGTGGAGAGAGAAACCCCGCTTCTGGAAACCGGACAGCCAGGCGCT 180
QY 66 TGATGTAGCCAAAGTTGAGCGCGATCCAGACAGCTGCGCAAGATGTCATCTCTTCT 125
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DB 661 GTATGGTGCAGAGACATGCGCGACAGCTGTGATCAACATGATGATGATGATGATCT 720
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DB 721 GGGTGGAGGCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 780
QY 666 TGCAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 725
DB 781 TGTCAATCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 840
QY 726 GCACAGAGGAGGCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 785
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QY 846 AGACCAACCAAGAGACCCGACCTGGCGGATGATGATGATGATGATGATGATGATGATG 905
DB 961 AGACCAACCAAGAGACCCGACCTGGCGGATGATGATGATGATGATGATGATGATGATG 1020
QY 906 CAGGAACCCCGGAGGCTTCACTCTGATGATGATGATGATGATGATGATGATGATGATG 965
DB 1021 CAGGAACCCCGGAGGCTTCACTCTGATGATGATGATGATGATGATGATGATGATGATG 1080
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QY 1386 CATCATGAGCTTAAAGAGAGCTTAAAGAGAGCTTAAAGAGAGCTTAAAGAGAGCTT 1445
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QY 1446 CACCGCAGCAGATCCCGAGCTAGGATAC 1476
DB 1561 TGGCTCTCGAGCGCGCAGCAGCTGCGGAGC 1591
RESULT 14
AR214216 2542 bp DNA linear PAT 25-SEP-2002
LOCUS AR214216
DEFINITION Sequence 5 from patent US 6406899.
ACCESSION AR214216
VERSION AR214216.1 GI:23111770

KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2542)
AUTHORS Hoejke, W., Muller, R., Burtcher, H. and Millan, J.L.
TITLE Highly active alkaline phosphatase
JOURNAL Patent: US 6406899-A 5 18-JUN-2002;
FEATURES Location/Qualifiers
source 1..2542
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ORIGIN
Query Match 89.9%; Score 1327; DB 6; Length 2542;
Best Local Similarity 93.9%; Pred. No. 1.5e-241;
Matches 1381; Conservative 0; Mismatches 90; Indels 0; Gaps 0;

QY 6 CCTCATCCAGCTGAGAGAGAAACCCGCTTCTGTGAACCGGCAGGCAAGCCGAGCCCT 65
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QY 666 TGGCAGTGTGAATGAGATCGGAGAGCAAGCAACCTGGTGAAGAAATGGCAGGCGAA 725
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DB 841 GCACCAAGGAGCCAGATATGTGTGAAACCGCAAGAGTCTCTTCAGGCGGCGATGATC 900
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QY 1446 CACCGCACACAGATCCCGAGTACG 1476
DB 1561 TGGCTCTTCGACGCGCGCACTTGGCGCC 1591

RESULT 15
AX012345 2542 bp DNA linear PAT 06-SEP-2000
LOCUS AX012345
DEFINITION Sequence 5 from Patent EP0955369.
ACCESSION AX012345
VERSION AX012345.1 GI:9998392
KEYWORDS
SOURCE Bos taurus (cow)
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.

REFERENCE 1
Burtcher, H.D., Mueller, R.D., Hoejke, W.D. and Millan, J.L.
AUTHORS
TITLE High active alkaline phosphatase
JOURNAL Patent: EP 0955369-A 5 10-NOV-1999;
ROCHE DIAGNOSTICS GMBH (DE)
FEATURES Location/Qualifiers
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ORIGIN
Query Match 89.9%; Score 1327; DB 6; Length 2542;
Best Local Similarity 93.9%; Pred. No. 1.5e-241;
Matches 1381; Conservative 0; Mismatches 90; Indels 0; Gaps 0;

QY 6 CCTCATCCAGCTGAGAGAGAAAAACCCGCTTCTGGAACCGGCAAGCCAGCCGCT 65
 Db 121 CTTGATCCAGCTGAGAGAGAGAAAAACCCGCTTCTGGAACCGGCAAGCCAGCCGCT 180
 QY 66 TGAATGAGCCAGAGAGTTGGAGCCGATCCAGACAGCTGCGAGAGATGTCACTCTTCT 125
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 QY 126 GGGGGATGGGATGGGGGTGCTTACGGTGACAGCCACTCGGATCTTAAAGGGGAGATGAA 185
 Db 241 GGGGGATGGGATGGGGGTGCTTACGGTGACAGCCACTCGGATCTTAAAGGGGAGATGAA 300
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QY 1086 TGTCTTCTCTTTTGTGGTACACACTGGGTGGGACCTCCATTTTGGTCTGGCCCCG 1145
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 QY 1146 CAAAGCCTTAAGACAGAAAGTCTTACACTTCCATCTCTATGCAATGGCCAGGCTATGC 1205
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 QY 1326 CCGGAGGCGCGGAGGCGACCTGTGCAAGGCTGTCAGAGAGAGAGAGAGAGAGAGAGAG 1385
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 Db 1501 CATCATGGCTTTTGGCGGCTGCTGAGAGCCCTTACACCGACTGCAATCTGCAAGCCCCG 1560
 QY 1446 CACCGCACAGGATCCCGACTAGGATAC 1476
 Db 1561 TGGCTCTCCAGCGCGCGCACCTGGCGGCG 1591

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